

Research Tools Completeness Score Report

NF-OSI

2025-11-07

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Executive Summary

This report provides a comprehensive analysis of the completeness scores for research tools and biobanks in the NF-OSI database. The scoring system evaluates resources across multiple dimensions:

- **Availability** (30 points): Biobank URL, vendor/developer info, RRID, and DOI
- **Critical Info** (30 points): Type-specific essential fields
- **Other Info** (15 points): Type-specific additional fields
- **Observations** (25 points): Scientific characterizations with DOI weighting

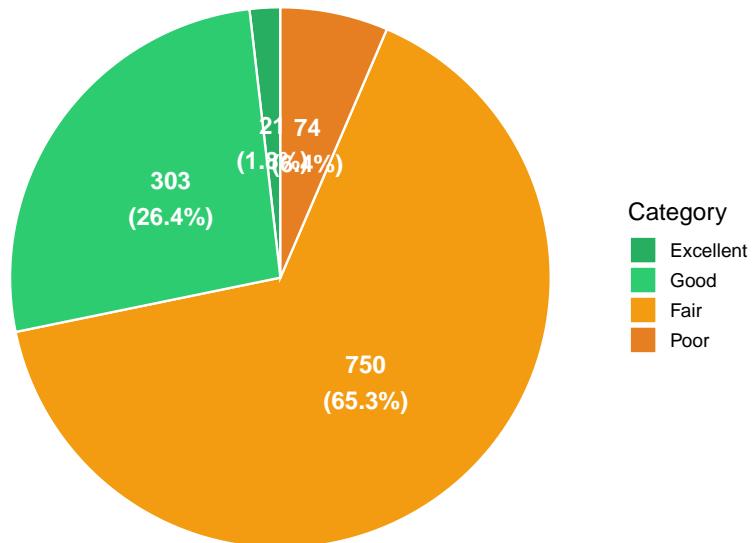
Total Maximum Score: 100 points

- **Excellent:** 80+ points
 - **Good:** 60+ points
 - **Fair:** 40+ points
 - **Poor:** 20+ points
 - **Minimal:** <20 points
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Completeness Category Distribution

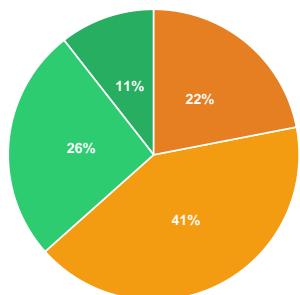
Overall Distribution of Completeness Categories

Total: 1148 resources

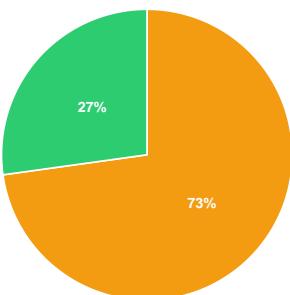


Completeness Category Distribution by Resource Type

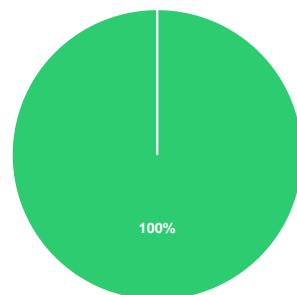
Animal Model (n=123)



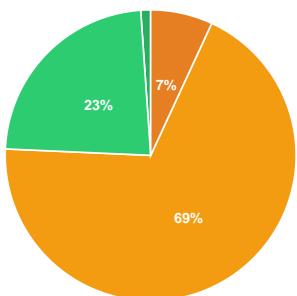
Antibody (n=261)



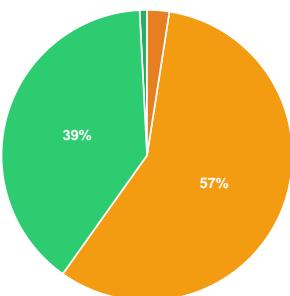
Biobank (n=4)



Cell Line (n=638)



Genetic Reagent (n=122)

