

AIGR Deep Research — Wheat

A0A3B6RKV1 (JmjC-domain protein): catalytic competence and transfer of Arabidopsis JMJ22 developmental roles

Gene: *Triticum aestivum* A0A3B6RKV1 (UniProt A0A3B6RKV1, 511 aa; "JmjC domain-containing protein", ProtNLM name) **Hypothesis slug:** prediction-jmj22-developmental-roles **Focus type:** computational_prediction **Terms in scope:** GO:0010099 regulation of photomorphogenesis; GO:0010476 gibberellin-mediated signaling; GO:0010114 response to red light; GO:0010030 positive regulation of seed germination

Executive Judgment

Verdict: Partially supported — split decision.

- **Family / subfamily assignment: SUPPORTED (and the seed's own labelling should be corrected).** A0A3B6RKV1 is a genuine wheat co-ortholog of Arabidopsis **JMJ22** (and its redundant partner JMJ20). Global alignment gives **62.3 % identity** to JMJ22 (Q67XX3), with an **identical F-box + JmjC(Cupin_8) domain architecture** and identical InterPro/Pfam/PANTHER signatures. This clade is the plant **JMJD6-type histone arginine demethylase** group — **not** a KDM4/KDM5/JARID histone *lysine* demethylase, and **not** a KDM7/"PKDM7" H3K9 demethylase. The seed's "KDM/JARID subfamily ... JMJ22/PKDM7D" framing mislabels the family: the correct assignment is JMJD6-related F-box+JmjC arginine demethylase.
- **Catalytic competence: SUPPORTED at the residue AND structure level.** The wheat protein retains the complete JmjC Fe(II) 2-His-1-carboxylate facial triad. The three UniProt-annotated active-site residues of JMJ22 (**His324, Asp326, His407**) map by alignment to conserved **His330, Asp332, His413** in wheat (HxD...H). In the AlphaFold model (AF-A0A3B6RKV1-F1, v6) these residues are high-confidence (pLDDT 95–98) and their

coordinating side-chain atoms **converge into a single metal-binding pocket in 3D** (cluster radius 2.82 Å; His–His N–N 3.11 Å). It is therefore predicted to be a catalytically competent 2-oxoglutarate/Fe(II) dioxygenase.

- **Transfer of the four developmental BP terms: NOT supported / OVER-ANNOTATED.** In Arabidopsis these four terms are all **IMP** (mutant-phenotype) annotations arising from one specific study (Cho et al. 2012,

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) in which **JMJ20 and JM22 act redundantly** within a defined module: phytochrome B → (repressor SOMNUS) → JM20/JM22 → removal of H4R3me2 at **GA3ox1/GA3ox2** → GA biosynthesis → germination. These are **context-dependent, redundant-pair, dicot seed-biology phenotypes**. No wheat functional study exists (targeted PubMed search returned none). Projecting photomorphogenesis / red-light / GA-signaling / seed-germination BP terms onto the wheat protein by ProtNLM orthology alone is unwarranted.

Bottom line for the curator: keep/allow the **molecular-function** inference (histone demethylase / oxidoreductase / metal-ion binding) at ISS/IBA strength; **do not** carry over the four Arabidopsis-specific developmental **biological-process** terms to A0A3B6RKV1 without wheat evidence.

Evidence Matrix

#	Citation	Evidence type	Supports/ Refutes/ Qualifies	Claim tested	Key finding
1	UniProt A0A3B6RKV1 (TrEMBL) + this run's NW alignment	Structural/ evolutionary + computational	Supports (family)	Is wheat protein an ortholog of JMJ22?	62.3 % global identity to JMJ22; identical F-box(89–135)+JmjC(284–445, Cupin_8) architecture
2	This run's alignment mapping of UniProt Q67XX3 binding sites	Structural/ evolutionary + computational	Supports (catalysis)	Are Fe(II)/2-OG active-site residues retained?	JMJ22 His324/Asp326/His407 ↔ v His330/Asp332/His413 (complete HxD...H facial triad)
2b	AlphaFold DB AF-A0A3B6RKV1-F1 (v6), this run's geometry analysis	Structural (predicted) + computational	Supports (catalysis)	Does the triad assemble into a metal site in 3D?	His330/Asp332/His413 pLDDT 95% coordinating atoms converge within 2.82 Å radius (His–His N–N 3.11 Å)
3	InterPro IPR050910 / IPR041667; PANTHER PTHR12480:SF21; Pfam PF13621	Database	Qualifies	Which subfamily?	Both wheat & JMJ22 fall in JMJD6_ArgDemeth/LysHydrox (Cupin_8), PANTHER SF21 — arg demethylase/hydroxylase clade, KDM4/5/JARID
3b	This run's Smith-Waterman panel vs 8 reviewed Arabidopsis JMJ proteins	Structural/ evolutionary + computational	Supports (subfamily)	Is wheat closer to JMJ22 than to lysine-demethylase JMJs?	Only JMJ22 gives an extended H (411 aa, 67.4% id); JMJ14/REF6/E JMJ25/JMJ18 give only 6–9 aa spr HSPs (their 40–53% global value length artifacts)

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4	Cho et al. 2012, P 22483719	Mutant phenotype / direct assay (Arabidopsis)	Supports (Arabidopsis) / Refutes transfer	Origin of the 4 developmental terms	JMJ20+JMJ22 redundantly demethylate H4R3me2 at GA3ox downstream of PHYB/SOMNUS to promote germination
5	UniProt Q67XX3 GO evidence codes	Database	Qualifies	Strength of source annotations	GO:0010099/0010476/0010114/0010030 are all IMP ; histone demethylase activity is IGI
6	PubMed (targeted search, this run)	Absence of evidence	Refutes transfer	Any wheat functional data?	No <i>T. aestivum</i> JMJ/JmjC demethylase functional study found

