

Structural  
Bioinformatics

# CHAPERONES

## SEQUENCE ANALYSIS

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MSA PARALOGS/ORTHOLOGS

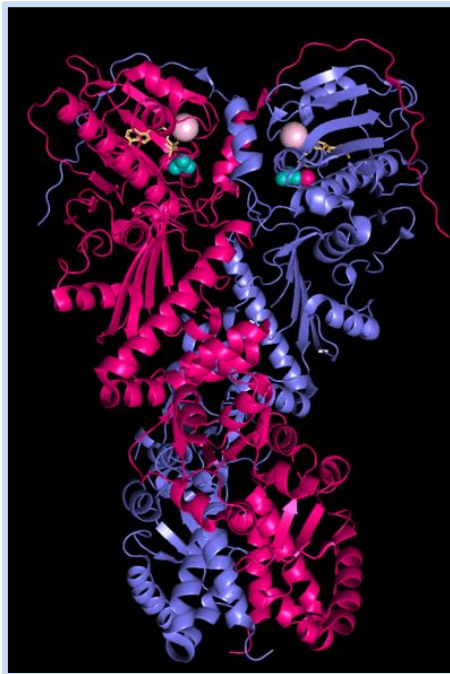
05

CONSERVED REGIONS

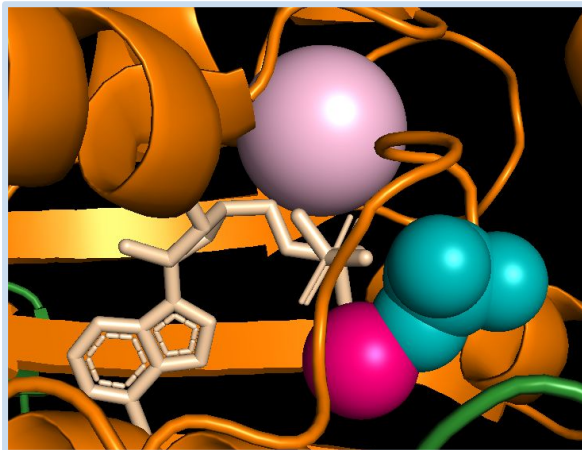
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MUTATION

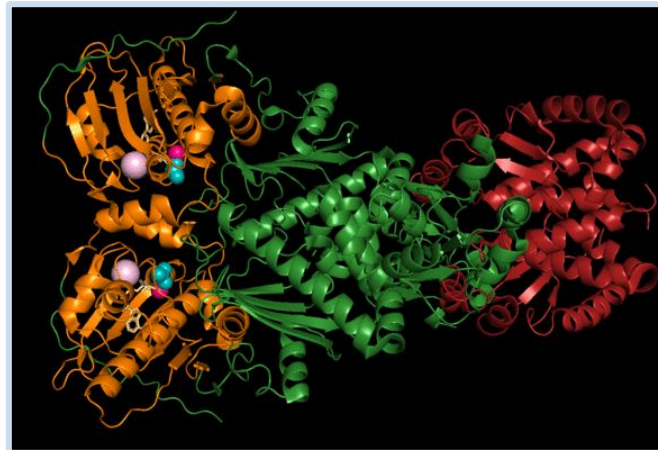
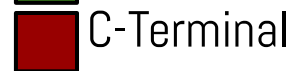
# 6XG6



Chains: **Alpha** / **Beta**



Ligands:



# HMM for 6XG6 in PFAM

These are the available models.