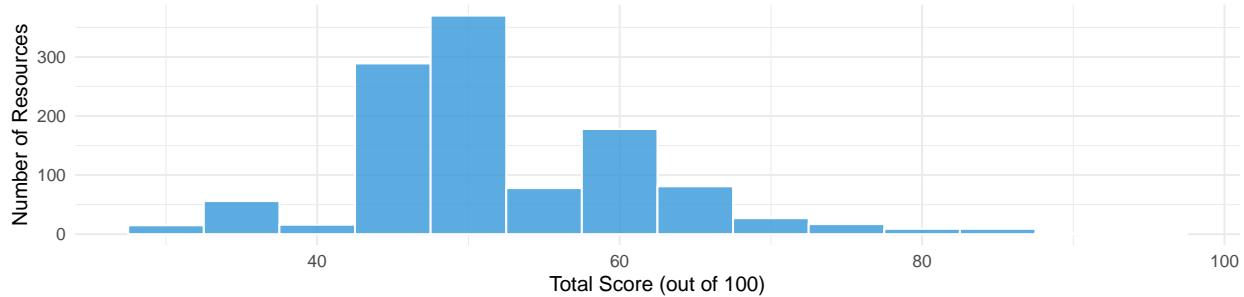


Category Excellent Good Fair Poor

Score Distribution

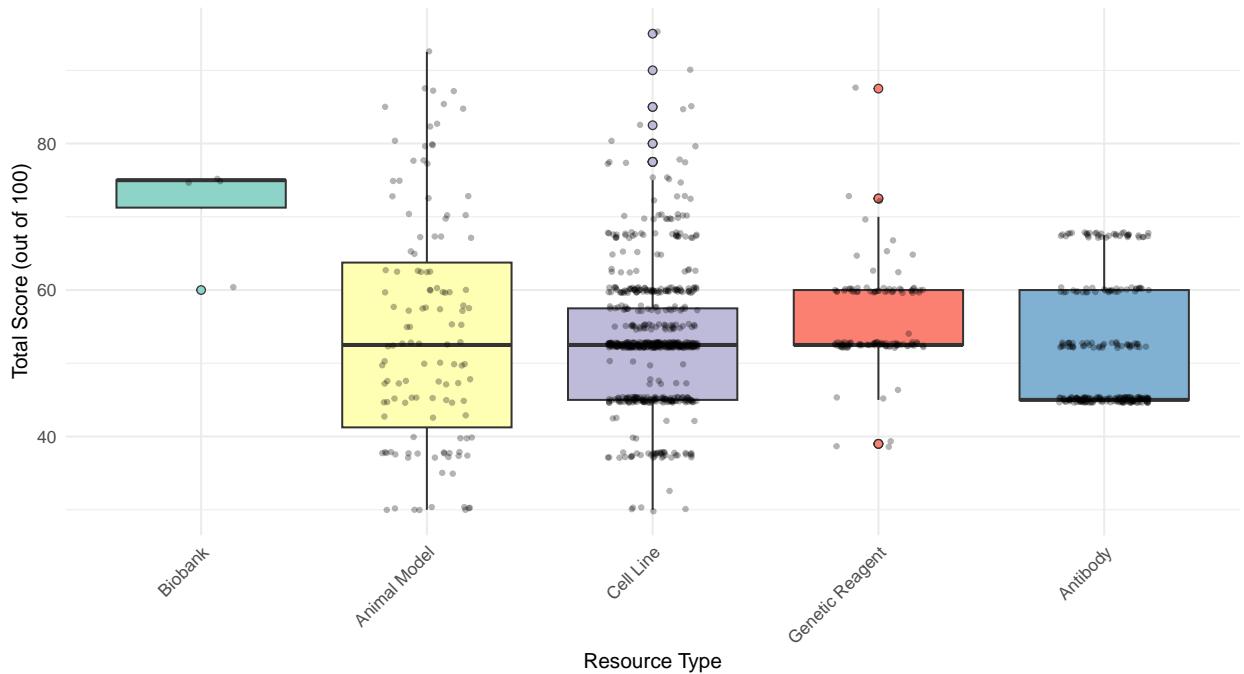
Overall Completeness Score Distribution

Mean: 53.3 | Median: 52.5 | N = 1148



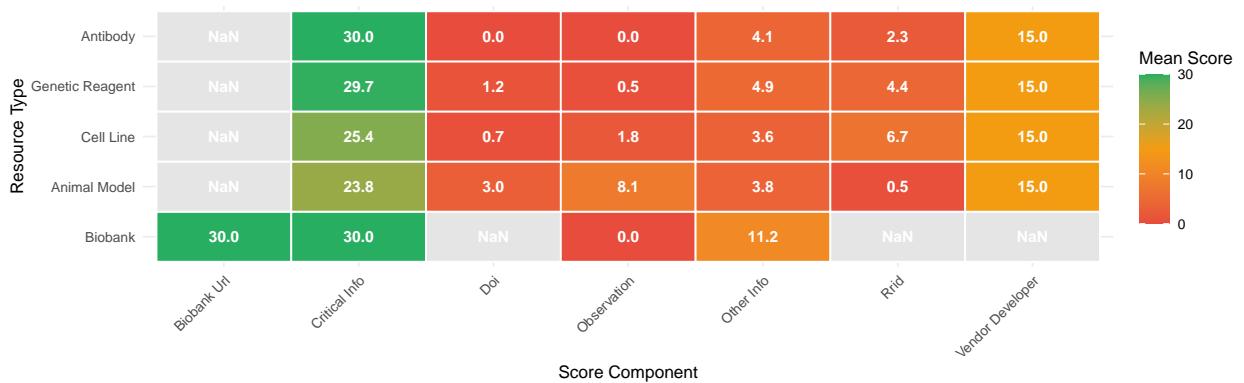
Completeness Score Distribution by Resource Type

Ordered by median score (highest to lowest)

