

Structural and Functional Analysis of MG53

Group 1

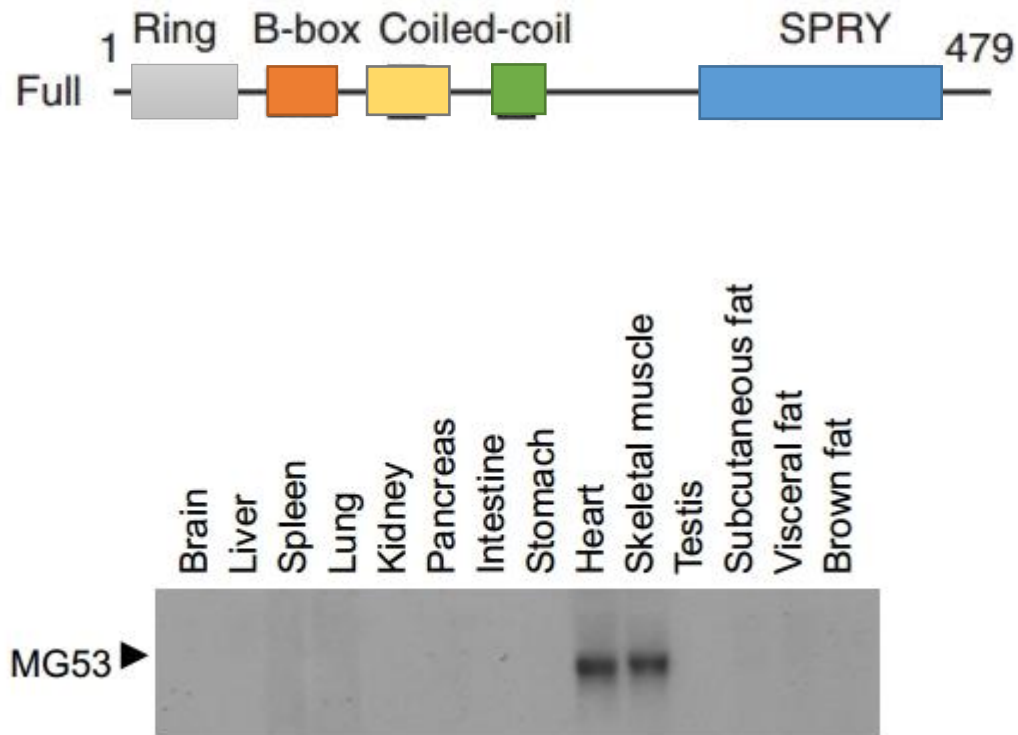
YAO Yuan, CUI Mingyao, ZHANG Huiyuan, CHEN Gengjia

Outline

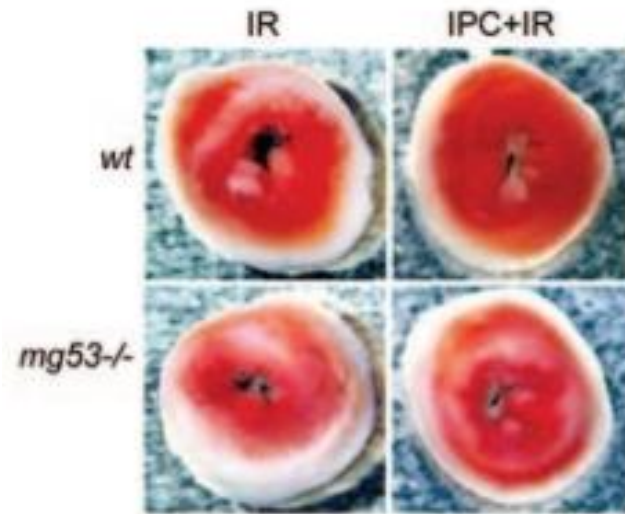
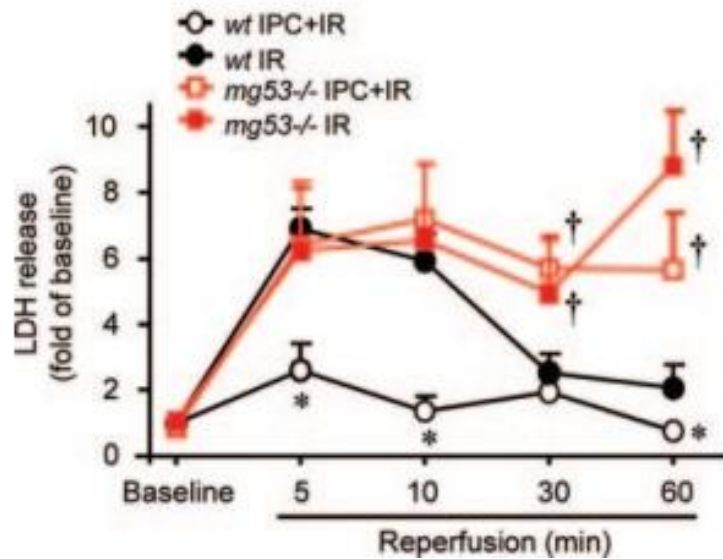
- Background
- Sequence Analysis
- Protein Structure Analysis
- Function Analysis

Background

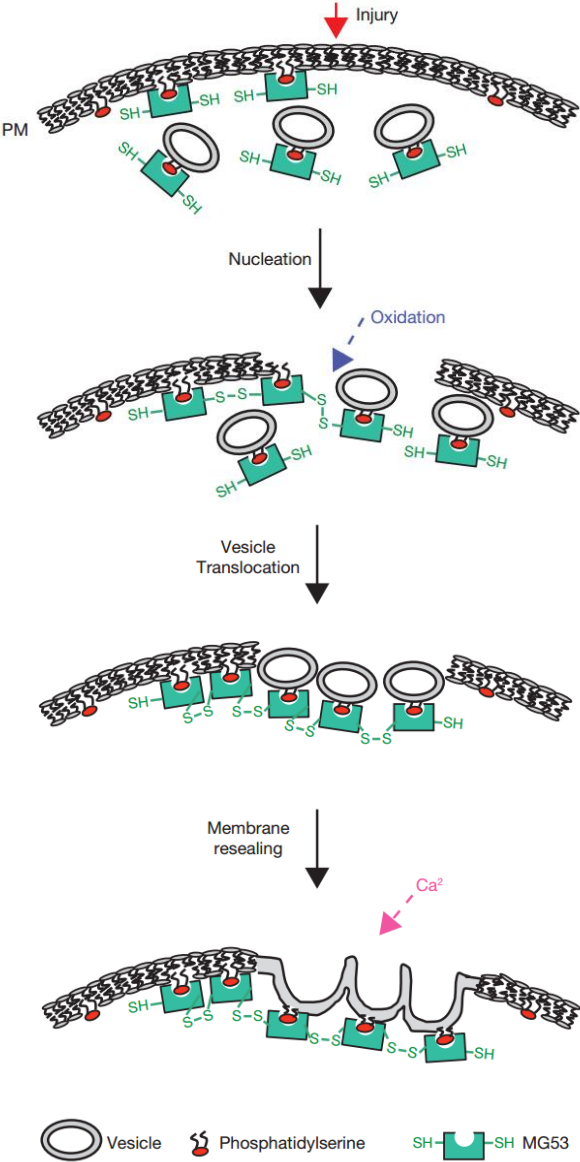
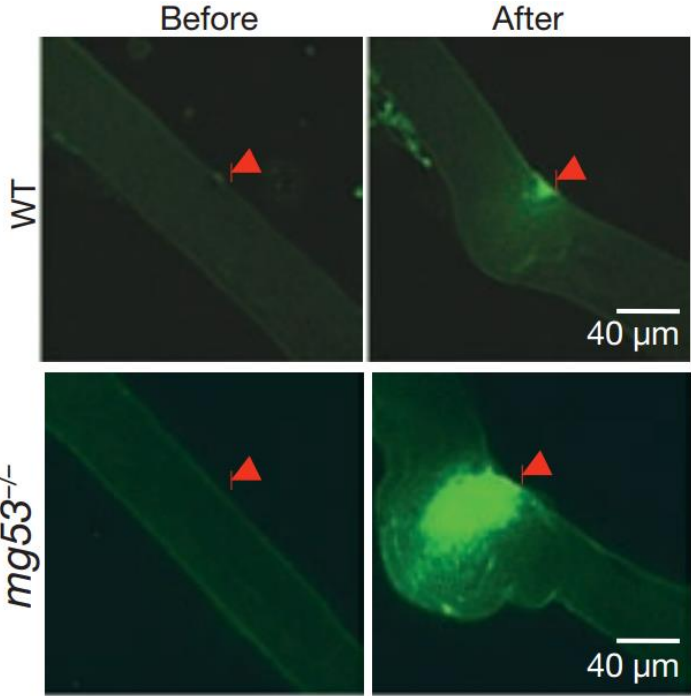
MG53 (TRIM72)