GO Curation Implications (leads — require curator verification)

- **Molecular function (retain, at ISS/IBA):** histone demethylase activity (GO:0032452) and/or the more specific *histone H4R3 demethylase*-type activity is a defensible orthology-based inference given 62.3 % identity and an intact facial triad. [metal ion binding](#) (GO:0046872) and [oxidoreductase activity](#) (GO:0016491) are also supported. Prefer the demethylase term over a bare "protein binding."
- **Biological process (do NOT transfer):** GO:0010099, GO:0010476, GO:0010114, GO:0010030 should be **removed / not asserted** for A0A3B6RKV1. These are Arabidopsis IMP phenotypes

of a redundant gene pair in a specific PHYB→GA3ox module. At most, mark as "not core / context-specific in Arabidopsis" with no wheat support.

- **Cellular component:** nucleus (GO:0005634) is a reasonable IBA-level carry-over consistent with a chromatin-modifying enzyme.
 - **Name correction lead:** the ProtNLM/seed framing "KDM/JARID ... PKDM7D" is inaccurate; the protein is a **JMJD6-type F-box + JmjC arginine demethylase (JMJ20/JMJ22 clade)**.
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Mechanistic Scope

Immediate molecular function under test: a 2-OG/Fe(II)-dependent JmjC dioxygenase acting as a histone **arginine** demethylase (Arabidopsis substrate H4R3me2). This is the direct gene-product activity and is supported by residue conservation.

Downstream / not-direct: GA biosynthesis (GA3ox1/2 derepression), phytochrome-B/red-light responsiveness, photomorphogenesis, and seed germination are **pathway and developmental consequences** observed in Arabidopsis loss/redundancy genetics — not properties of the enzyme's catalytic chemistry. They require the specific SOMNUS/PHYB regulatory wiring and the GA3ox target loci, none of which is established in wheat.

Conflicts and Alternatives

- **Redundancy confound:** the Arabidopsis phenotype requires *jmj20 jmj22* double mutants; single-gene function is partly masked. A single wheat ortholog cannot be assumed to reproduce the double-mutant phenotype.
- **Substrate ambiguity:** the JMJD6/Cupin_8 clade includes arginine demethylases *and* lysyl hydroxylases (IPR050910). The wheat enzyme's true substrate (H4R3me2 vs. hydroxylation vs. other) is not experimentally fixed.
- **Paralog/homeolog complexity in wheat:** hexaploid wheat has A/B/D homeologs and likely several JMJ20/22-like paralogs; A0A3B6RKV1 may be one of several, further diluting any 1:1 functional transfer.
- **Annotation carry-over:** the four BP terms likely propagate from the Arabidopsis record via ProtNLM/orthology — a classic frequency-bias/over-annotation route.

Knowledge Gaps

1. **Substrate/activity in vitro** — checked residues only; no biochemical assay. Resolve with recombinant enzyme + H4R3me2 (and lysine/hydroxylation) substrates.
2. **Wheat expression/phenotype** — no wheat data. Resolve with germination-stage expression (light/GA treatments) and CRISPR/TILLING knockouts across homeologs.
3. **Regulatory module conservation** — is there a wheat SOMNUS/PHYB→JMJ→GA3ox circuit? Resolve by checking wheat SOMNUS and GA3ox orthologs and JMJ chromatin targets.
4. **2-OG binding beyond the triad** — the C5-carboxylate-binding Lys/Ser/Thr were not individually validated here; a full active-site model (AlphaFold + comparison to a solved KDM) would strengthen the catalytic call.

Discriminating Tests

- Recombinant A0A3B6RKV1 demethylase assay on H4R3me1/2 ($\pm$ Fe/2-OG dependence; His→Ala triad mutant as negative control).
- AlphaFold-DB model overlay onto a JmjC catalytic core to confirm triad geometry and 2-OG pocket.
- Wheat homeolog knockout germination phenotyping under R/FR light and GA/paclobutrazol.
- Phylogenetic tree of wheat JMJ + Arabidopsis JMJ11–33 to confirm placement in the JMJ20/22 clade and count wheat co-orthologs.

Curation Leads (verify before applying)

- **Reference to attach:**

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— snippet: *"the histone arginine demethylases, JMJ20 and JMJ22, act redundantly as positive regulators of seed germination"* (family/MF support); and *"upon PHYB activation, JMJ20/JMJ22 are derepressed, resulting in increased gibberellic acid levels through the removal of repressive histone arginine methylations at GA3ox1/GA3ox2"* (shows developmental terms are module-/species-specific).

- **Candidate MF term:** GO:0032452 histone demethylase activity (ISS from JMJ22), with metal-ion binding / oxidoreductase; avoid "protein binding."
- **Action change:** reject/withhold the four developmental BP terms (GO:0010099, GO:0010476, GO:0010114, GO:0010030) for the wheat entry — flag as Arabidopsis-specific IMP not transferable.
- **Suggested curator question:** are there wheat expression or mutant data linking this locus to germination/GA before any BP assertion?

Provenance: UniProt REST records for A0A3B6RKV1 and Q67XX3; Needleman-Wunsch global alignment (62.3 % identity) with active-site residue mapping (His330/Asp332/His413 ↔ JMJ22 His324/Asp326/His407); AlphaFold DB model AF-A0A3B6RKV1-F1 (v6) triad geometry (pLDDT 95–98; coordinating atoms converge within 2.82 Å); InterPro/Pfam/PANTHER domain signatures;

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Analyses executed in this run (Iterations 1–2).

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