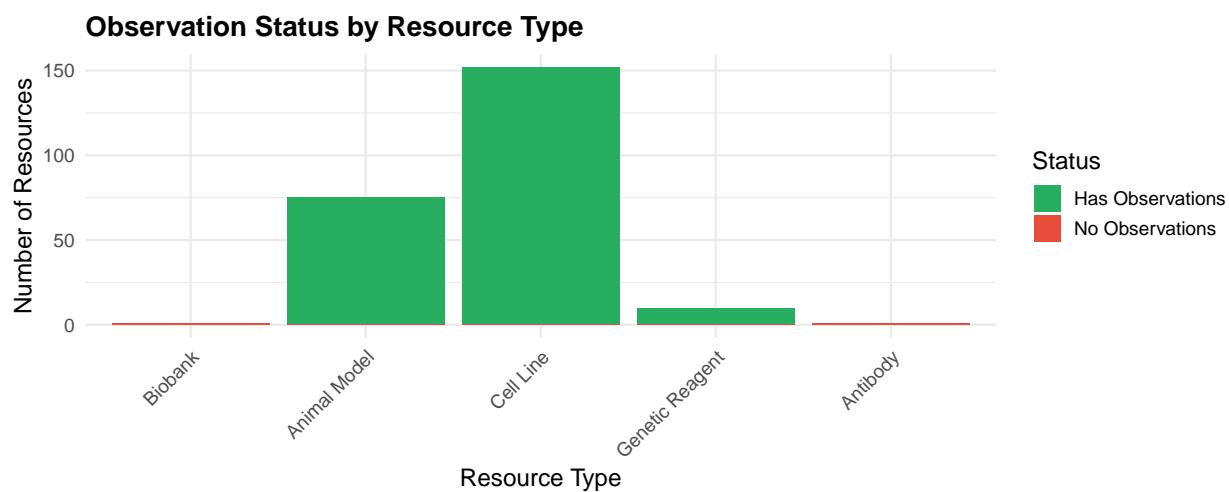
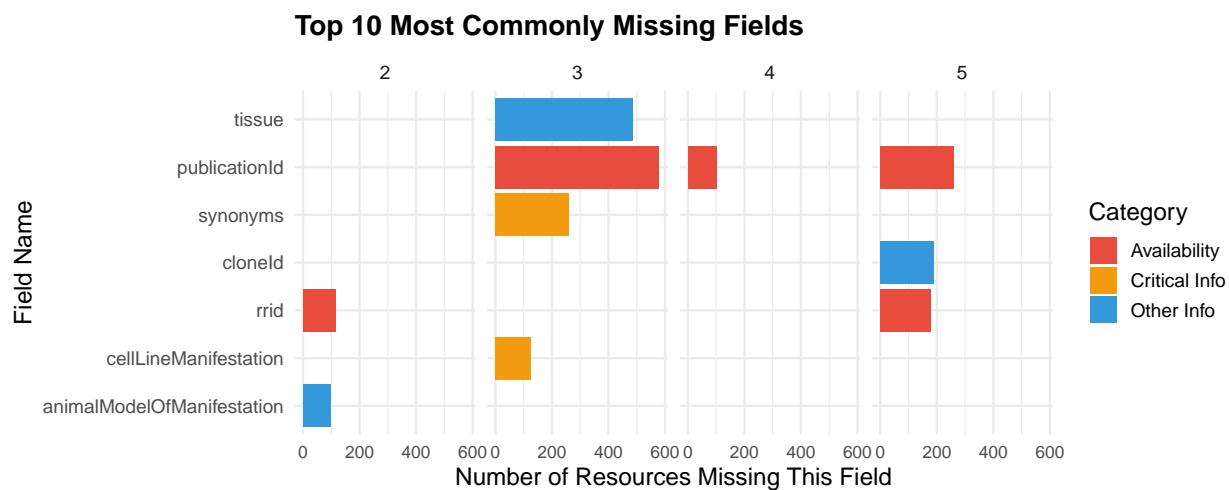
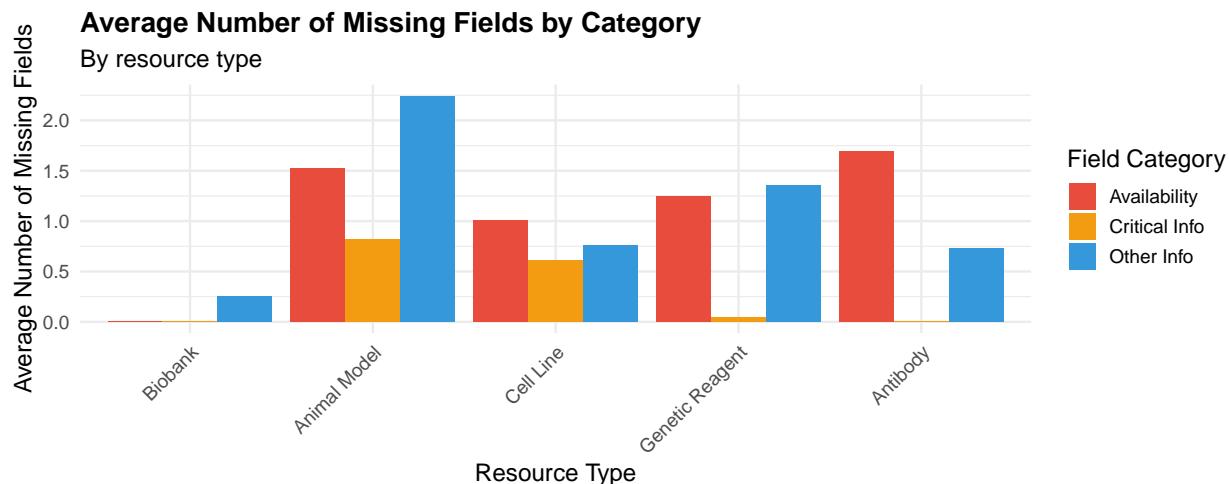


Mean Score by Component and Resource Type

Higher values indicate better completeness



Missing Fields Analysis



Summary Statistics Tables

Table 1: Overall Summary Statistics

Metric	Value
Total Resources	1148.00
Mean Score	53.29
Median Score	52.50
Std Dev	9.70
Min Score	30.00
Max Score	95.00
Range	65.00