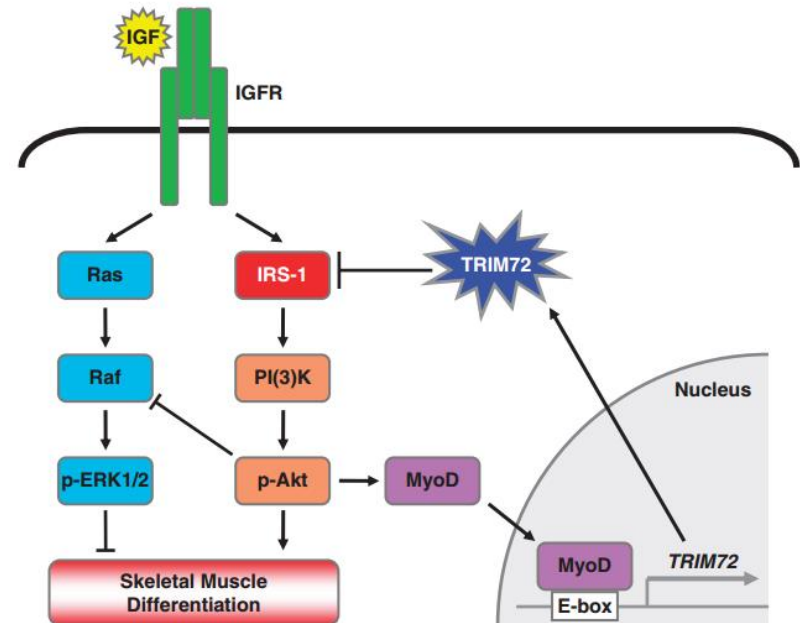
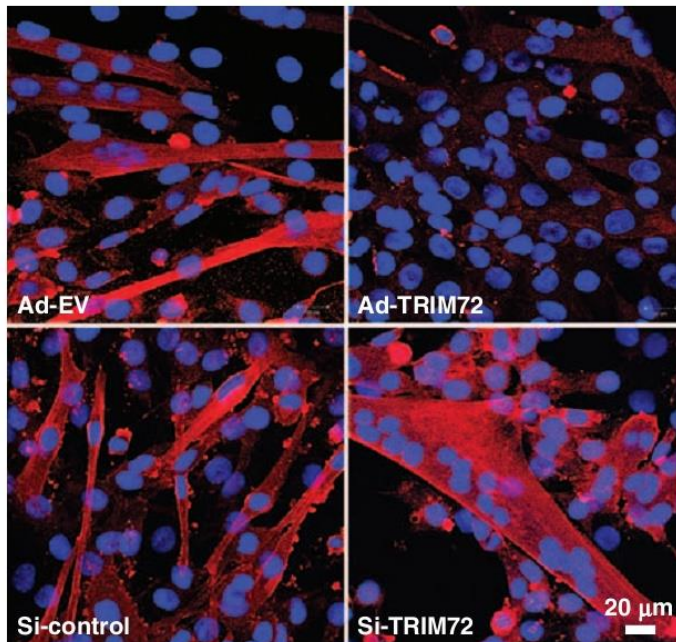
Primary component of the cardiac IPC response



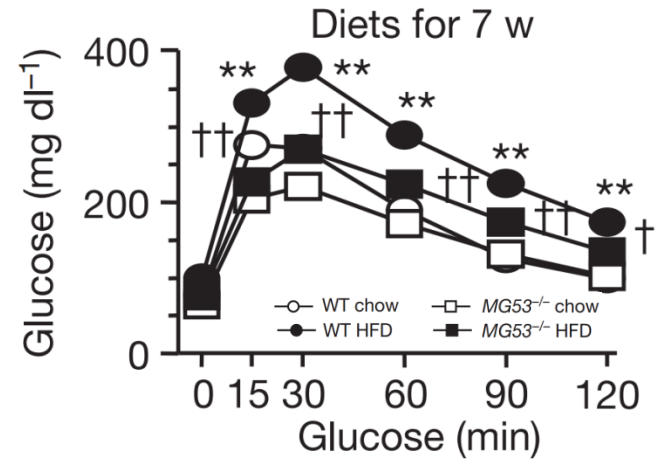
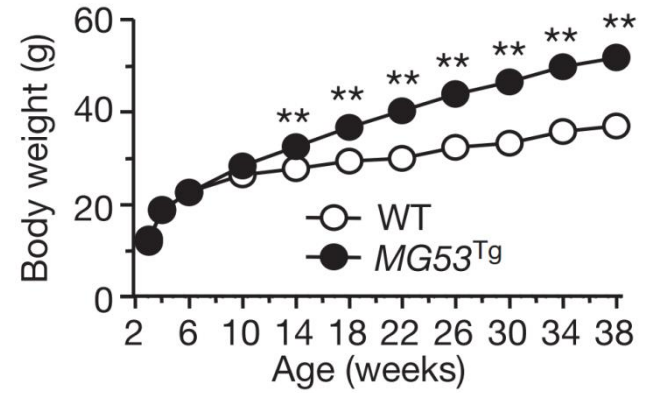
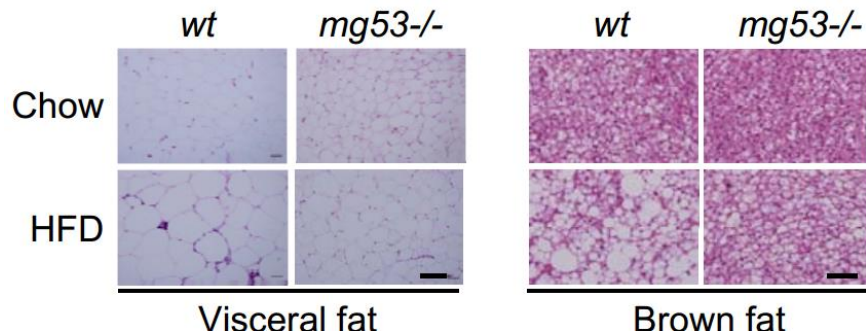
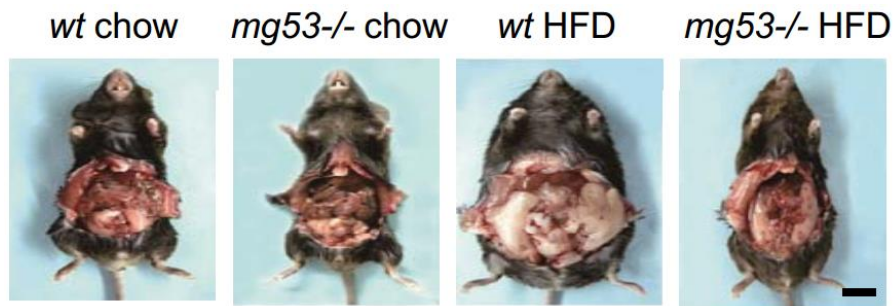
Cell membrane repair