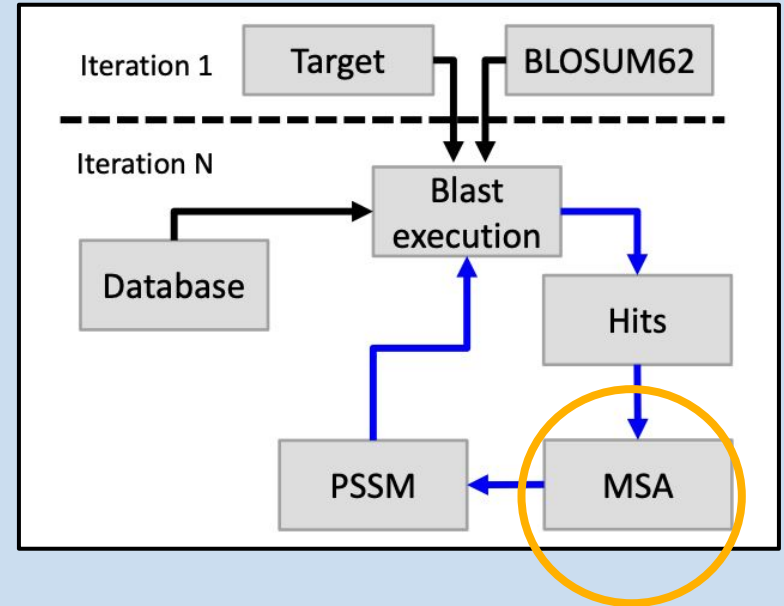
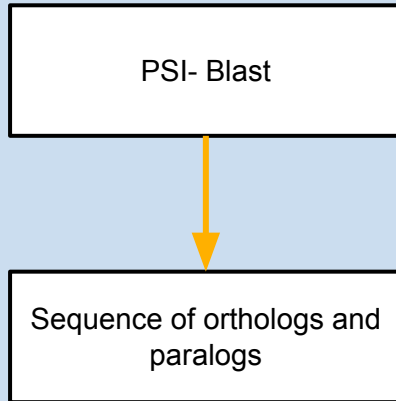
ACCESSION	NAME	SOURCE DATABASE	MATCHES		
PF00183	Hsp90 protein	Pfam	200	400	600
PF02986	Fibronectin binding repeat	Pfam	200	400	600
PF13085	2Fe-2S iron-sulfur cluster binding domain	Pfam	200	400	600
PF13589	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase	Pfam	200	400	600
PF17802	Prealbumin-like fold domain	Pfam	200	400	600

USE **HMMSCAN** ON  
FASTA SEQUENCE

USE **HMMFETCH** TO  
EXTRACT PROFILE

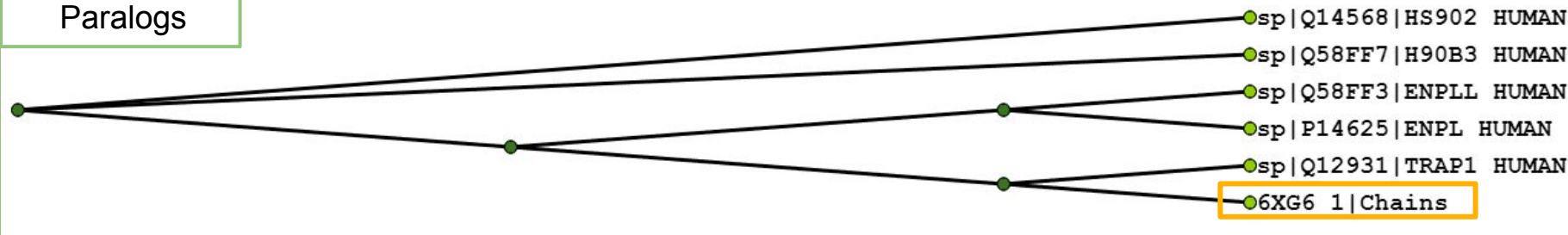
HSP90:  
Most representative  
(best e-value)