Table 2: Summary Statistics by Resource Type

Resource Type	Count	Mean	Median	Std Dev	Min	Max
Biobank	4	71.25	75.0	7.50	60	75.0
Genetic Reagent	122	55.75	52.5	6.30	39	87.5
Animal Model	123	54.35	52.5	15.98	30	92.5
Cell Line	638	53.26	52.5	8.91	30	95.0
Antibody	261	51.41	45.0	8.35	45	67.5

Table 3: Top 10 Most Complete Resources

Resource Name	Type	RRID	Score	Category
SK-N-AS	Cell Line	rrid:CVCL_1700	95.0	Excellent
Nf14F/4F;CAGGCre-ERTM	Animal Model	NA	92.5	Excellent
GI-ME-N	Cell Line	rrid:CVCL_1232	90.0	Excellent
NF1flox4/Arg681*;Dhh-Cre	Animal Model	NA	87.5	Excellent
Nf1+/-GFAPCKO	Animal Model	NA	87.5	Excellent
NF1fl/fl;Dhh-Cre	Animal Model	NA	87.5	Excellent
pAMP-CY1_NF1 T1 (+minintr, KDR)	Genetic Reagent	rrid:Addgene_119200	87.5	Excellent
2XSB	Cell Line	rrid:CVCL_A7NI	85.0	Excellent
Capan-1	Cell Line	rrid:CVCL_0237	85.0	Excellent
Nf1tm1.1Kest	Animal Model	NA	85.0	Excellent

Table 4: Resources Needing Improvement (N = 74)

Resource Name	Type	Score	Category
Dh5 alpha	Cell Line	30.0	Poor
ELK-TAD Luciferase Reporter HEK293 Stable	Cell Line	30.0	Poor
c.1149C > A NF1-mutant hiPSCs	Cell Line	30.0	Poor
c.3431-32_dupGT NF1-mutant hiPSCs	Cell Line	30.0	Poor
U87-NF1-419	Cell Line	30.0	Poor
Krox20;Nf1flox/-	Animal Model	30.0	Poor
MPNST-Nf1-001	Animal Model	30.0	Poor

