

Protein Knowledge Report — Q00987

1. Target summary

- Input type: uniprot_accession
- Label: Q00987
- Length: 491 aa
- UniProt accession: Q00987
- Submitted: 2026-07-15T13:00:10Z
- Sequence:

MCNTNMSVPTDGAVTTSQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVYCSNDLLGDLFGVPSFSVKEHRKIYT
MIYRNLVVVNQEQSSDGTSVSENCHLEGGSDQKDLVQELQEEKPSSSHLVSRPSTSSRRRAISETEENSDELSGERQQRKRHKSDSISLSFDESLALC

2. Family classification

- Family: zf-C3HC4_3 (PF13920) — Zinc finger, C3HC4 type (RING finger)
- E-value: 1.10e-10 Bit score: 41.9
- Model span: 26-32 of model (305-311 of query)
- Passes family's curated gathering threshold: yes

Source: HMMER hmmscan vs Pfam-A (local)

3. Known ligand precedent

- Total structures in this family: 74
- Distinct ligand scaffolds curated below: 8

PDB ID	Ligand(s)	Resolution (Å)	Why selected
13SY	W2J	1.29	highest-resolution structure...
13SQ	U0P	1.30	highest-resolution structure...
13SL	JHP	1.34	highest-resolution structure...
13ST	A1H9V	1.37	highest-resolution structure...
13SW	A1AJM	1.37	highest-resolution structure...
13SM	GW1	1.40	highest-resolution structure...
13SE	T1J	1.44	highest-resolution structure...
13SN	Q7L	1.44	highest-resolution structure...

Source: RCSB PDB REST API, curated top-N by distinct ligand scaffold + resolution

Interaction fingerprints (Evidence Integration Layer, Phase 1)

8 ligand-bound structure(s) exist for this target's Pfam family (PF13920), but none checked aligned to the query at >=50% sequence coverage — likely other members of the same broad family (e.g. related kinases), not this specific protein. Interaction fingerprints require a structure of the query protein itself.

Source: PLIP (Protein-Ligand Interaction Profiler), run on representative structures from known ligand precedent

4. Conservation

- Family: PF13920
- Seed alignment size: 309 sequences
- Mean pairwise identity (seed alignment): 29.4%
- Note: computed over a sample of 40/309 seed sequences

Source: Pfam seed alignment (via InterPro API), mean pairwise identity across aligned members at matched-region columns

5. Structural analysis

- Structure provider: AlphaFold DB (model created 2025-08-01T00:00:00Z)
- Pocket detector: fpocket (default parameters)
- Mean per-residue confidence: 0.6258
- Conformational ensemble: 5 conformers (ANM, 5 frames)
- Static (single-frame) pocket count: 32
- Residue numbering: pipeline-sequential, with literature (author-deposited PDB 6Q9L) numbering shown in parentheses — 94/491 residues cross-walked
- Ensemble-informed ranked pocket clusters (customer-visible top): 3

Rank (cluster id)	Frames present	Persistence	Residues
1 (cluster 4)	5/5	1.0	23(23), 24(24), 25(25), 26(2...
2 (cluster 24)	5/5	1.0	263(?), 266(?), 268(?), 270(...
3 (cluster 29)	5/5	1.0	275(?), 276(?), 277(?), 278(...

Pocket functional context (UniProt features + ClinVar variants):