# PSI-BLAST & UNIPROT

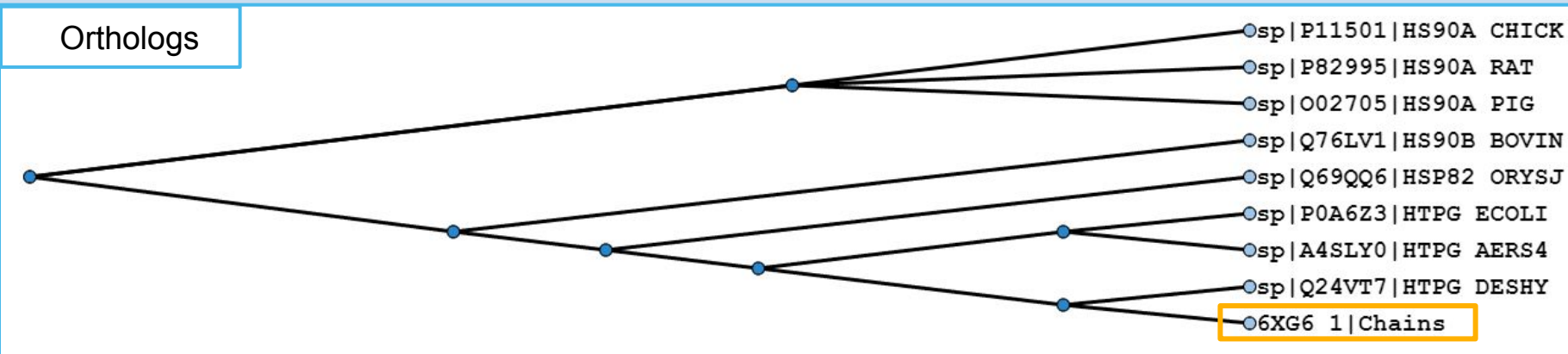


# EVOLUTIONARY HISTORY HSP90

## Paralogs



## Orthologs



# MULTIPLE SEQUENCE ALIGNMENT

## Paralogs

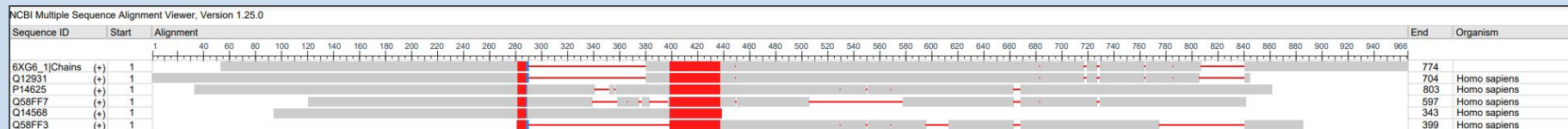
<b>sp Q12931 TRAP1_HUMAN Heat shock protein 75 kDa, mitochondrial ...</b>	<b>1328</b>	<b>0.0</b>
sp P14625 ENPL_HUMAN Endoplasmic reticulum protein OS=Homo sapiens GN=HSP90B1 PE=...	330	6e-100
sp Q58FF7 H90B3_HUMAN Putative heat shock protein HSP 90-beta-3...	183	3e-48
sp Q14568 HS902_HUMAN Putative heat shock protein HSP 90-alpha ...	176	7e-48
sp Q58FF3 ENPLL_HUMAN Putative endoplasmic reticulum protein OS=Homo...	104	9e-23

## Orthologs

<b>sp Q12931 TRAP1_HUMAN Heat shock protein 75 kDa, mitochondrial ...</b>	<b>1328</b>	<b>0.0</b>
sp Q24VT7 HTPG_DESHY Chaperone protein htpG OS=Desulfitobacteri...	511	6e-172
sp A4SLY0 HTPG_AERS4 Chaperone protein htpG OS=Aeromonas salmon...	408	8e-132
sp P0A6Z3 HTPG_ECOLI Chaperone protein htpG OS=Escherichia coli...	385	6e-123
sp Q69QQ6 HSP82_ORYSJ Heat shock protein 81-2 OS=Oryza sativa s...	345	6e-107
sp O02705 HS90A_PIG Heat shock protein HSP 90-alpha OS=Sus scro...	189	1e-49
sp P82995 HS90A_RAT Heat shock protein HSP 90-alpha OS=Rattus n...	189	3e-49
sp P11501 HS90A_CHICK Heat shock protein HSP 90-alpha OS=Gallus...	187	8e-49
sp Q76LV1 HS90B_BOVIN Heat shock protein HSP 90-beta OS=Bos tau...	183	2e-47