Negative regulator of IGF-induced muscle differentiation



E3 ubiquitin ligase

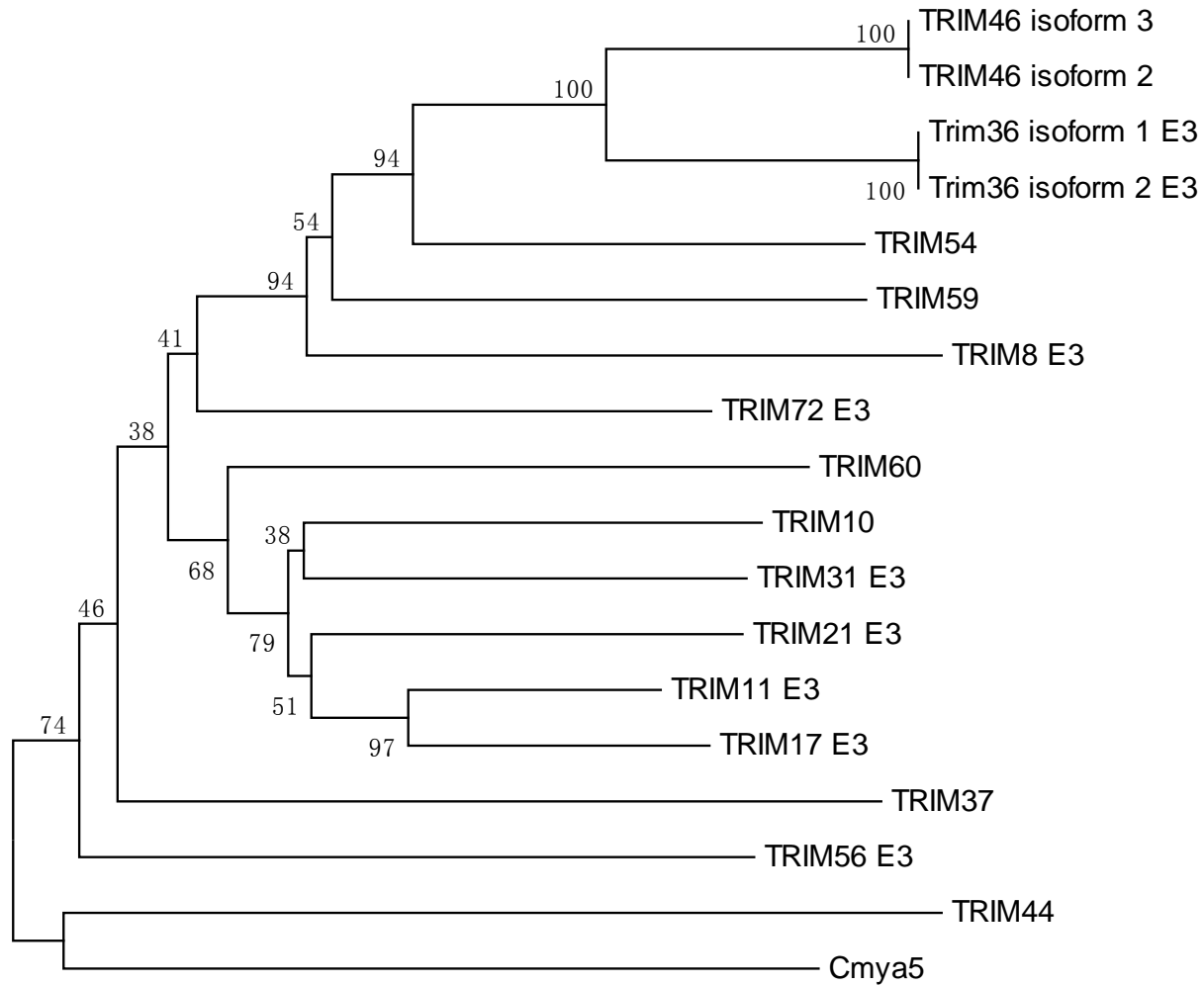


Sequence Analysis

Sequence alignment

Species	Accession	Score	Identity	Similarity	Gaps
Human/ Mouse	NP_001008275/ NP_001073401	2293.0	435/477 (91.2%)	456/477 (95.6%)	0/477 (0.0%)
Human/ Rat	NP_001008275/ NP_001071143	2274.0	433/477 (90.8%)	451/477 (94.5%)	0/477 (0.0%)
Mouse/ Rat	NP_001073401/ NP_001071143	2380.0	455/477 (95.4%)	465/477 (97.5%)	0/477 (0.0%)

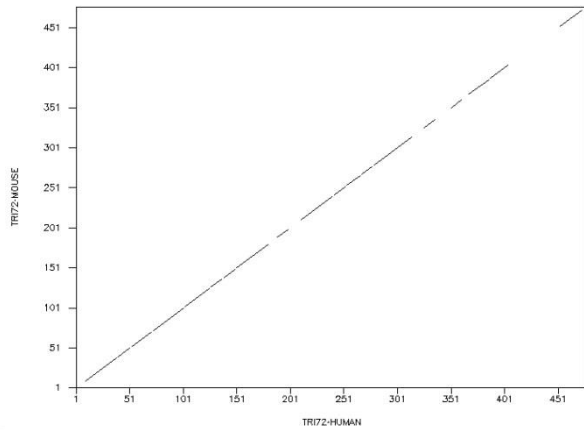
Phylogenetic tree



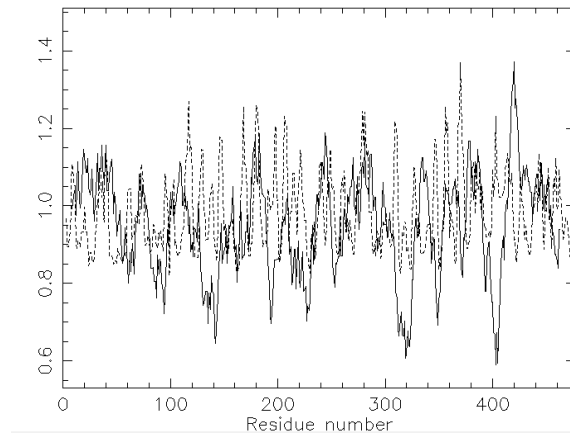
0.2

MEGA

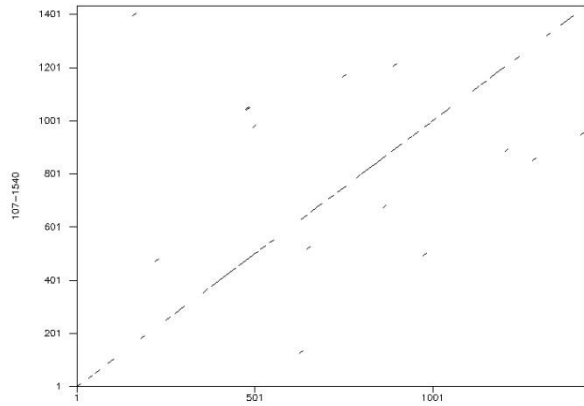
Dottup – A.A.



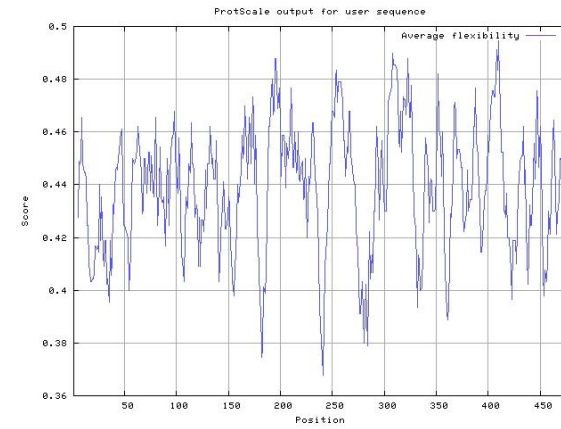
Tmap – Transmembrane



Dottup – mRNA

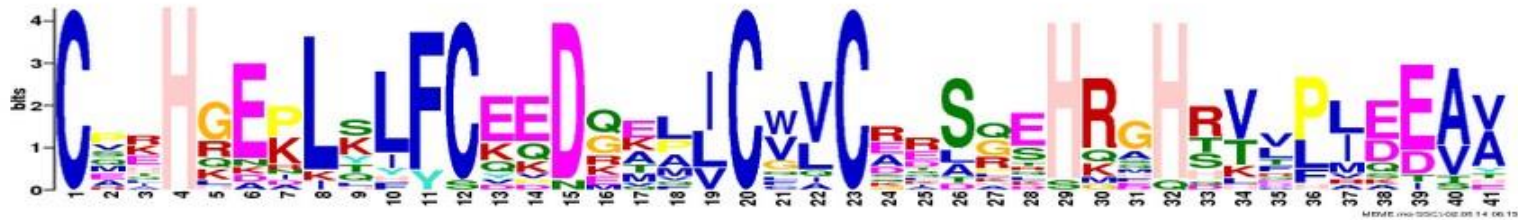


ProtScale – Flexibility

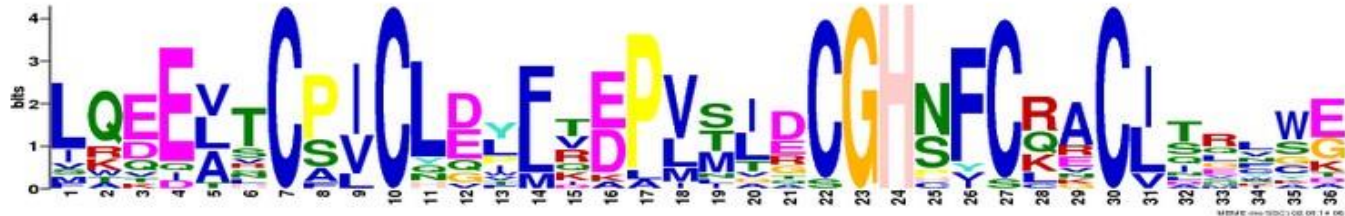


Motif elicitation

- ✓ **Motif 1** (E-value=2.0e-204; Width=41; Sites=16)



