KRAS IP Portfolio Analysis

Executive Summary

This report applies the rDNA.ai four-stage KC scoring pipeline to 1,777 recent USPTO biopharma patents in the KRAS / RAS-pathway target class, including 154 patents directly classified into the KRAS_RAS_Pathway therapeutic area. Each patent is scored on six Key Component (KC) dimensions on a 1–5 scale and aggregated into a four-scheme ensemble (Meta Baseline / AbbVie / Amgen / Genentech weighting), which determines the patent's investment-grade tier.

Portfolio-level results are summarized below by therapeutic-area cut, by top assignee, and at the patent level for the top decile after a V2 pairwise-tournament calibration. The KRAS_RAS_Pathway cut is the strongest in the corpus (mean ensemble 4.482; 121 of 154 patents at TIER 1 PREMIUM), reflecting the concentrated composition-of-matter and platform IP held by Revolution Medicines, Mirati/BMS, Ranok, Treeline, Affini-T, Astellas, Genentech/Roche, CureVac, Incyte, Alterome, and others.

This is one of an expanding set of target-class KC Quality Analyses generated from a four-stage KC scoring pipeline applied to all USPTO biopharma issued and published patents assigned to each of the 25 most active global biopharma companies from January 2020 through April 2026. A parallel Top-25 Consolidated cross-portfolio analysis covering all 14,552 company patents in the biopharma cohort is available upon request.

Key Component (KC) Scoring Framework

Each patent is scored on six Key Component (KC) dimensions on a 1–5 scale. The ensemble score is the mean of the six dimensions (with confidence and standard deviation tracked alongside).

- **KC1** measures abstract and therapeutic specificity: target specificity, therapeutic positioning, structural disclosure, and technical differentiation.
- **KC2** measures independent-claim quality: scope, structure, enforceability, and enablement vulnerability.
- **KC3** measures dependent-claim quality: fallback hierarchy, embodiment coverage, prosecution flexibility, and structural diversity.

- **KC4** measures novelty and differentiation: prior-art positioning, inventive-step quality, and field positioning.
- **KC5** measures specification enablement: enablement gap, structure-function insight, data breadth, and translational completeness.
- **KC6** measures working examples: working/prophetic example quality, structural diversity, experimental rigor, and in vivo / translational validation.

Portfolio-Level Metrics

- Total Biopharma patents scored: 1777 most recent KRAS patent publications retrieved via a USPTO patent publication search carried out in April 2026
- Patents dropped (batch_12_D — Sonnet workaround, policy-block on rescore): 5
- Average KC scores — KC1: 3.24 KC2: 3.54 KC3: 3.53 KC4: 3.54 KC5: 3.72 KC6: 3.27
- Average ensemble mean across portfolio: 3.468

Investment-grade distribution:

- TIER_1_PREMIUM: 539
- TIER_1_HIGH: 319
- TIER_2_MODERATE: 476
- TIER_3_SPECULATIVE: 443

Top Assignees

Rank	Assignee	Patent Count
1	GUARDANT HEALTH	31
2	UNIVERSITY OF CALIFORNIA SAN DIEGO UCSD	30
3	AMGEN	26
4	MIRATI	26
5	FOUNDATION MEDICINE	25
6	REVOLUTION MEDICINES	23

7	MASSACHUSETTS INSTITUTE OF TECHNOLOGY; BROAD INSTITUTE	21
8	UNIVERSITY OF TEXAS SYSTEM	20
9	SINGULAR GENOMICS SYSTEMS	19
10	GILEAD	17
11	LELAND STANFORD JUNIOR UNIVERSITY	15
12	CHUGAI	15
13	INDIVIDUAL	14
14	MASSACHUSETTS INSTITUTE OF TECHNOLOGY; BROAD INSTITUTE ; HARVARD UNIVERSITY	13
15	GENENTECH	13

Therapeutic Area Analysis (n ≥ 5 patents)

Sixteen therapeutic areas have at least 5 patents and receive their own KC breakdown. For each area: average KC1-KC6 (1-5 scale), average ensemble mean, average TA-weighted score, and tier distribution. KRAS_RAS_Pathway, CAR_T_CellTherapy, Gene_Therapy_Editing, Immunotherapy_Checkpoint, and Protein_Degrader_PROTAC carry small TA multipliers (1.02-1.05).

