

Supplementary Materials

BIAPSS: A comprehensive physicochemical analyzer of proteins undergoing liquid-liquid phase separation

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The original results generated within BIAPSS web platform for FUS (UniProt identifier: P35637)

1.1 Entry Summary and Annotation web app: https://biapss.chem.iastate.edu/single_seq.html

Analysis of *Single* LLPS Sequence

Select UniProt ID

Select Name

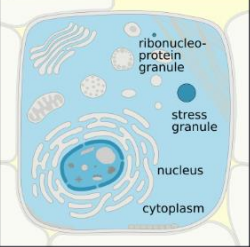
Select Gene

Select Organism

Select from all deposits

1 501

P35637



see cellular location at
COMPARTMENTS

ORGANISM: Homo sapiens
GENE: FUS
NAME: RNA-binding protein FUS

Parameter	Value
Sequence length:	526
LLPS fragment(s):	1-526 PMID:29961577
LLPS PSPredictor [↗] :	0.17 (NO)
Disorder fraction:	0.84
Secondary structure:	0.08: 0.03 (H) 0.05 (E)
Solvent accessibility:	0.08 (buried) 0.8 (exposed)
Charge:	0.17: 0.1 (pos) 0.07 (neg)
Charge pattern:	0.02 (FCR) 1.27 (OCS) 0.99 (SCD)
Polarity:	0.4
Hydrophobicity:	0.42
Aromatic:	0.1