- Pocket 1 (cluster 4):
 - Residue 23: Region — Necessary for interaction with USP2
 - Residue 23: Region — Sufficient to promote the mitochondrial pathway of apoptosis
 - Residue 24: Region — Necessary for interaction with USP2
 - Residue 24: Region — Sufficient to promote the mitochondrial pathway of apoptosis
 - Residue 25: Region — Necessary for interaction with USP2
 - Residue 25: Region — Sufficient to promote the mitochondrial pathway of apoptosis
 - Residue 26: Region — Necessary for interaction with USP2
 - Residue 26: Region — Sufficient to promote the mitochondrial pathway of apoptosis
 - Residue 49: Region — Necessary for interaction with USP2
 - Residue 49: Region — Sufficient to promote the mitochondrial pathway of apoptosis
 - Residue 50: Region — Necessary for interaction with USP2
 - Residue 50: Region — Sufficient to promote the mitochondrial pathway of apoptosis
 - Residue 51: Region — Necessary for interaction with USP2
 - Residue 51: Region — Sufficient to promote the mitochondrial pathway of apoptosis
 - Residue 94: Region — Necessary for interaction with USP2
 - Residue 94: Region — Sufficient to promote the mitochondrial pathway of apoptosis
 - Residue 95: Region — Necessary for interaction with USP2
 - Residue 95: Region — Sufficient to promote the mitochondrial pathway of apoptosis
 - Residue 96: Region — Necessary for interaction with USP2
 - Residue 96: Region — Sufficient to promote the mitochondrial pathway of apoptosis
 - Residue 97: Region — Necessary for interaction with USP2
 - Residue 97: Region — Sufficient to promote the mitochondrial pathway of apoptosis
 - Residue 98: Region — Necessary for interaction with USP2
 - Residue 98: Region — Sufficient to promote the mitochondrial pathway of apoptosis
 - Residue 100: Region — Necessary for interaction with USP2
 - Residue 100: Region — Sufficient to promote the mitochondrial pathway of apoptosis
 - Residue 101: Region — Necessary for interaction with USP2
 - Residue 101: Region — Sufficient to promote the mitochondrial pathway of apoptosis
 - Residue 104: Region — Necessary for interaction with USP2
 - Residue 190: Region — Interaction with PYHIN1 and necessary for interaction with RFFL and RNF34
 - Residue 190: Region — Interaction with MTBP
 - Residue 190: Modified residue — Phosphoserine
 - Residue 191: Region — Interaction with PYHIN1 and necessary for interaction with RFFL and RNF34
 - Residue 191: Region — Interaction with MTBP
 - Residue 192: Region — Interaction with PYHIN1 and necessary for interaction with RFFL and RNF34
 - Residue 192: Region — Interaction with MTBP
 - Residue 193: Region — Interaction with PYHIN1 and necessary for interaction with RFFL and RNF34

- Residue 193: Region — Interaction with MTBP
- Residue 194: Region — Interaction with PYHIN1 and necessary for interaction with RFFL and RNF34
- Residue 194: Region — Interaction with MTBP
- Residue 195: Region — Interaction with PYHIN1 and necessary for interaction with RFFL and RNF34
- Residue 195: Region — Interaction with MTBP
- Residue 196: Region — Interaction with PYHIN1 and necessary for interaction with RFFL and RNF34
- Residue 196: Region — Interaction with MTBP
- Residue 197: Region — Interaction with PYHIN1 and necessary for interaction with RFFL and RNF34
- Residue 197: Region — Interaction with MTBP
- Residue 198: Region — Interaction with PYHIN1 and necessary for interaction with RFFL and RNF34
- Residue 198: Region — Interaction with MTBP
- Pocket 2 (cluster 24):
 - Residue 263: Region — Interaction with MTBP
 - Residue 263: Region — Mediates interaction with RAD54B
 - Residue 263: Region — ARF-binding
 - Residue 263: Region — Region II
 - Residue 263: Region — Disordered
 - Residue 266: Region — Interaction with MTBP
 - Residue 266: Region — Mediates interaction with RAD54B
 - Residue 266: Region — ARF-binding
 - Residue 266: Region — Region II
 - Residue 266: Region — Disordered
 - Residue 268: Region — Interaction with MTBP
 - Residue 268: Region — Mediates interaction with RAD54B
 - Residue 268: Region — ARF-binding
 - Residue 268: Region — Region II
 - Residue 268: Region — Disordered
 - Residue 270: Region — Interaction with MTBP
 - Residue 270: Region — Mediates interaction with RAD54B
 - Residue 270: Region — ARF-binding
 - Residue 270: Region — Region II
 - Residue 270: Region — Disordered
 - Residue 271: Region — Interaction with MTBP
 - Residue 271: Region — Mediates interaction with RAD54B
 - Residue 271: Region — ARF-binding
 - Residue 271: Region — Region II
 - Residue 271: Region — Disordered
 - Residue 272: Region — Interaction with MTBP
 - Residue 272: Region — Mediates interaction with RAD54B
 - Residue 272: Region — ARF-binding
 - Residue 272: Region — Region II
 - Residue 272: Region — Disordered
 - Residue 273: Region — Interaction with MTBP
 - Residue 273: Region — Mediates interaction with RAD54B
 - Residue 273: Region — ARF-binding
 - Residue 273: Region — Region II
 - Residue 273: Region — Disordered
 - Residue 274: Region — Interaction with MTBP
 - Residue 274: Region — Mediates interaction with RAD54B
 - Residue 274: Region — ARF-binding
 - Residue 274: Region — Region II
 - Residue 274: Region — Disordered
 - Residue 275: Region — Interaction with MTBP
 - Residue 275: Region — Mediates interaction with RAD54B