Therapeutic Area	N	KC1	KC2	KC3	KC4	KC5	KC6	Ens Mean	TA-W	T1 Prem	T1 High	T2 Mod	T3 Spec
Other_Therapeutic	763	2.94	3.4	3.38	3.32	3.62	3.1	3.277	3.277	182	125	216	240
Oncology_Other	287	3.14	3.33	3.45	3.36	3.48	3.07	3.309	3.309	50	53	99	85
KRAS_RAS_Pathway	154	4.72	4.28	4.12	4.7	4.37	4.53	4.482	4.706	121	25	3	5
Antibody_Biologic	121	3.37	3.88	3.81	3.71	4.09	3.39	3.7	3.7	51	23	33	14
CNS_Neurological	110	2.75	3.17	3.18	3.12	3.35	2.76	3.054	3.054	20	16	33	41
Small_Molecule_Kinase	72	3.93	3.9	3.86	3.89	3.99	3.74	3.896	3.896	29	22	19	2
Gene_Therapy_Editing	47	3.64	4.02	4	4.23	4.32	3.66	3.987	4.067	21	15	9	2
RNA_Therapeutics	40	3	3.45	3.42	3.58	3.75	2.98	3.371	3.371	7	9	11	13
CAR_T_CellTherapy	29	3.69	3.9	3.9	3.83	4.03	3.48	3.818	3.894	12	9	5	3
Immunotherapy_Checkpoint	29	3.55	3.66	3.59	3.76	3.86	3.45	3.653	3.726	12	5	6	6
Platform_Delivery	27	3	3.56	3.56	3.33	3.59	3.22	3.357	3.357	6	4	12	5
Vaccine_Immunization	24	3.46	3.38	3.5	3.67	3.92	3.33	3.534	3.534	9	3	8	4
Microbiome_Bacterial	24	2.83	3.21	3.42	3.12	3.25	3.17	3.137	3.137	2	5	9	8

Protein_Degrader_PROTAC	23	3.57	3.96	3.7	4	4.22	3.61	3.841	3.956	12	4	4	3
Stem_Cell_Regenerative	12	2.58	3.25	3.33	3	2.92	2.75	2.983	2.983	1	1	5	5
Inflammation_Autoimmune	11	3	3.18	3.18	3.09	3.45	3	3.134	3.134	4	0	2	5

Therapeutic Area Narratives

Other_Therapeutic (n=763)

Average ensemble mean: 3.277. Highest KC: KC5 (avg 3.62). Lowest KC: KC1 (avg 2.94). TIER_1_PREMIUM: 182, TIER_1_HIGH: 125. Top 3 patents (by TA-weighted score): US20260071236A1; US12571005B2; US20260062425A1.

Oncology_Other (n=287)

Average ensemble mean: 3.309. Highest KC: KC5 (avg 3.48). Lowest KC: KC6 (avg 3.07). TIER_1_PREMIUM: 50, TIER_1_HIGH: 53. Top 3 patents (by TA-weighted score): US12545670B2; US20250332239A1; US20250268894A1.

KRAS_RAS_Pathway (n=154)

Average ensemble mean: 4.482. Highest KC: KC1 (avg 4.72). Lowest KC: KC3 (avg 4.12). TIER_1_PREMIUM: 121, TIER_1_HIGH: 25. Top 3 patents (by TA-weighted score): US20260070929A1; US12565476B2; US20260042740A1.

Antibody_Biologic (n=121)

Average ensemble mean: 3.7. Highest KC: KC5 (avg 4.09). Lowest KC: KC1 (avg 3.37). TIER_1_PREMIUM: 51, TIER_1_HIGH: 23. Top 3 patents (by TA-weighted score): US20260098098A1; US12594325B2; US12508311B2.

CNS_Neurological (n=110)

Average ensemble mean: 3.054. Highest KC: KC5 (avg 3.35). Lowest KC: KC1 (avg 2.75). TIER_1_PREMIUM: 20, TIER_1_HIGH: 16. Top 3 patents (by TA-weighted score): US12571049B2; US20260055387A1; US20250257396A1.