CrossRefs

PHASEPRO

LLPSDB go

PHASEPDB go

DRLLPS

DISPROT

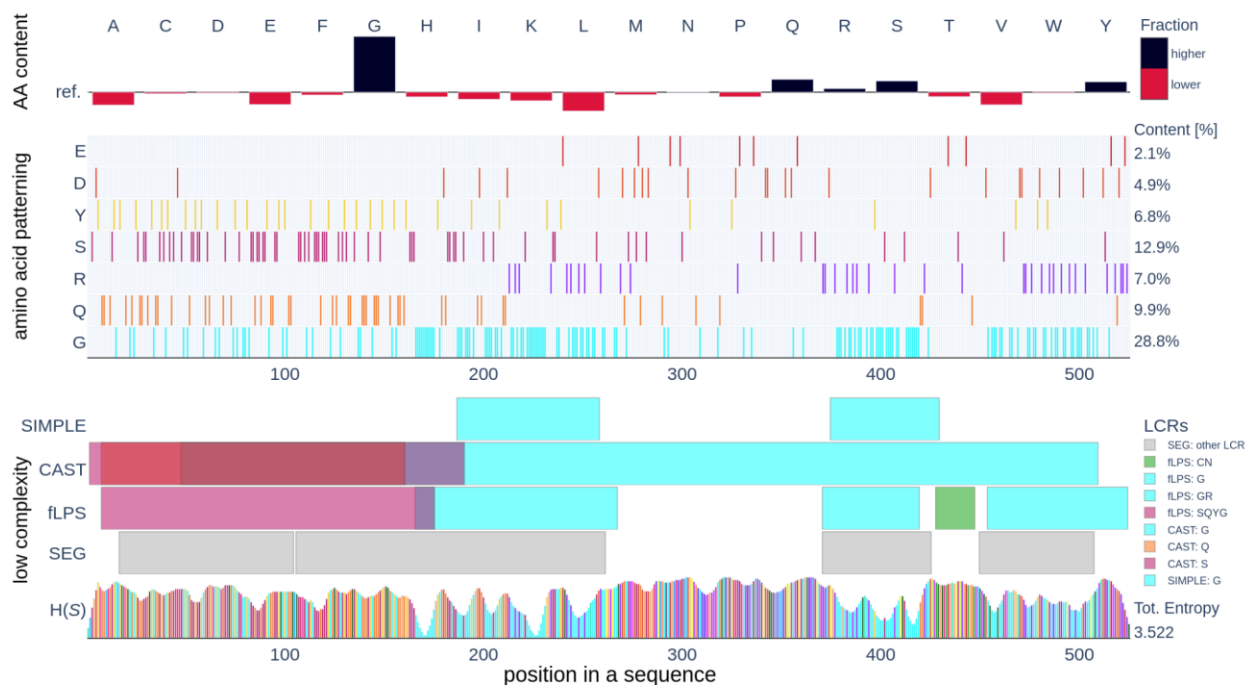
UNIPROT

STRUCTURE go

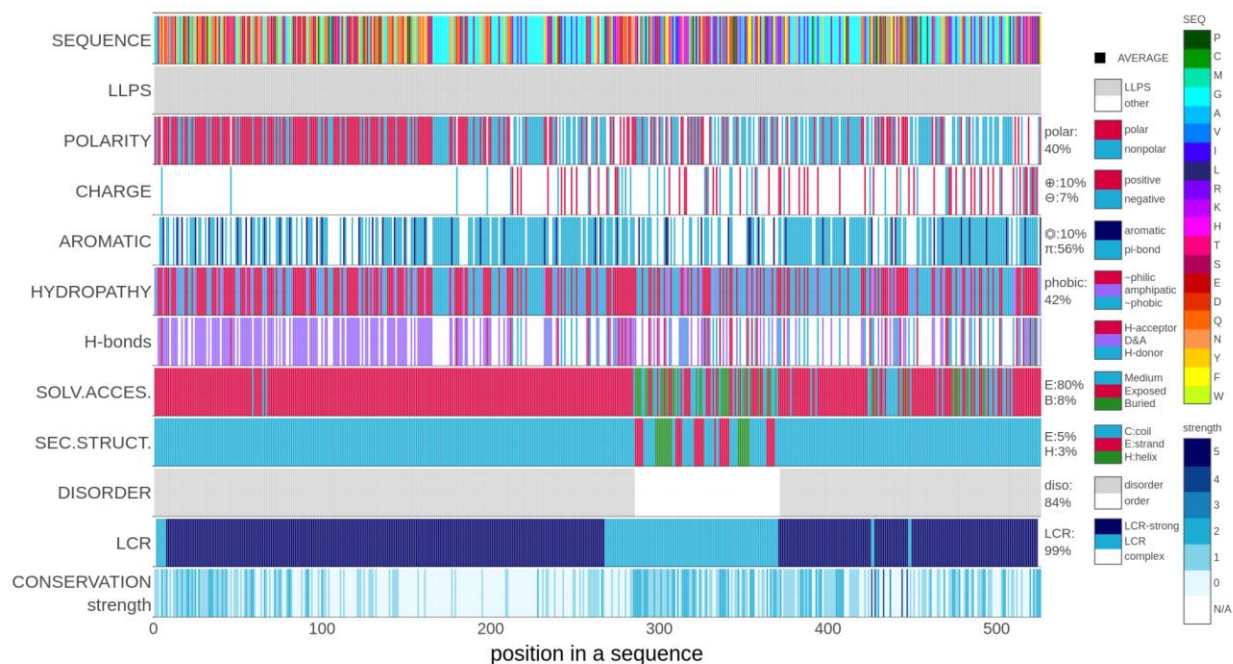
