CERTIFICATE OF ANALYSIS

ACE 031 1 mg

LOT NUMBER	REPORT NUMBER	COA ISSUE DATE
APX-2026-0702-A	APX-COA-2026-0702-A	2026-07-02

COMPOUND REFERENCE

Material family
protein or glycoprotein

Material form
lyophilized solid in vial

MATERIAL & COMPOSITION

Nominal component amounts
ACE 031 1 mg: 1 mg

Recorded storage
-20 +/-5 C, protected from light; sealed dry vial

RECORDED RESULTS	Purity % integrated detector area	Active content
ACE 031 1 mg	99.863%	1.00209 mg/vial

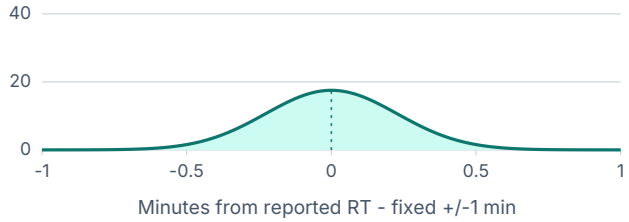
ESTIMATED PEAK PROFILE

Reported RT: 16.079 min

Reported integrated area: 9,986,300 counts

Modeled area density (10^6 counts/min)

0-20 min model view



Minutes from reported RT - fixed +/-1 min

Gaussian model; N = 5,000 assumed. Width and height estimated; not detector measurements.

68 recorded endpoints across 21 test groups. Results apply to this configuration and lot. For research use only; not for human or animal use.

APPROVED BY

K. Norwood

COA issued 2026-07-02

ONLINE REPORT
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Contamination & microbiology

All applicable tested criteria met

32 applicable endpoints reviewed against their stated specifications.

ELEMENTAL IMPURITIES

Lead	✓ PASS
Cadmium	✓ PASS
Arsenic	✓ PASS
Mercury	✓ PASS
Cobalt	✓ PASS
Vanadium	✓ PASS
Nickel	✓ PASS
Palladium	✓ PASS
Platinum	✓ PASS
Rhodium	✓ PASS
Ruthenium	✓ PASS
Iridium	✓ PASS

RESIDUAL SOLVENTS

Methanol	✓ PASS
Acetonitrile	✓ PASS
Dichloromethane	✓ PASS
N, N-dimethylformamide	✓ PASS
Ethanol	✓ PASS
Acetone	✓ PASS
Ethyl acetate	✓ PASS
Toluene	✓ PASS
n-Hexane	✓ PASS
Benzene	✓ PASS

MICROBIOLOGY & ENDOTOXINS

Sterility: FTM	✓ PASS
Sterility: SCDM	✓ PASS
Bacterial endotoxins	✓ PASS
TAMC	✓ PASS
TYMC	✓ PASS
Escherichia coli	✓ PASS
Staphylococcus aureus	✓ PASS
Pseudomonas aeruginosa	✓ PASS
Salmonella species	✓ PASS
Candida albicans	✓ PASS

PASS indicates that the recorded result meets its stated criterion for the tested sample. Exact values, detection limits, sampling scope and methods follow in the complete results. For research use only.

Complete assay results

Reported values, units and acceptance outcomes are reproduced separately for each endpoint. Method keys link to the method reference section.