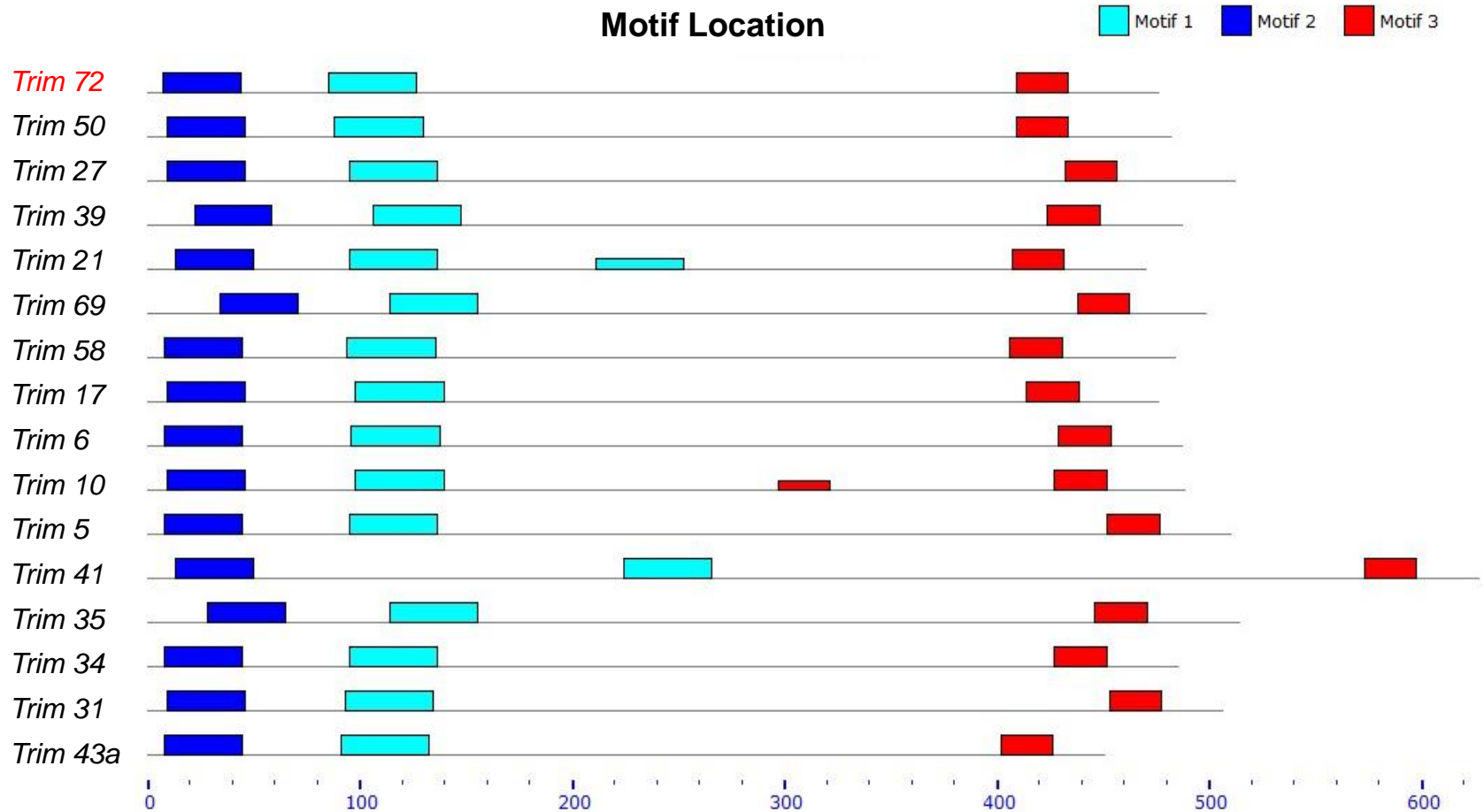
- ✓ **Motif 2** (E-value=9.9e-207; Width=36; Sites=16)



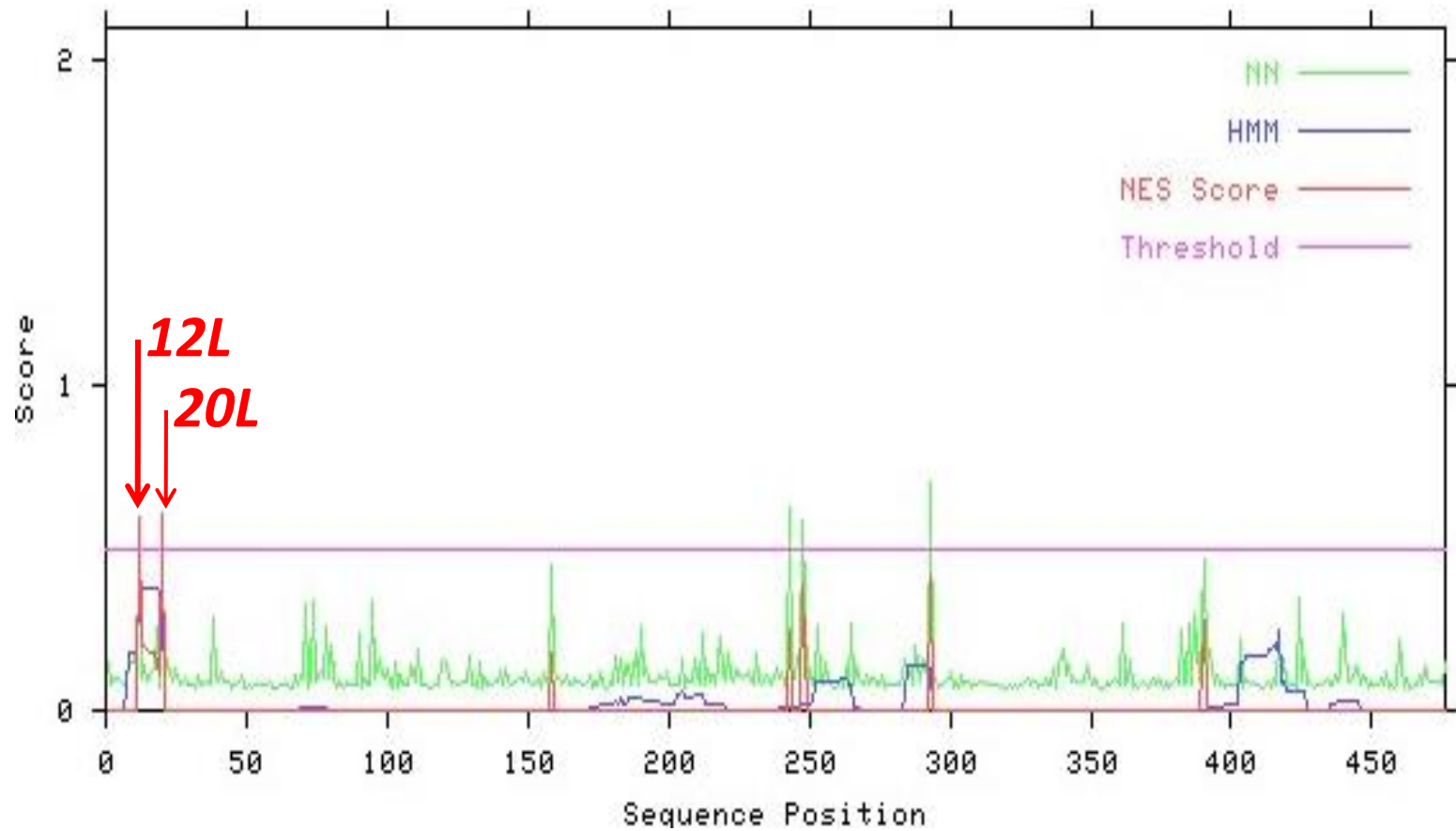
- ✓ **Motif 3** (E-value= 4.8e-134; Width=24; Sites=16)