Resource Name	Type	Score	Category
MPNST-Nf1-002	Animal Model	30.0	Poor
MPNST-SP-001	Animal Model	30.0	Poor
MPSNT-SP-002	Animal Model	30.0	Poor
Nf1 GEM	Animal Model	30.0	Poor
Nf1-/- Drosophila	Animal Model	30.0	Poor
Nf1Fcr	Animal Model	30.0	Poor
Prx1-Cre+/- Nf1flox/+	Animal Model	30.0	Poor
HS-PSS	Cell Line	32.5	Poor
miR-155 +/-;Nf1flox/+	Animal Model	35.0	Poor
Nf1bdelta55 zebrafish	Animal Model	35.0	Poor
HEK293 NF1 -/- with R1306X mNf1 cDNA	Cell Line	37.5	Poor
WT ES	Cell Line	37.5	Poor
HEK293 NF1 -/- Exon 47 insT #14	Cell Line	37.5	Poor
HEK293 NF1 -/- with R1947X mNf1 cDNA	Cell Line	37.5	Poor
Dhh-Cre; NF1Arg681*/flox Schwann Cells	Cell Line	37.5	Poor
Schwann cell NF1 -/- (iPN97.4 #24)	Cell Line	37.5	Poor
ELK-TAD Luciferase Reporter HEK293 Stable NF1 -/-	Cell Line	37.5	Poor
Schwann cell NF1 -/- with R816X mNf1 cDNA	Cell Line	37.5	Poor
Schwann cell NF1 -/- with WT tagged mNf1 cDNA	Cell Line	37.5	Poor
HEK293 NF1 -/- with R461X mNf1 cDNA	Cell Line	37.5	Poor
Nf1-/- HEK 293	Cell Line	37.5	Poor
iPSC NF1 WT	Cell Line	37.5	Poor
Nf1Arg681*/+ ES	Cell Line	37.5	Poor
Nf1Arg681/ <i>Arg681</i> ES	Cell Line	37.5	Poor
Nf1-/- Epithelial lung cells	Cell Line	37.5	Poor
HEK293 NF1 -/- Exon 52 R2550X #5	Cell Line	37.5	Poor
NF1-R68X Embryonic cells	Cell Line	37.5	Poor
iPSC NF1 +/- BJFF.6 bkgd	Cell Line	37.5	Poor
HEK293 NF1 -/- with R2550X mNf1 cDNA	Cell Line	37.5	Poor
HEK293 NF1 -/- Exon 17 #A15 G629R cryptic splice	Cell Line	37.5	Poor
ScienCell Schwann cells	Cell Line	37.5	Poor
HEK293 NF1 -/- with R816X mNf1 cDNA	Cell Line	37.5	Poor
Schwann cell NF1 -/- with R681X mNf1 cDNA	Cell Line	37.5	Poor
HEK293 NF1 -/- with R192X mNf1 cDNA	Cell Line	37.5	Poor
SIGTR ES cell line AA0320	Cell Line	37.5	Poor
CPTC-NF1-1	Cell Line	37.5	Poor
CPTC-NF1-2	Cell Line	37.5	Poor
CPTC-NF1-3	Cell Line	37.5	Poor
FMS-1	Cell Line	37.5	Poor
MCF10A_NF1_1	Cell Line	37.5	Poor
MCF10A_NF1_7A1	Cell Line	37.5	Poor
MCF10A_NF1_7B2	Cell Line	37.5	Poor
MPNST-90	Cell Line	37.5	Poor
MPNST-91	Cell Line	37.5	Poor
MPNST-92	Cell Line	37.5	Poor
NFS-1	Cell Line	37.5	Poor
NMS-2PC	Cell Line	37.5	Poor
XL110	Cell Line	37.5	Poor
B6;CBA-Nf1/F1mg	Animal Model	37.5	Poor
C57BL/6JSmoc-Nf1em1Smoc	Animal Model	37.5	Poor
C57BL/6JSmoc-Nf1tm1(flox)Smoc	Animal Model	37.5	Poor
Nf1-/-	Animal Model	37.5	Poor

Resource Name	Type	Score	Category
CisNf1+/-; p53+/-	Animal Model	37.5	Poor
Nf1 flox/+; DhhCre/+	Animal Model	37.5	Poor
Nf1P1/Nf1E1 Drosophila	Animal Model	37.5	Poor
Nf1+/-MyoD	Animal Model	37.5	Poor
Nf1:p53	Animal Model	37.5	Poor
Nf1+/Arg681	Animal Model	37.5	Poor
Nf1flox/-;P0A-Cre-	Animal Model	37.5	Poor
Nf1flox/+;P0A-Cre(+)	Animal Model	37.5	Poor
Nf1flox/flox;P0A-cre-	Animal Model	37.5	Poor
Nf1flox/mut	Animal Model	37.5	Poor
Nf1P1 Drosophila	Animal Model	37.5	Poor
Nf1tm1a(KOMP)Wtsi	Animal Model	37.5	Poor
Neurofibromin CRISPR Plasmids (h)	Genetic Reagent	39.0	Poor
Neurofibromin CRISPR Plasmids (m)	Genetic Reagent	39.0	Poor
Neurofibromin siRNA and shRNA Plasmids	Genetic Reagent	39.0	Poor

Recommendations

Based on the analysis above, here are key recommendations for improving resource completeness:

- Focus on Low-Scoring Components:** Identify which score components (availability, critical info, other info, observations) have the lowest average scores across resource types and prioritize filling those fields.
 - Resource Type Priorities:** Target resource types with lower median scores for systematic improvement efforts.
 - Observation Documentation:** Encourage researchers to submit observations with publication DOIs, as these contribute more points (7.5 vs 2.5) to the completeness score.
 - RRID Registration:** Ensure all resources have registered RRIDs to improve findability and citation.
 - Vendor/Developer Information:** Complete vendor or developer information for resources to improve availability scores.
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