Endpoint	Reported result / basis	Acceptance criterion	Method / outcome
T01 / Identity and structure			
01 / Orthogonal identity against specified reference	Conforms to the assigned reference; see identity basis Unit: qualitative Basis B01	Conforms to the specified acceptance criterion Unit: qualitative	M01 PASS C01
02 / Orthogonal fingerprint similarity	= 0.9994 similarity (0-1) Basis B02	>= 0.995 Unit: similarity (0-1)	M01 PASS C02
T02 / Chromatographic purity			
03 / ACE 031 1 mg chromatographic purity	= 99.863 % integrated detector area Basis B03	99.7 to 100 Unit: % integrated detector area	M02 PASS C02
T03 / Active content and assay			
08 / ACE 031 1 mg active content	= 1.00209 mg/vial Basis B06	0.98 to 1.02 Unit: mg/vial	M04 PASS C02
09 / ACE 031 1 mg label claim assay	= 100.209 % label claim Basis B07	98 to 102 Unit: % label claim	M04 PASS C02
T04 / Blend composition			
13 / Applicability decision	Not applicable — One declared active or a water/preservative reagent. Preservative is separately quantified under T14; there is no multi-active blend ratio. Unit: qualitative Basis B08	Same as reported result Unit: qualitative Basis B09	M06 N/A — justified C05
T05 / Related substances and degradants			
04 / ACE 031 1 mg Unknown U1	= 0.069 % integrated detector area Basis B04	<= 0.1 Unit: % integrated detector area	M03 PASS C03
05 / ACE 031 1 mg Unknown U2	= 0.041 % integrated detector area Basis B04	<= 0.1 Unit: % integrated detector area	M03 PASS C03
06 / ACE 031 1 mg Unknown U3	= 0.027 % integrated detector area Basis B04	<= 0.1 Unit: % integrated detector area	M03 PASS C03

Endpoint	Reported result / basis	Acceptance criterion	Method / outcome
07 / ACE 031 1 mg total related peaks	= 0.137 % integrated detector area Basis B05	<= 0.3 Unit: % integrated detector area	M03 PASS C02
T06 / Water content			
14 / Residual water	= 0.539 % w/w finished fill Basis B12	<= 2 Unit: % w/w finished fill	M07 PASS C02
T07 / Counterions and associated species			
15 / Acetate content relative to parent active mass	= 1.5 % acetate/parent mass Basis B13	0.5 to 3 Unit: % acetate/parent mass	M08 PASS C02
T08 / Residual solvents			
16 / Methanol	= 19.828 ug/g finished fill Basis B14	<= 3000 Unit: ug/g finished fill	M09 PASS C06
17 / Acetonitrile	= 8.88 ug/g finished fill Basis B14	<= 410 Unit: ug/g finished fill	M09 PASS C07
18 / Dichloromethane	= 3.368 ug/g finished fill Basis B14	<= 600 Unit: ug/g finished fill	M09 PASS C08
19 / N, N-dimethylformamide	= 4.398 ug/g finished fill Basis B14	<= 880 Unit: ug/g finished fill	M09 PASS C09
20 / Ethanol	= 40.861 ug/g finished fill Basis B14	<= 5000 Unit: ug/g finished fill	M09 PASS C06
21 / Acetone	= 13.09 ug/g finished fill Basis B14	<= 5000 Unit: ug/g finished fill	M09 PASS C09
22 / Ethyl acetate	= 8.795 ug/g finished fill Basis B14	<= 5000 Unit: ug/g finished fill	M09 PASS C09
23 / Toluene	= 1.803 ug/g finished fill Basis B14	<= 890 Unit: ug/g finished fill	M09 PASS C10
24 / n-Hexane	= 1.1 ug/g finished fill Basis B14	<= 290 Unit: ug/g finished fill	M09 PASS C10
25 / Benzene	= 0.074 ug/g finished fill Basis B14	<= 2 Unit: ug/g finished fill	M09 PASS C11