Small_Molecule_Kinase (n=72)

Average ensemble mean: 3.896. Highest KC: KC5 (avg 3.99). Lowest KC: KC6 (avg 3.74). TIER_1_PREMIUM: 29, TIER_1_HIGH: 22. Top 3 patents (by TA-weighted score): US12594349B2; US12570672B2; US12539305B2.

Gene_Therapy_Editing (n=47)

Average ensemble mean: 3.987. Highest KC: KC5 (avg 4.32). Lowest KC: KC1 (avg 3.64). TIER_1_PREMIUM: 21, TIER_1_HIGH: 15. Top 3 patents (by TA-weighted score): US20260071198A1; US20260071237A1; US12570972B2.

RNA_Therapeutics (n=40)

Average ensemble mean: 3.371. Highest KC: KC5 (avg 3.75). Lowest KC: KC6 (avg 2.98). TIER_1_PREMIUM: 7, TIER_1_HIGH: 9. Top 3 patents (by TA-weighted score): US12552743B2; US20250353872A1; US20260022378A1.

CAR_T_CellTherapy (n=29)

Average ensemble mean: 3.818. Highest KC: KC5 (avg 4.03). Lowest KC: KC6 (avg 3.48). TIER_1_PREMIUM: 12, TIER_1_HIGH: 9. Top 3 patents (by TA-weighted score): US12576135B2; US20250250318A1; US20260008832A1.

Immunotherapy_Checkpoint (n=29)

Average ensemble mean: 3.653. Highest KC: KC5 (avg 3.86). Lowest KC: KC6 (avg 3.45). TIER_1_PREMIUM: 12, TIER_1_HIGH: 5. Top 3 patents (by TA-weighted score): US12570745B2; US20250382365A1; US12479917B2.

Platform_Delivery (n=27)

Average ensemble mean: 3.357. Highest KC: KC5 (avg 3.59). Lowest KC: KC1 (avg 3.0). TIER_1_PREMIUM: 6, TIER_1_HIGH: 4. Top 3 patents (by TA-weighted score): US20250257342A1; US20260069538A1; US20250353906A1.

Vaccine_Immunization (n=24)

Average ensemble mean: 3.534. Highest KC: KC5 (avg 3.92). Lowest KC: KC6 (avg 3.33). TIER_1_PREMIUM: 9, TIER_1_HIGH: 3. Top 3 patents (by TA-weighted score): US20250213643A1; US20250269002A1; US12582609B2.

Microbiome_Bacterial (n=24)

Average ensemble mean: 3.137. Highest KC: KC3 (avg 3.42). Lowest KC: KC1 (avg 2.83). TIER_1_PREMIUM: 2, TIER_1_HIGH: 5. Top 3 patents (by TA-weighted score): US12569439B2; US20250382613A1; US20260077000A1.

Protein_Degrader_PROTAC (n=23)

Average ensemble mean: 3.841. Highest KC: KC5 (avg 4.22). Lowest KC: KC1 (avg 3.57). TIER_1_PREMIUM: 12, TIER_1_HIGH: 4. Top 3 patents (by TA-weighted score): US20250276981A1; US12570626B2; US20250382278A1.

Stem_Cell_Regenerative (n=12)

Average ensemble mean: 2.983. Highest KC: KC3 (avg 3.33). Lowest KC: KC1 (avg 2.58). TIER_1_PREMIUM: 1, TIER_1_HIGH: 1. Top 3 patents (by TA-weighted score): US12472209B2; US12517112B2; US12379372B2.

Inflammation_Autoimmune (n=11)

Average ensemble mean: 3.134. Highest KC: KC5 (avg 3.45). Lowest KC: KC1 (avg 3.0). TIER_1_PREMIUM: 4, TIER_1_HIGH: 0. Top 3 patents (by TA-weighted score): US20250296938A1; US20250289825A1; US12459951B2.