Motif elicitation



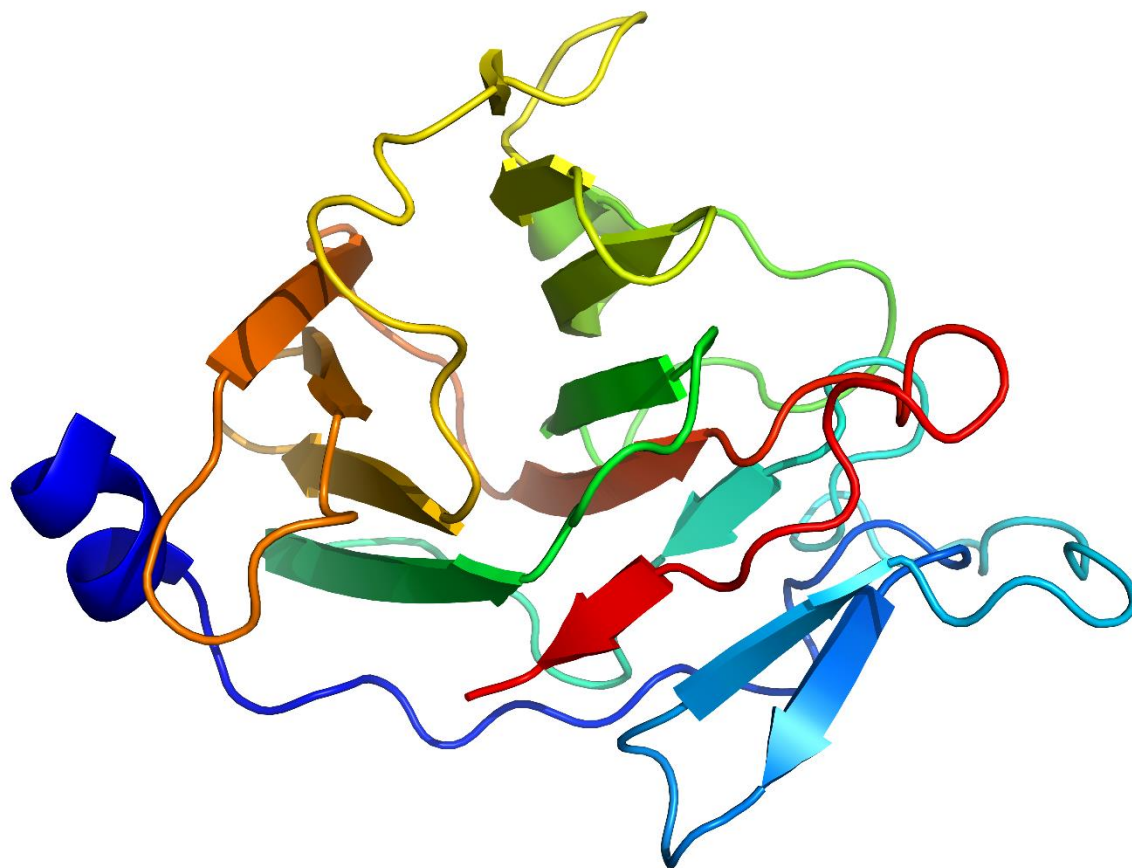
Nuclear export signal



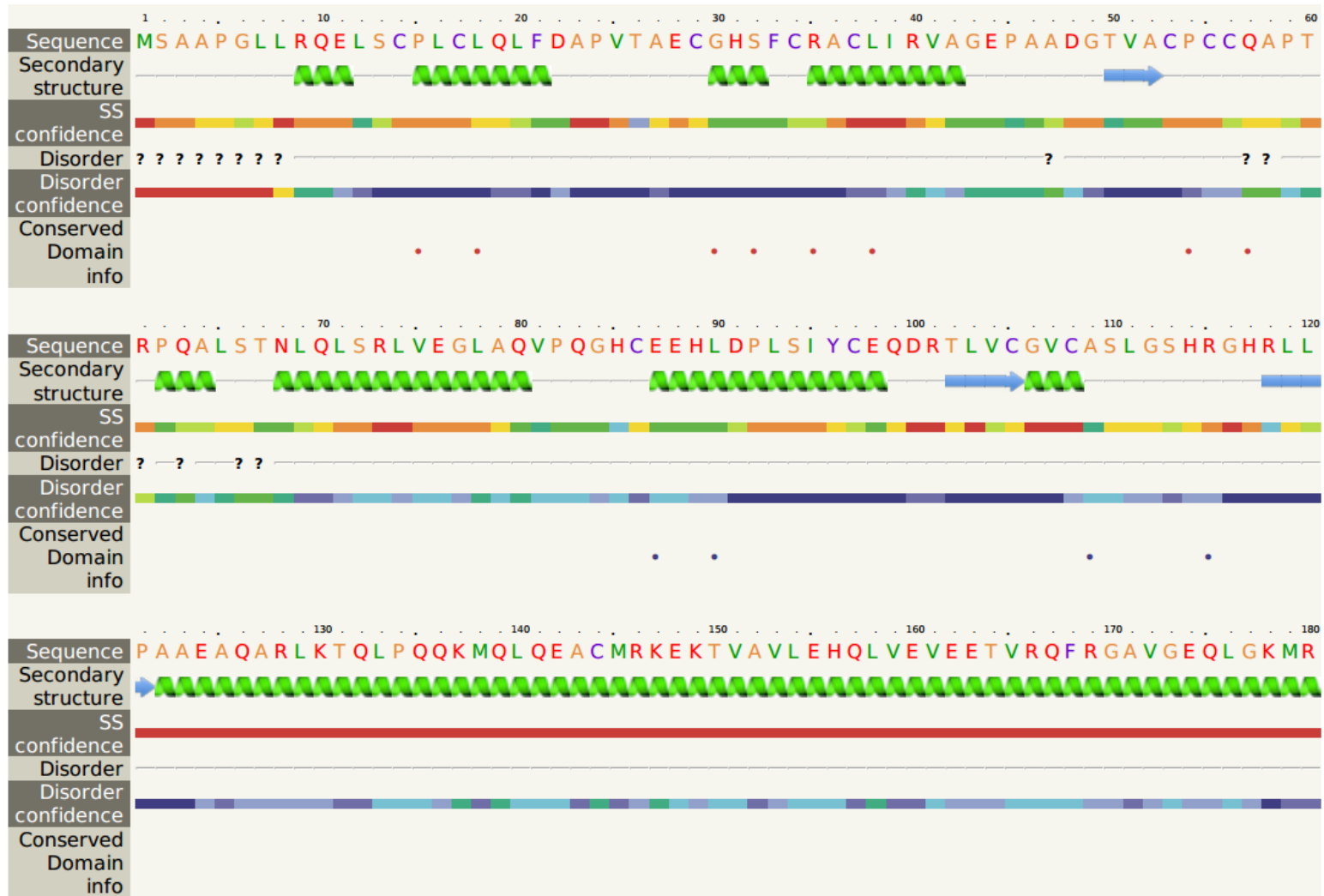
Protein Structure Analysis

PRY-SPRY domain of human TRIM72

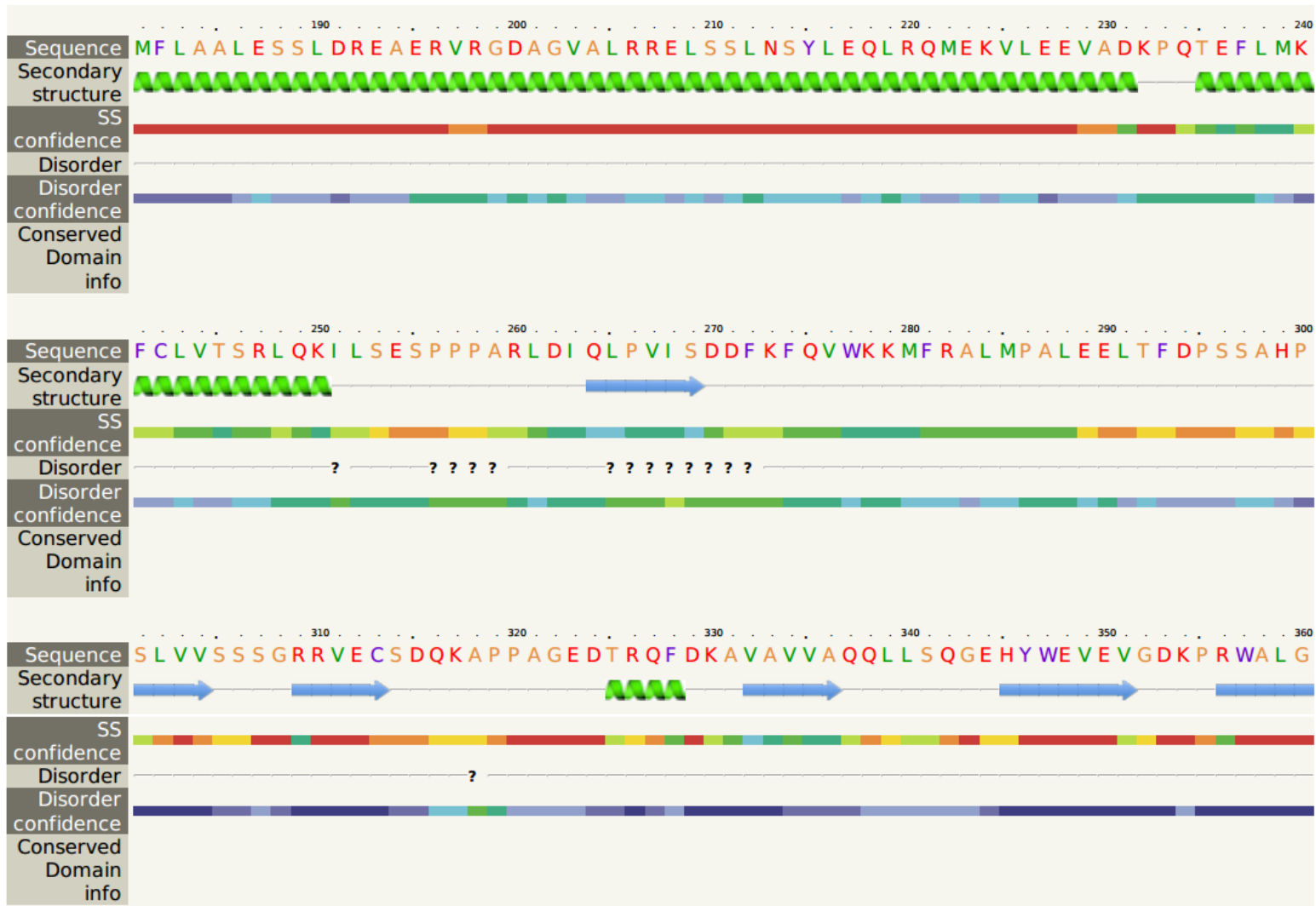