CELLATLAS

1.2 Sequence Complexity & Composition web app:

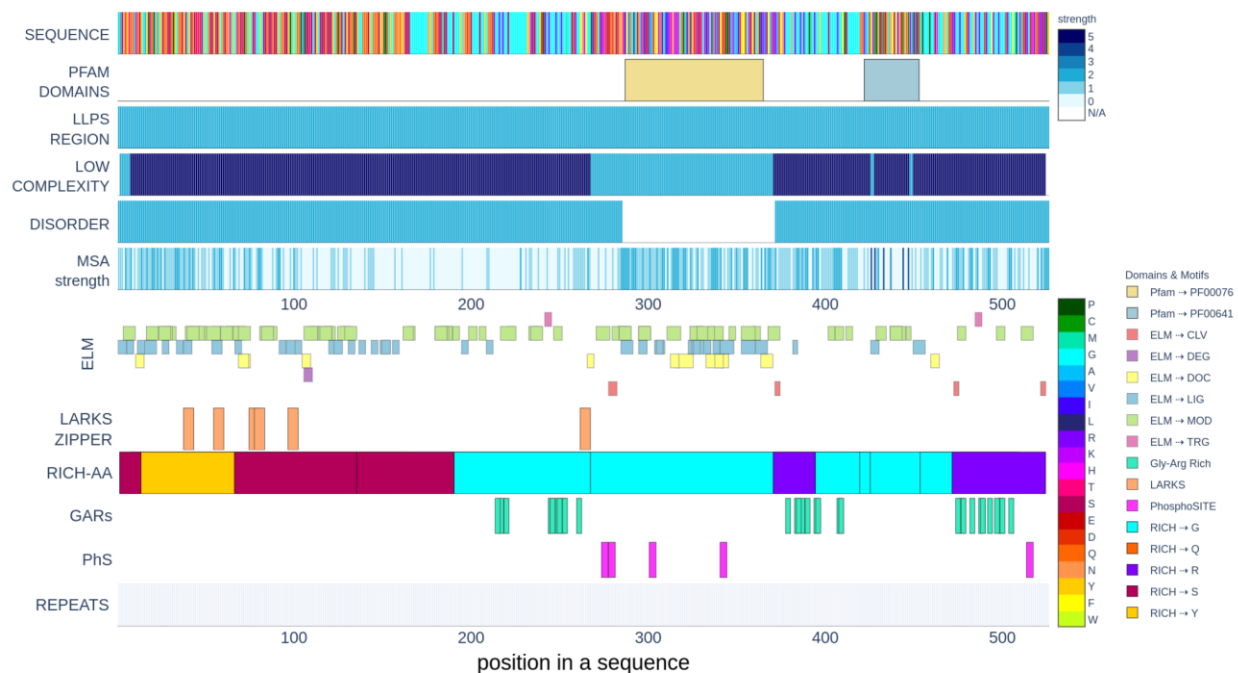
https://biapss.chem.iastate.edu/single_seq.html#complexity