Top-Decile Calibration: Pairwise Tournament Results

Rank	Patent	Assignee	KC1	KC2	KC3	KC4	KC5	KC6	Cal Ens
1	US20260042740A1	REVOLUTION MEDICINES	5	5	5	5	5	5	5.0
2	US20260028353A1	REVOLUTION MEDICINES	5	5	4	5	5	5	4.85
3	US20260035389A1	MIRATI	5	5	4	5	4	5	4.748
4	US20260042764A1	LAWRENCE LIVERMORE NATIONAL SECURIT	5	5	5	4	5	4	4.69
5	US20260070929A1	RANOK HANGZHOU	5	4	5	5	4	4	4.612
6	US20260022132A1	TREELINE	5	5	4	4	5	4	4.54
7	US20260027208A1	AFFINI T	5	4	4	5	4	4	4.463

8	US20260021097A1	GENENTECH ; HOFFMANN LA ROCHE	5	4	5	4	4	5	4.447
9	US12528855B2	CUREVAC SE	5	5	4	4	4	4	4.438
10	US20260022118A1	UNIVERSITY OF TEXAS SYSTEM	4	5	5	4	4	4	4.362
11	US20260042771A1	ASTELLAS PHARMA	5	4	4	5	3	4	4.36
12	US20260034126A1	INCYTE	4	5	5	3	4	4	4.125
13	US12528828B2	ALTEROME	4	5	4	3	5	4	4.078
14	US12565476B2	REVOLUTION MEDICINES	4	4	3	4	4	4	3.85
15	US12527795B2	MIRATI	4	4	4	3	4	4	3.763

Top-Decile Assignee Ranking

Rank	Assignee	Count	Best Patent Rank	Avg Rank	Avg Score
1	REVOLUTION MEDICINES	3	1	5.67	4.567
2	MIRATI	2	3	9.0	4.255
3	LAWRENCE LIVERMORE NATIONAL SECURITY ; LEIDOS	1	4	4.0	4.69
4	RANOK HANGZHOU	1	5	5.0	4.612
5	TREELINE	1	6	6.0	4.54
6	AFFINI T	1	7	7.0	4.463

7	GENENTECH ; HOFFMANN LA ROCHE	1	8	8.0	4.447
8	CUREVAC SE	1	9	9.0	4.438
9	UNIVERSITY OF TEXAS SYSTEM	1	10	10.0	4.362
10	ASTELLAS PHARMA	1	11	11.0	4.36
11	INCYTE	1	12	12.0	4.125
12	ALTEROME	1	13	13.0	4.078

Bottom-Decile Assignee Ranking

Bottom-decile assignees are ranked by frequency in the bottom KRAS_RAS_Pathway decile, then by weaker average original ensemble score.

Rank	Assignee	Count	Avg Original Score	Weakest Score
1	AMGEN	4	3.489	2.965
2	KHR BIOTEC	2	3.535	3.535
3	INDIVIDUAL	1	2.535	2.535
4	ASCENTAWITS	1	2.788	2.788
5	KOREA INSTITUTE OF RADIOLOGICAL AND MEDICAL	1	3.123	3.123
6	TEXAS MD ANDERSON CANCER A STATE INSTITUTION OF HIGHER	1	3.225	3.225
7	EMORY UNIVERSITY	1	3.462	3.462

8	TOSK	1	3.535	3.535
9	REVOLUTION MEDICINES	1	3.752	3.752
10	CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE CNRS; INST	1	3.76	3.76
11	MIRATI	1	3.788	3.788

Top 15 Tournament Calibration KRAS Patents

#1 US20260042740A1 - REVOLUTION MEDICINES

RAS inhibitors

Calibrated KC profile: KC1=5, KC2=5, KC3=5, KC4=5, KC5=5, KC6=5; calibrated ensemble=5.0; pairwise record=14-0.

Revolution macrocyclic RAS(ON) inhibitor filing remained the cleanest top-decile winner: direct pan-RAS/KRAS positioning, broad composition-of-matter scope, clinically anchored RMC-class commercial relevance, deep Markush hierarchy, and strong enablement support.

#2 US20260028353A1 - REVOLUTION MEDICINES

MACROCYCLIC RAS INHIBITORS

Calibrated KC profile: KC1=5, KC2=5, KC3=4, KC4=5, KC5=5, KC6=5; calibrated ensemble=4.85; pairwise record=13-1.