Endpoint	Reported result / basis	Acceptance criterion	Method / outcome
T09 / Elemental impurities			
26 / Lead	= 0.0118 ug/g finished fill Basis B15	<= 0.5 Unit: ug/g finished fill	M10 PASS C12
27 / Cadmium	= 0.0085 ug/g finished fill Basis B15	<= 0.2 Unit: ug/g finished fill	M10 PASS C12
28 / Arsenic	= 0.019 ug/g finished fill Basis B15	<= 0.5 Unit: ug/g finished fill	M10 PASS C12
29 / Mercury	= 0.0056 ug/g finished fill Basis B15	<= 0.1 Unit: ug/g finished fill	M10 PASS C12
30 / Cobalt	= 0.0239 ug/g finished fill Basis B15	<= 1 Unit: ug/g finished fill	M10 PASS C12
31 / Vanadium	= 0.022 ug/g finished fill Basis B15	<= 1 Unit: ug/g finished fill	M10 PASS C12
32 / Nickel	= 0.0365 ug/g finished fill Basis B15	<= 2 Unit: ug/g finished fill	M10 PASS C12
33 / Palladium	= 0.0117 ug/g finished fill Basis B15	<= 1 Unit: ug/g finished fill	M10 PASS C12
34 / Platinum	= 0.0096 ug/g finished fill Basis B15	<= 1 Unit: ug/g finished fill	M10 PASS C12
35 / Rhodium	= 0.0066 ug/g finished fill Basis B15	<= 1 Unit: ug/g finished fill	M10 PASS C12
36 / Ruthenium	= 0.009 ug/g finished fill Basis B15	<= 1 Unit: ug/g finished fill	M10 PASS C12
37 / Iridium	= 0.0059 ug/g finished fill Basis B15	<= 1 Unit: ug/g finished fill	M10 PASS C12
T10 / Sterility test			
42 / Sterility: FTM	No growth at 14 days in all 20 units Unit: qualitative Basis B20	Conforms to the specified acceptance criterion Unit: qualitative	M14 PASS C13

Endpoint	Reported result / basis	Acceptance criterion	Method / outcome
43 / Sterility: SCDM	No growth at 14 days in all 20 units Unit: qualitative Basis B21	Conforms to the specified acceptance criterion Unit: qualitative	M14 PASS C13
T11 / Bacterial endotoxins			
44 / Bacterial endotoxins	<0.025 EU/mg active-equivalent Basis B22	<= 0.1 Unit: EU/mg active-equivalent	M15 PASS C14
T12 / Microbial enumeration			
45 / TAMC	<1 CFU/g finished fill Basis B23	<= 100 Unit: CFU/g finished fill	M16 PASS C15
46 / TYMC	<1 CFU/g finished fill Basis B23	<= 10 Unit: CFU/g finished fill	M16 PASS C15
47 / Escherichia coli	Not detected in 1g Unit: qualitative Basis B24	Conforms to the specified acceptance criterion Unit: qualitative	M16 PASS C16
48 / Staphylococcus aureus	Not detected in 1g Unit: qualitative Basis B24	Conforms to the specified acceptance criterion Unit: qualitative	M16 PASS C16
49 / Pseudomonas aeruginosa	Not detected in 1g Unit: qualitative Basis B24	Conforms to the specified acceptance criterion Unit: qualitative	M16 PASS C16
50 / Salmonella species	Not detected in 1g Unit: qualitative Basis B24	Conforms to the specified acceptance criterion Unit: qualitative	M16 PASS C16
51 / Candida albicans	Not detected in 1g Unit: qualitative Basis B24	Conforms to the specified acceptance criterion Unit: qualitative	M16 PASS C16
T13 / pH and analytical solution			
38 / pH of specified buffered analytical solution	= 4.8 pH Basis B16	4.1 to 5.5 Unit: pH	M11 PASS C02
T14 / Excipients and preservatives			
39 / Trehalose content	= 5.004 mg/vial Basis B17	4.75 to 5.25 Unit: mg/vial	M12 PASS C02
T15 / Unit uniformity			
10 / ACE 031 1 mg individual-unit mean	= 100.209 % label claim Basis B08	98 to 102 Unit: % label claim Basis B09	M05 PASS C04