PDB ID: 3KB5



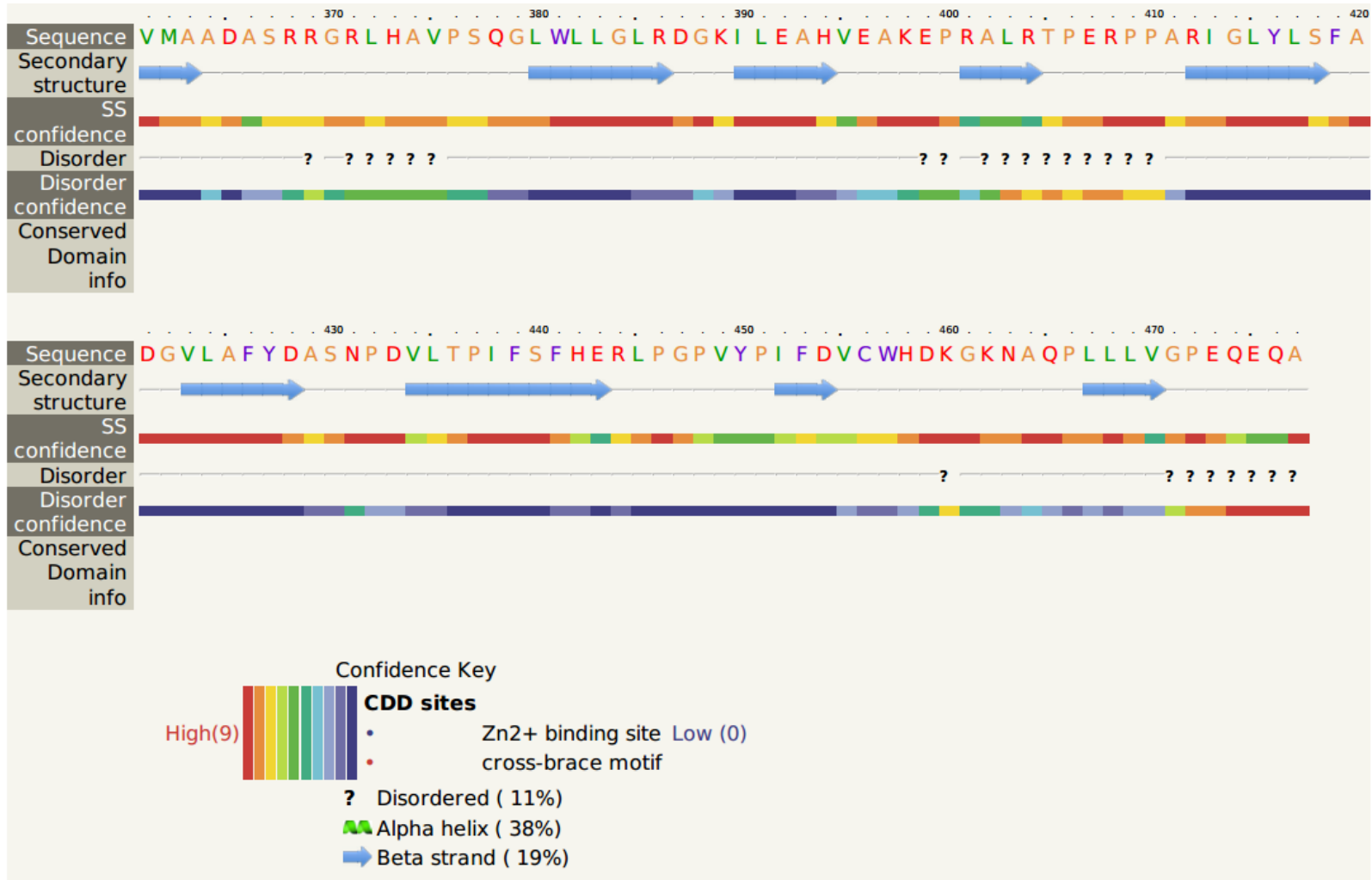
Secondary structure and disorder prediction



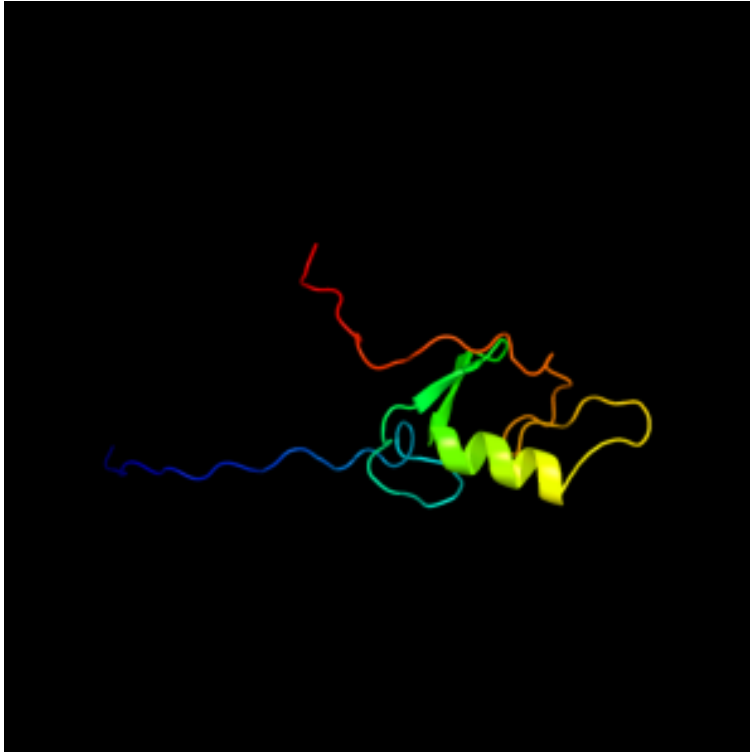
Secondary structure and disorder prediction