Second Revolution macrocyclic RAS filing has exceptional platform value and specification depth; the only calibration haircut is dependent-claim hierarchy because the active claim count is denser than it is numerous.

#3 US20260035389A1 - MIRATI

Tetrahydropyridopyrimidine pan-KRAS inhibitors

Calibrated KC profile: KC1=5, KC2=5, KC3=4, KC4=5, KC5=4, KC6=5; calibrated ensemble=4.748; pairwise record=12-2.

Mirati/BMS pan-KRAS inhibitor claims are highly enforceable and commercially validated, but score just behind Revolution because the file is more follow-on to the approved adagrasib franchise and has less disclosed breadth than the leading RevMed packets.

#4 US20260042764A1 - LAWRENCE LIVERMORE NATIONAL SECURITY ; LEIDOS BIOMEDICAL RESEARCH ; THERAS

Compositions and methods for inhibition of KRAS

Calibrated KC profile: KC1=5, KC2=5, KC3=5, KC4=4, KC5=5, KC6=4; calibrated ensemble=4.69; pairwise record=11-3.

The Lawrence Livermore/Leidos/Theras pan-KRAS filing has extraordinary claim depth and enablement architecture, but pairwise loses to the top three because commercial execution and field-defining clinical validation are less clear.

#5 US20260070929A1 - RANOK HANGZHOU

METHODS AND COMPOSITIONS FOR MODULATING KRAS(G12D)

Calibrated KC profile: KC1=5, KC2=4, KC3=5, KC4=5, KC5=4, KC6=4; calibrated ensemble=4.612; pairwise record=10-4.

Ranok's CHAMP KRAS(G12D) degrader is mechanistically differentiated and strategically strong; pairwise calibration places it below the broadest pan-RAS composition-of-matter leaders but above narrower lifecycle, vaccine, and cell-therapy assets.

#6 US20260022132A1 - TREELINE

SPIROCYCLIC DIHYDROPYRANOPYRIMIDINE KRAS INHIBITORS

Calibrated KC profile: KC1=5, KC2=5, KC3=4, KC4=4, KC5=5, KC6=4; calibrated ensemble=4.54; pairwise record=9-5.

Treeline's spirocyclic KRAS inhibitor packet has excellent specification scale and composition claims, but the crowded KRAS small-molecule landscape pulls novelty below the RevMed/Mirati leaders.

#7 US20260027208A1 - AFFINI T

HOST CELLS BEARING KRAS BINDING PROTEIN AND KNOCKOUT OF ENDOGENOUS TCR AND METHODS OF USE THEREOF

Calibrated KC profile: KC1=5, KC2=4, KC3=4, KC4=5, KC5=4, KC6=4; calibrated ensemble=4.463; pairwise record=8-6.

Affini-T's KRAS G12D TCR-T plus endogenous TCR knockout is highly differentiated, but HLA restriction and cell-therapy execution narrow the enforceable commercial footprint relative to small-molecule pan-RAS filings.

#8 US20260021097A1 - GENENTECH ; HOFFMANN LA ROCHE

COMBINATION THERAPIES COMPRISING A KRAS G12C INHIBITOR AND PEMBROLIZUMAB

Calibrated KC profile: KC1=5, KC2=4, KC3=5, KC4=4, KC5=4, KC6=5; calibrated ensemble=4.447; pairwise record=7-7.

Genentech/Roche divarasib-pembrolizumab-steroid scheduling is extremely commercial and well laddered, but it is calibrated below de novo composition-of-matter assets because it is a combination and toxicity-mitigation lifecycle filing.

#9 US12528855B2 - CUREVAC SE

KRAS variant mRNA molecules

Calibrated KC profile: KC1=5, KC2=5, KC3=4, KC4=4, KC5=4, KC6=4; calibrated ensemble=4.438; pairwise record=6-8.

CureVac's issued KRAS variant mRNA vaccine patent has strong structural construct and formulation coverage across major KRAS variants, offset by translational uncertainty for therapeutic KRAS vaccines.