Endpoint	Reported result / basis	Acceptance criterion	Method / outcome
11 / ACE 031 1 mg acceptance value (n=10)	= 0.8458 % label claim Basis B10	<= 15 Unit: % label claim	M05 PASS C04
12 / ACE 031 1 mg individual-unit RSD	= 0.3517 % Basis B11	<= 2 Unit: %	M05 PASS C04
T16 / Biological activity			
52 / Activin A inhibition of SMAD2/3 reporter by ActRIIB-Fc relative potency	= 100.05 % reference response potency Basis B25	90 to 110 Unit: % reference response potency	M17 PASS C02
T17 / Protein and conjugate characterization			
53 / Size-exclusion main defined population	= 99.863 % SEC response Basis B26	99.7 to 100 Unit: % SEC response	M18 PASS C02
54 / High molecular weight aggregate fraction	= 0.069 % SEC response Basis B08	<= 0.1 Unit: % SEC response Basis B09	M18 PASS C02
55 / Low molecular weight non-reference fraction	= 0.068 % SEC response Basis B08	<= 0.1 Unit: % SEC response Basis B09	M18 PASS C02
56 / Orthogonal construct/fingerprint mapping	Conforms to explicit reference specification Unit: qualitative Basis B27	Conforms to the specified acceptance criterion Unit: qualitative	M18 PASS C01
60 / Released N-glycan composition-profile cosine similarity	= 0.999999 similarity0-1 Numeric value: 0.9999993368264456 Basis B31	0.995 to 1 Unit: similarity0-1	M20 PASS C02
61 / Nonreducing CE-SDS intended chain-population fraction	= 99.88 % integrated CE-SDS area Basis B32	99.7 to 100 Unit: % integrated CE-SDS area	M21 PASS C02
62 / Reducing CE-SDS intended chain-population fraction	= 99.9 % integrated CE-SDS area Basis B32	99.7 to 100 Unit: % integrated CE-SDS area	M21 PASS C02
T18 / Process impurities			
57 / Residual source-process protein impurities	= 2.1 ng/mg assigned target material Basis B28	<= 100 Unit: ng/mg assigned target material	M19 PASS C17
58 / Residual source DNA	= 0.012 ng/vial Basis B29	<= 1 Unit: ng/vial	M19 PASS C18

Endpoint	Reported result / basis	Acceptance criterion	Method / outcome
59 / Residual Protein A	= 0.15 ng/mg target protein Basis B30	<= 10 Unit: ng/mg target protein	M19 PASS C19
T19 / Particles and container closure			
63 / Subvisible particles >= 10um	= 21 particles/container Basis B33	<= 6000 Unit: particles/container	M22 PASS C20
64 / Subvisible particles >= 25um	= 2 particles/container Basis B33	<= 600 Unit: particles/container	M22 PASS C20
65 / Vacuum decay package integrity	10/10test closures conform; positive-leak controls detected Unit: qualitative Basis B34	Conforms to the specified acceptance criterion Unit: qualitative	M22 PASS C21
T20 / Stability observations			
66 / Reported 6 month assay retention	= 99.9102 % of initial assay Basis B35	98 to 102 Unit: % of initial assay	M23 PASS C02
67 / Reported 6 month minimum component purity	= 99.821 % integrated detector area Basis B36	99.7 to 100 Unit: % integrated detector area	M23 PASS C02
68 / Dating disposition	6 month review point; actual expiry/retest not assigned Unit: qualitative Basis B35	Conforms to the specified acceptance criterion Unit: qualitative	M23 PASS C01
T21 / Appearance and physical inspection			
40 / Appearance	white to off-white; uniform lyophilized cake Unit: qualitative Basis B18	Conforms to the specified acceptance criterion Unit: qualitative	M13 PASS C01
41 / Visible foreign matter	None observed in 3 inspected units Unit: qualitative Basis B19	Conforms to the specified acceptance criterion Unit: qualitative	M13 PASS C01

Method reference

The keys below identify the methods referenced in the result tables.