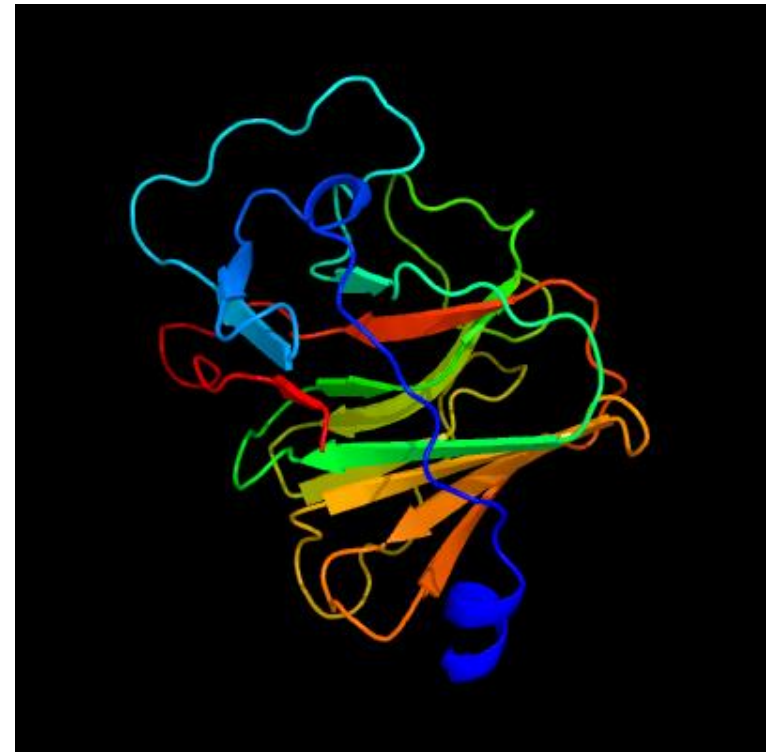
Secondary structure and disorder prediction



Homologous modeling

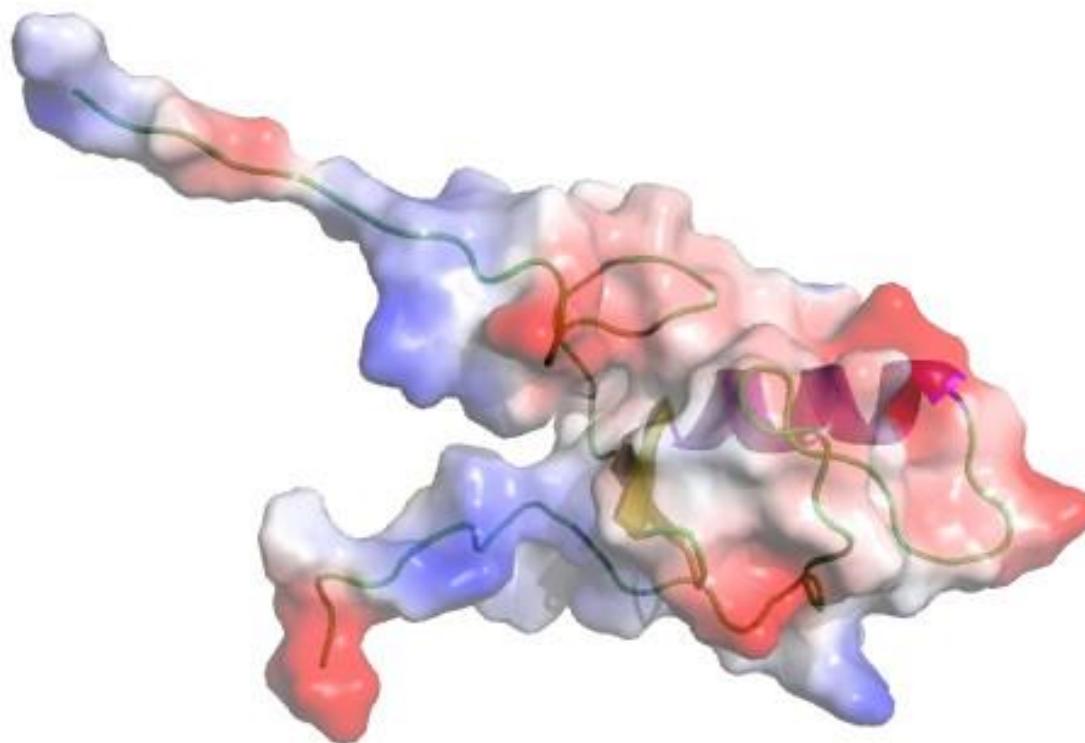


PDB header: apoptosis
PDB Molecule: tripartite motif-containing protein 30;
Confidence: 99.5%
Coverage: 15%
Residues: 1-76

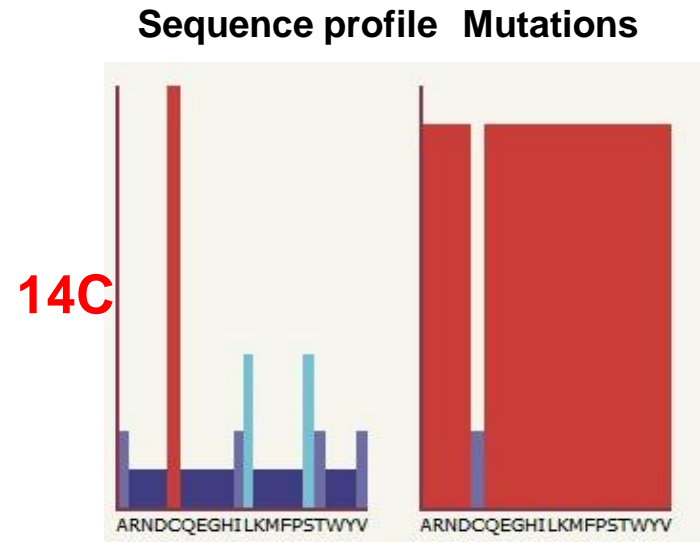
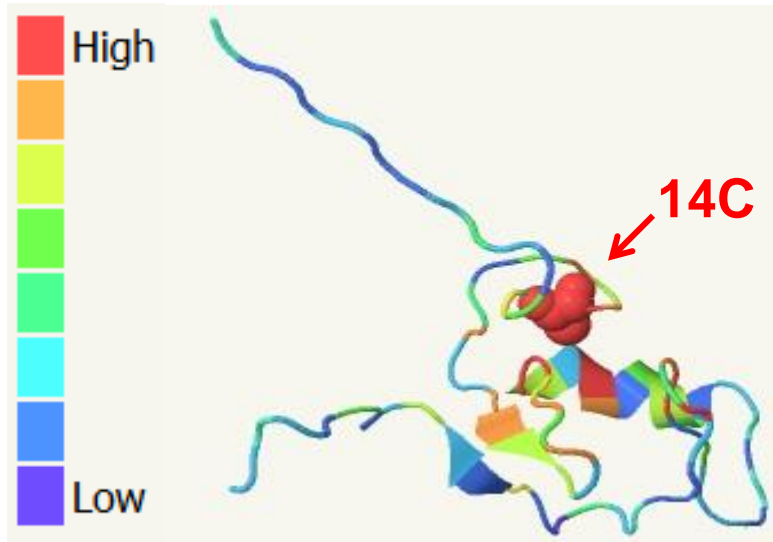


PDB header: membrane protein;
PDB Molecule: tripartite motif-containing protein 72;
Confidence: 100%
Coverage: 40%
Residues: 278-470