# MULTIPLE SEQUENCE ALIGNMENT

## Paralogs



## Orthologs





# MUTATION

**R>H**

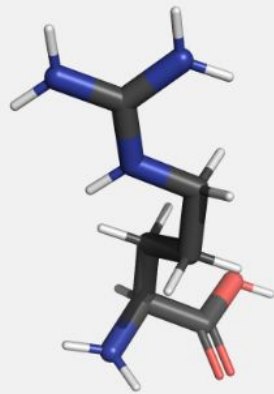
cGc/cAc (-)

Missense

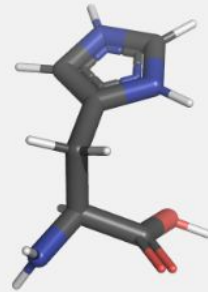
Conservation score: 0.808

Position: 469

$\Delta\Delta G_{\text{pred}}$  : 3.91427

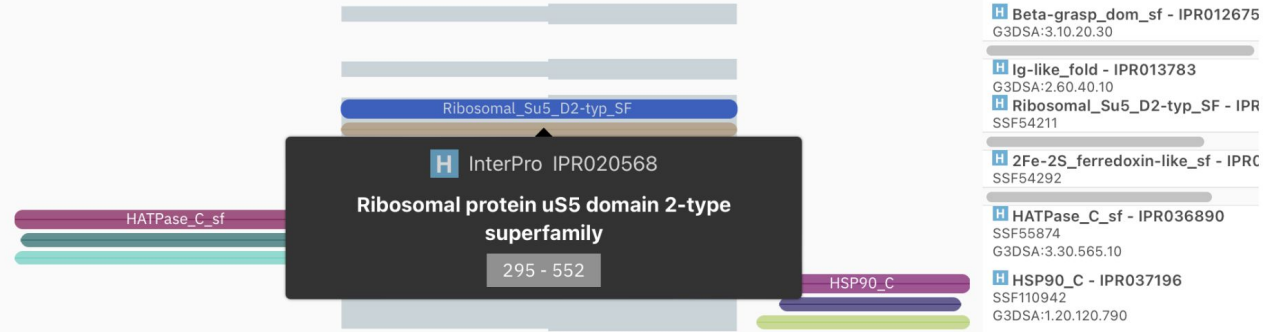


Arginine



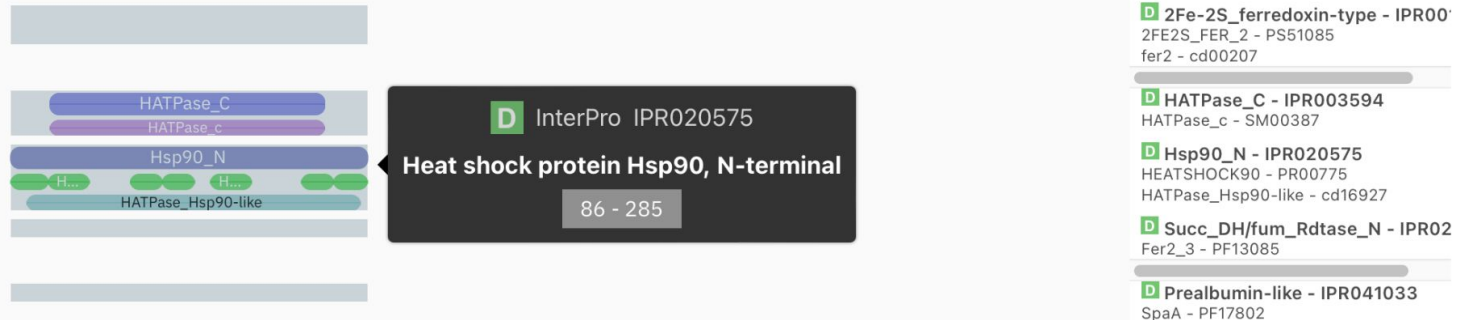
Histidine

▼ Homologous Superfamily



The mutation (469 aa) is not in any of the main domains, yet it is in a Ribosomal Protein domain

▼ Domain



**THE END!**