- Residue 275: Region — ARF-binding
- Residue 275: Region — Region II
- Residue 276: Region — Interaction with MTBP
- Residue 276: Region — Mediates interaction with RAD54B
- Residue 276: Region — ARF-binding
- Residue 276: Region — Region II
- Residue 276: Region — Necessary for interaction with USP2
- Residue 462: Region — Necessary for interaction with USP2
- Residue 463: Region — Necessary for interaction with USP2
- Residue 466: Region — Necessary for interaction with USP2
- Residue 467: Region — Necessary for interaction with USP2
- Residue 469: Region — Necessary for interaction with USP2
- Residue 470: Region — Necessary for interaction with USP2
- Residue 484: Region — Necessary for interaction with USP2
- Residue 485: Region — Necessary for interaction with USP2
- Residue 486: Region — Necessary for interaction with USP2
- Residue 487: Region — Necessary for interaction with USP2
- Residue 489: Region — Necessary for interaction with USP2
- Pocket 3 (cluster 29):
 - Residue 275: Region — Interaction with MTBP
 - Residue 275: Region — Mediates interaction with RAD54B
 - Residue 275: Region — ARF-binding
 - Residue 275: Region — Region II
 - Residue 276: Region — Interaction with MTBP
 - Residue 276: Region — Mediates interaction with RAD54B
 - Residue 276: Region — ARF-binding
 - Residue 276: Region — Region II
 - Residue 276: Region — Necessary for interaction with USP2
 - Residue 277: Region — Interaction with MTBP
 - Residue 277: Region — Mediates interaction with RAD54B
 - Residue 277: Region — ARF-binding
 - Residue 277: Region — Region II
 - Residue 277: Region — Necessary for interaction with USP2
 - Residue 278: Region — Interaction with MTBP
 - Residue 278: Region — Mediates interaction with RAD54B
 - Residue 278: Region — ARF-binding
 - Residue 278: Region — Region II
 - Residue 278: Region — Necessary for interaction with USP2
 - Residue 279: Region — Interaction with MTBP
 - Residue 279: Region — Mediates interaction with RAD54B
 - Residue 279: Region — ARF-binding
 - Residue 279: Region — Region II
 - Residue 279: Region — Necessary for interaction with USP2
 - Residue 280: Region — Interaction with MTBP
 - Residue 280: Region — Mediates interaction with RAD54B
 - Residue 280: Region — ARF-binding
 - Residue 280: Region — Region II
 - Residue 280: Region — Necessary for interaction with USP2
 - Residue 282: Region — Interaction with MTBP
 - Residue 282: Region — Mediates interaction with RAD54B
 - Residue 282: Region — ARF-binding
 - Residue 282: Region — Region II
 - Residue 282: Region — Necessary for interaction with USP2
 - Residue 428: Region — Necessary for interaction with USP2

- Residue 429: Region — Necessary for interaction with USP2
- Residue 429: Modified residue — Phosphoserine; by ATM
- Residue 430: Region — Necessary for interaction with USP2
- Residue 431: Region — Necessary for interaction with USP2
- Residue 449: Region — Necessary for interaction with USP2
- Residue 458: Region — Necessary for interaction with USP2
- Residue 486: Region — Necessary for interaction with USP2
- Residue 487: Region — Necessary for interaction with USP2
- Residue 488: Region — Necessary for interaction with USP2
- Residue 489: Region — Necessary for interaction with USP2
- Residue 490: Region — Necessary for interaction with USP2
- Residue 491: Region — Necessary for interaction with USP2