Homologous modeling



Mutation sensitivity

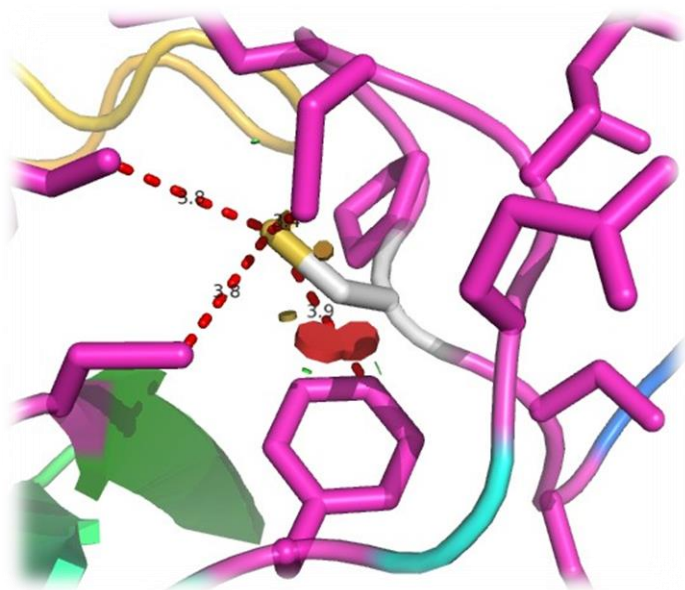


14C

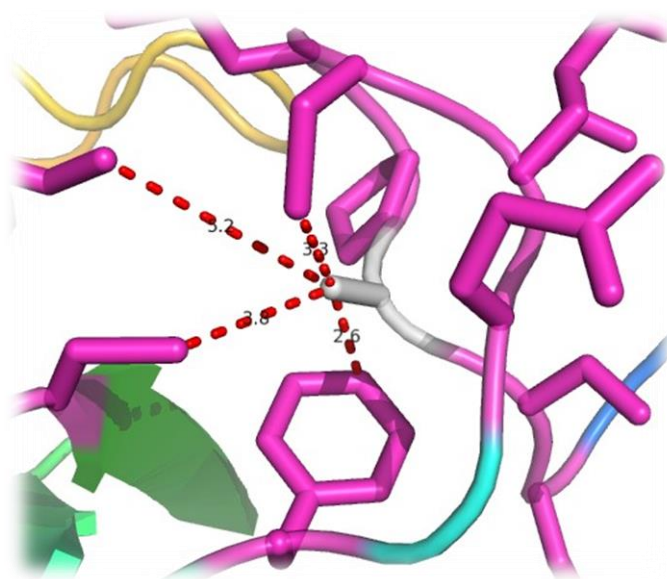
Phyre

Mutation sensitivity

14C



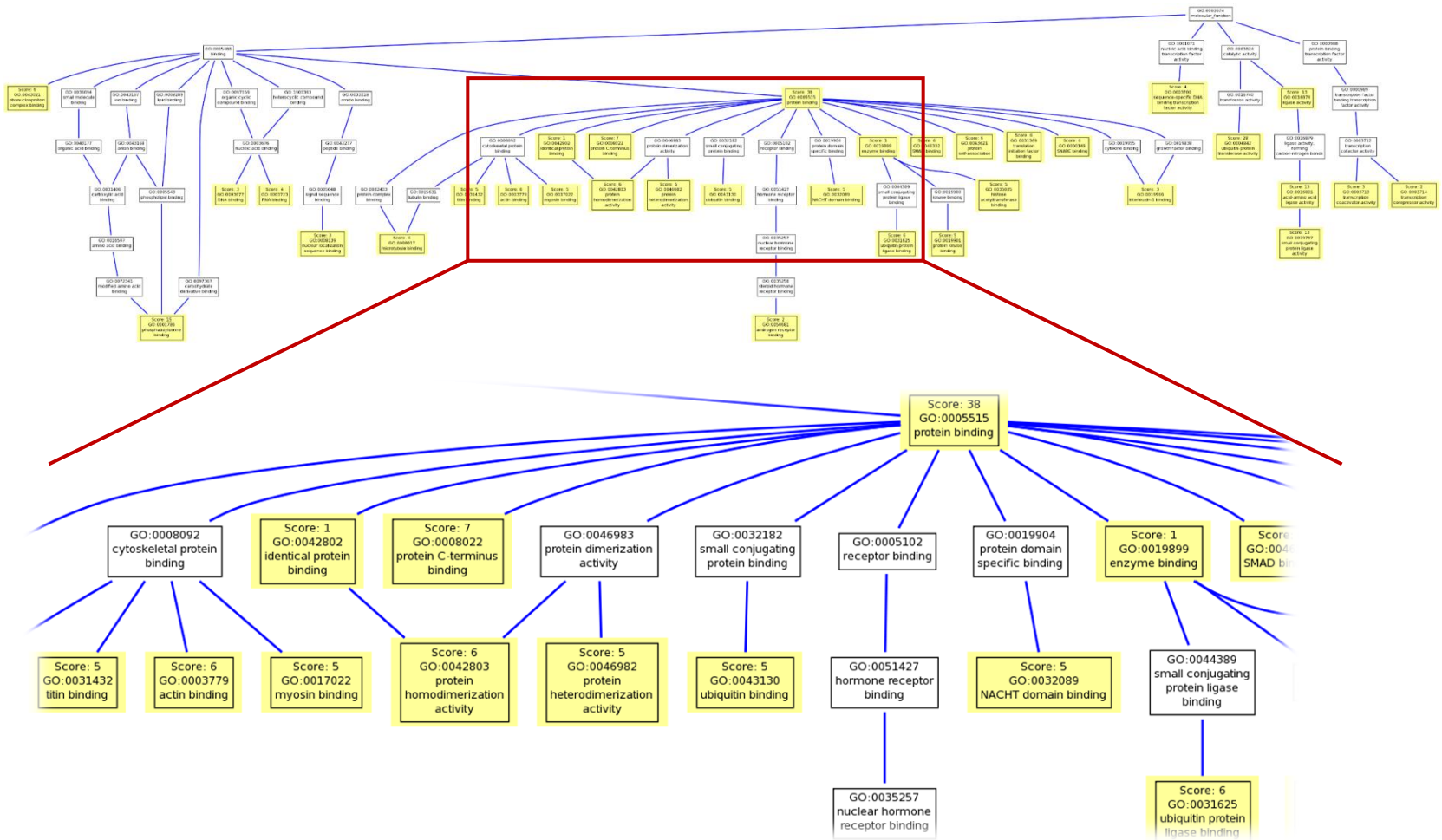
14A



Functional Analysis

Gene ontology prediction

GO : Molecular Function



Gene ontology prediction

Molecular Function Ontology				
#	GO ID ↕	GO Term ↕	Reliability (%) ↕	✓
1	GO:0005515	protein binding	38	✓
2	GO:0004842	ubiquitin-protein ligase activity	28	✓
3	GO:0001786	phosphatidylserine binding	15	✓
4	GO:0016881	acid-amino acid ligase activity	13	✓
5	GO:0019787	small conjugating protein ligase activity	13	✓
6	GO:0016874	ligase activity	13	✓
7	GO:0008022	protein C-terminus binding	7	✓
8	GO:0046332	SMAD binding	6	✓
9	GO:0043621	protein self-association	6	✓
10	GO:0003779	actin binding	6	✓
11	GO:0000149	SNARE binding	6	✓
12	GO:0031369	translation initiation factor binding	6	✓
13	GO:0042803	protein homodimerization activity	6	✓
14	GO:0031625	ubiquitin protein ligase binding	6	✓
15	GO:0043021	ribonucleoprotein binding	6	✓
16	GO:0035035	histone acetyltransferase binding	5	✓
17	GO:0017022	myosin binding	5	✓
18	GO:0032089	NACHT domain binding	5	✓
19	GO:0031432	titin binding	5	✓
20	GO:0046982	protein heterodimerization activity	5	✓
21	GO:0019901	protein kinase binding	5	✓
22	GO:0043130	ubiquitin binding	5	✓
23	GO:0008017	microtubule binding	4	✓
24	GO:0003700	transcription factor activity	4	✓
25	GO:0003723	RNA binding	4	✓

Biological Process Ontology				
#	GO ID ↕	GO Term ↕	Reliability (%) ↕	✓
1	GO:0003012	muscle system process	39	✓
2	GO:0006900	membrane budding	28	✓
3	GO:0006887	exocytosis	26	✓
4	GO:0007517	muscle organ development	26	✓
5	GO:0051260	protein homooligomerization	26	✓
6	GO:0001778	plasma membrane repair	26	✓
7	GO:0007275	multicellular organismal development	10	✓
8	GO:0051865	protein autoubiquitination	9	✓
9	GO:0006629	lipid metabolic process	9	✓
10	GO:0006915	apoptosis	9	✓
11	GO:0006281	DNA repair	9	✓
12	GO:0006633	fatty acid biosynthetic process	9	✓
13	GO:0006350	transcription	9	✓
14	GO:0007026	negative regulation of microtubule depolymerization	8	✓
15	GO:0045449	regulation of transcription	8	✓
16	GO:0045787	positive regulation of cell cycle	8	✓
17	GO:0007049	cell cycle	8	✓
18	GO:0044419	interspecies interaction between organisms	8	✓
19	GO:0032728	positive regulation of interferon-beta production	8	✓
20	GO:0006816	calcium ion transport	8	✓
21	GO:0019835	cytolysis	8	✓
22	GO:0006355	regulation of transcription, DNA-dependent	8	✓
23	GO:0045087	innate immune response	8	✓
24	GO:0009405	pathogenesis	8	✓
25	GO:0009615	response to virus	8	✓

Acknowledgements

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THANK YOU!