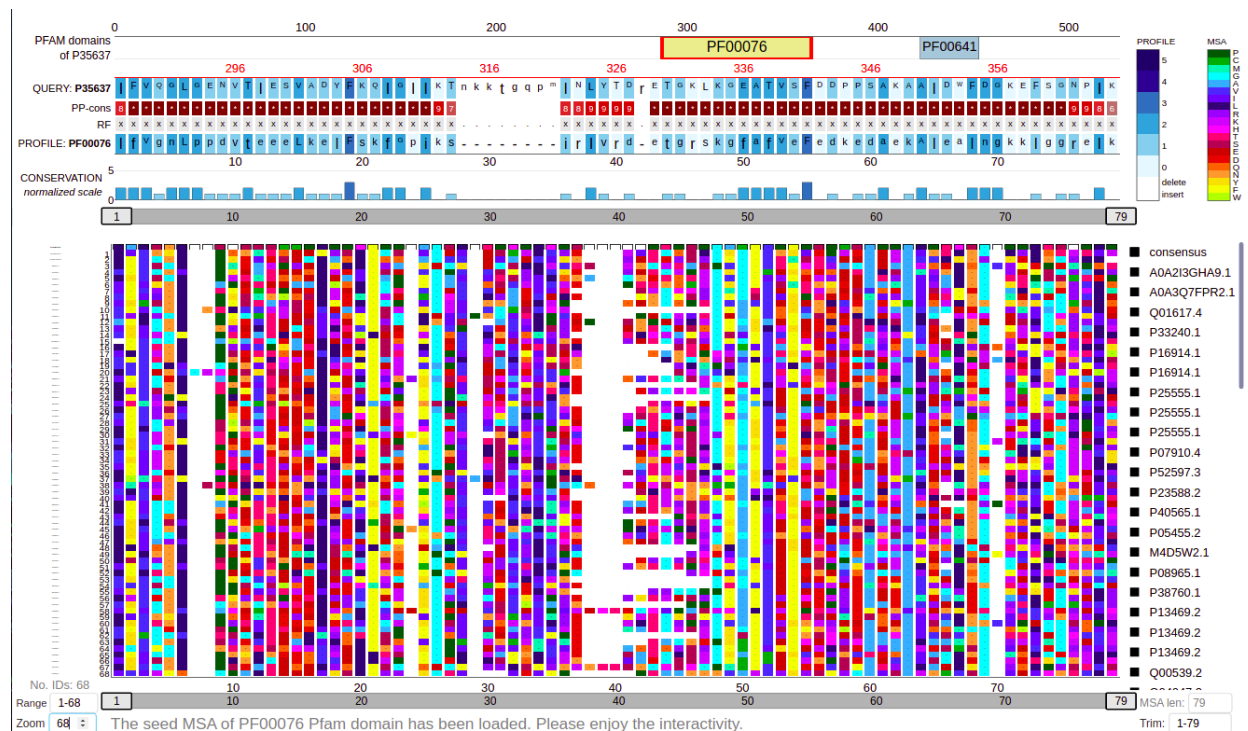
1.3 Patterns of Chemical Decoration web app: https://biapss.chem.iastate.edu/single_seq.html#pattern