#10 US20260022118A1 - UNIVERSITY OF TEXAS SYSTEM

HETEROCYCLIC COMPOUNDS AS NRAS INHIBITORS

Calibrated KC profile: KC1=4, KC2=5, KC3=5, KC4=4, KC5=4, KC6=4; calibrated ensemble=4.362; pairwise record=5-9.

UT/MD Anderson NRAS inhibitor claims are structurally deep and well layered; calibration lowers KRAS-portfolio priority because the target is NRAS rather than KRAS despite high standalone RAS-family patent quality.

#11 US20260042771A1 - ASTELLAS PHARMA

Heterocyclic compound for inducing degradation of G12V mutant KRAS protein

Calibrated KC profile: KC1=5, KC2=4, KC3=4, KC4=5, KC5=3, KC6=4; calibrated ensemble=4.36; pairwise record=4-10.

Astellas G12V-selective KRAS degrader wins on novelty but loses several pairwise comparisons on specification size, data breadth, and translational completeness.

#12 US20260034126A1 - INCYTE

KRAS INHIBITORS

Calibrated KC profile: KC1=4, KC2=5, KC3=5, KC4=3, KC5=4, KC6=4; calibrated ensemble=4.125; pairwise record=3-11.

Incyte's KRAS inhibitor filing has broad structural coverage, but the pairwise pass found less product-specific differentiation than the higher-ranked pan-KRAS assets.

#13 US12528828B2 - ALTEROME

Substituted pyrido[4,3-d]pyrimidines as KRAS modulators

Calibrated KC profile: KC1=4, KC2=5, KC3=4, KC4=3, KC5=5, KC6=4; calibrated ensemble=4.078; pairwise record=2-12.

Alterome has very strong specification depth around a validated KRAS scaffold, but novelty is moderated by the crowded pyridopyrimidine KRAS inhibitor space.

#14 US12565476B2 - REVOLUTION MEDICINES

2,5-disubstituted 3-methyl pyrazines and 2,5,6-trisubstituted 3-methyl pyrazines as allosteric SHP2 inhibitors

Calibrated KC profile: KC1=4, KC2=4, KC3=3, KC4=4, KC5=4, KC6=4; calibrated ensemble=3.85; pairwise record=1-13.

Revolution's SHP2 inhibitor patent is valuable for KRAS combinations, but it is pathway-adjacent rather than direct KRAS/RAS inhibitor composition-of-matter and has fewer active dependent claims.

#15 US12527795B2 - MIRATI

Compositions of adagrasib and mTOR inhibitors and methods of treatment therewith

Calibrated KC profile: KC1=4, KC2=4, KC3=4, KC4=3, KC5=4, KC6=4; calibrated ensemble=3.763; pairwise record=0-14.

Mirati's adagrasib-mTOR combination is commercially useful lifecycle IP around an approved drug, but pairwise calibration placed it last among the top decile because novelty and field-positioning are narrower than new composition-of-matter filings.

Methodology

The initial KRAS analysis contained 1,777 scored biopharma patents, including 154 KRAS_RAS_Pathway patents. The top-decile calibration cohort was operationalized as the 15 patents in KRAS_Top15_Predictions.csv, matching roughly 10% of the KRAS_RAS_Pathway group.

The original top-decile plateau assigned all 15 patents KC1–KC6=5 and TA-weighted score=5.25. The V2 calibration intentionally re-read the top-decile patent packets against the V2 rubric and ran a pairwise tournament to separate composition-of-matter platform assets from narrower lifecycle, combination, pathway-adjacent, or less-enabled filings.

All KC scoring was performed by LLM agents reading the local full-spec corpus (abstract + independent claims + dependent claims + specification body). Ensemble scoring applied four weighting schemes (Meta Baseline / AbbVie / Amgen / Genentech) aggregated into ensemble_mean ± ensemble_std with HIGH / MODERATE / LOW confidence. Tier thresholds are absolute (TIER 1 PREMIUM ≥ 4.5; TIER 1 HIGH 4.0–4.49; TIER 2 MODERATE 3.0–3.99; TIER 3 SPECULATIVE < 3.0).