Source: UniProt REST API (features) + ClinVar via NCBI E-utilities (variants, filtered by clinical significance)

4 pocket cluster(s) (of 11 total, filtered to those present in >=2 frames) appear only in later ensemble frames, absent from the static structure-provider output:

Cluster id	Frames present	Persistence	Residues
33	4/5	0.8	332(?), 333(?), 334(?), 335(...
35	2/5	0.4	392(?), 393(?), 394(?)
36	2/5	0.4	234(?), 235(?), 236(?)
38	2/5	0.4	208(?), 209(?), 210(?), 211(...

3 pocket cluster(s) in the customer-visible top ranking; static (first-frame-only) fpocket found 32 pocket(s); the ensemble-informed ranker considered 43 cluster(s) across 5 conformers — compare static_pocket_count against pocket_ranking.clusters to see whether the ensemble surfaces anything the static structure alone misses; no binding-site ground truth supplied, so no recovery/overlap metrics are reported; residue numbers above are pipeline-sequential, NOT necessarily literature convention — see numbering_crosswalk (ref: 6Q9L) for author-deposited numbering

Source: StructureProvider + PocketDetector abstraction (see api/knowledge_protein/structural.py)

6. Confidence flags

1 caution flag(s) — discount confidence accordingly:

- [Structural analysis] numbering_low_coverage: Numbering cross-walk against 6Q9L only mapped 94/491 residues (19%) — the reference structure found is a poor match for most of this sequence (e.g. a short peptide/fragment, or a construct covering only a small domain of a larger protein). Most residues will show as unmapped ('?'); treat any '(literature)' number that DOES appear as coincidental unless independently checked, not as evidence the cross-walk is reliable for this target.

Source: rules-based checks in api/knowledge_protein/confidence_flags.py — fixed thresholds on numbers already computed elsewhere in this report, no learned calibration, no combined/weighted score.

7. Similar known proteins

Sequence-based (Pfam family co-membership, top 5 by identity):

PDB ID	Sequence identity to query	Ligand(s)
3T6P	4.4%	(none recorded)
9SA1	0.0%	(none recorded)
9SA2	0.0%	(none recorded)
6SQP	0.0%	(none recorded)
13SY	0.0%	W2J

Structure-based (Foldseek vs. full PDB structural index, Evidence Integration Layer Phase 2):

PDB ID	TM-score	Sequence identity	In sequence-based list...	Description
4HFZ	1.000	97.5%	no	Crystal Structure of a...

3LNZ	1.000	100.0%	no	Crystal structure of h...
3TPX	1.000	100.0%	no	Crystal structure of h...
5UMM	1.000	100.0%	no	CRYSTAL STRUCTURE OF H...
3IWY	1.000	100.0%	no	Crystal structure of h...

5/5 top structural neighbor(s) — 4HFZ, 3LNZ, 3TPX, 5UMM, 3IWY — are not in the small cached sequence-based sample above (similar_protein.py surveys only the ~60 highest-resolution structures per family, itself capped for query cost, while Foldseek searches the full PDB structural index) — this does not mean they're unrelated, only that they weren't in that capped sample; treat both lists as complementary, partial views, not a contradiction

Source: sequence-based: Pfam family co-membership among cached PDB reference structures (sequence-based); Foldseek vs local PDB structural database (structure-based)

8. Limitations & data provenance

Auto-populated from each section's own status — not hand-maintained.

Section	Status	Detail
Family classification	returned data	
Known ligand precedent	returned data	
Interaction fingerprints	no self-matching ligand-bound structur...	8 ligand-bound structure(s) exist for ...
Functional context (UniProt + ClinVar)	returned data	1 variant position(s) exceeded the can...
Conservation	returned data	computed over a sample of 40/309 seed ...
Structural analysis	returned data	3 pocket cluster(s) in the customer-vi...
Similar known proteins	returned data	
Similar known proteins (structure-base...	returned data	

1 of 8 sections did not return data this run: Interaction fingerprints.