1.4 Domains, Motifs, Repeats web app: https://biapss.chem.iastate.edu/single_seq.html#motifs

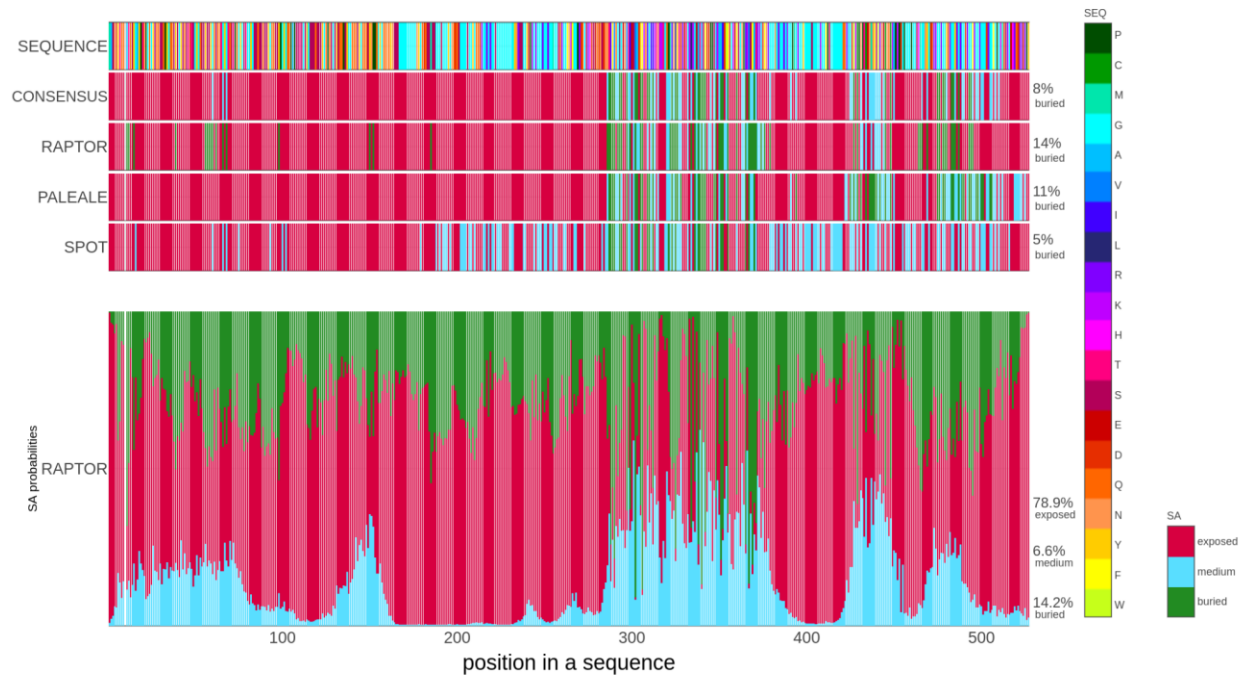


1.5 Sequence Conservation web app: https://biapss.chem.iastate.edu/single_seq.html#conservation

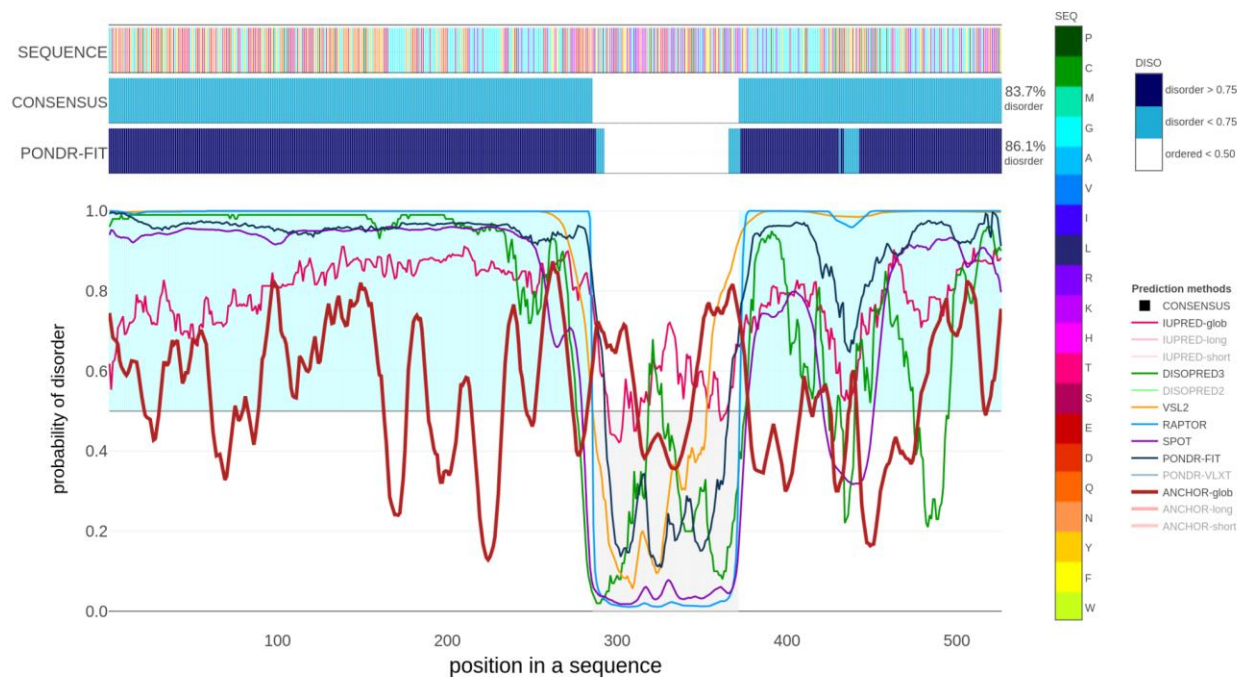


Domain PF00076

1.7 The Solvent Accessibility web app: https://biapss.chem.iastate.edu/single_seq.html#solventacc



1.8 The Structural Disorder web app: https://biapss.chem.iastate.edu/single_seq.html#disorder



1.9 Contact Map web app: https://biapss.chem.iastate.edu/single_seq.html#contacts