Key / method ID	Method	Technique
M01 M-T01-DEFAULT	Orthogonal chemical/structural identity	LC-HRMS/MS plus sequence/connectivity-sensitive reference comparison
M02 M-T02-SEC-UV280	Reference-defined protein size-population response purity	Size-exclusion chromatography with UV detection at 280 nm
M03 M-T05-DEFAULT	Related substances	Stability-indicating LC integration; orthogonal size/charge separation for biologics
M04 M-T03-DEFAULT	Calibrated material content	Independent quantitative LC/CAD, protein assay or bioactivity calibration for IU
M05 M-T15-DEFAULT	Individual-unit uniformity	Ten separate unit preparations and fill measurements
M06 M-T04-DEFAULT	Component-resolved blend assay	Separate calibrated selective assay for every declared component
M07 M-T06-KF	Residual formulation water on a defined mass basis	Coulometric Karl Fischer with oven transfer
M08 M-T07-DEFAULT	Counterion composition	Ion chromatography and stoichiometric accounting
M09 M-T08-DEFAULT	Residual solvent panel	headspace GC-MS
M10 M-T09-DEFAULT	Elemental impurity panel	ICP-MS
M11 M-T13-DEFAULT	pH and solution state	Calibrated potentiometry
M12 M-T14-DEFAULT	Excipients/preservatives	Component-specific quantitative LC/CAD or formulation identity
M13 M-T21-DEFAULT	Appearance	Controlled visual examination
M14 M-T10-DEFAULT	Sterility observations in two media with matrix-specific preparation	Membrane filtration/rinsing or neutralized direct inoculation for Lemon dispersion
M15 M-T11-DEFAULT	Bacterial endotoxins	Recombinant factor C fluorometric assay
M16 M-T12-DEFAULT	Microbial enumeration/organisms	Membrane filtration enumeration and enrichment
M17 M-T16-DEFAULT	Functional biological activity	Reference-relative concentration-response assay
M18 M-T17-DEFAULT	Protein/conjugate characterization	SEC-MALS, CE-SDS, peptide mapping, glycan/PEG profiling

Key / method ID	Method	Technique
M19 M-T18-DEFAULT	Biological process impurity panel	Host/process-specific ELISA and qPCR
M20 M-T17-GLYCAN-COMPOSITION-PROFILE	Released N-glycan composition-profile comparison	PNGase-F release with composition-resolved, response-calibrated LC-MS
M21 M-T17-PROTEIN-CHAIN-PROFILE	Reference-defined reduced/nonreducing protein-chain populations	CE-SDS with independent chain-reference migration and subunit identity comparison
M22 M-T19-DEFAULT	Particles and package integrity	Light obscuration plus vacuum decay
M23 M-T20-DEFAULT	Stability observation	Time-zero/1/3/6-month trend

Analytical detail appendix

Basis keys preserve the exact analytical scope of each result. Detection limits and sampling context are reported separately from measured values. N/A limits are not numerical detection limits and are omitted from the context key.

Result and criterion bases

Key	Basis
B01	ACE-031/ramatercept reference construct: each chain is human ACVR2B precursor residues20-134 (construct1-115), GGG linker(116-118), human IGHG1*03 Fc H-CH2-CH3 fragment(119-343), including CH2 A115V at construct226; interchain disulfides122-122' and 125-125'. Two-chain glycosylated dimer; CHO-expressed material.
B02	spectrum/peptide-map comparison; score is not proof of stereochemistry
B03	Single analyte method scope; intended blend co-components and excipients excluded by analyte-specific selectivity, not denominator manipulation
B04	Same analyte-specific chromatogram as T02; response factor assumed 1.00 for unknowns; area only
B05	Sum of U1+U2+U3; purity plus related areas = 100%
B06	Assigned component material basis; excludes vehicle/excipient/water; salt basis explicitly in identity specification
B07	Independent calibrated amount / nominal amount x 100; not chromatographic area purity
B08	specified sample/form only
B09	material-specific limit
B10	AV=abs(M-mean)+2.4 sample SD; target 100%; M=mean within 98.5-101.5
B11	Precision criterion for the listed specification, independently of AV
B12	Water as percentage of total net formulation, not peptide area purity
B13	Explicit process/counterion basis; acetate-associated material. No fixed stoichiometric salt is asserted; acidic peptides may contain residual process acetate rather than a counterion.
B14	Material-based limit. Liquid numerical limits are listed specification and not ICH Option1 mass ppm.
B15	Total element; no speciation. material-based criterion, not a dose/route-derived safety limit.
B16	1.000 mg active/mL in 25mM acetate buffer, pH4.80,25.0C; buffer-solution compatibility is not the pH of dry material
B17	Separate excipient-specific assay; not label active
B18	Three containers under diffuse white illumination
B19	Visual observation only; subvisible particles reported separately
B20	FTM30-35C; tested units only; growth-promotion/suitability controls conform
B21	SCDM20-25C; tested units only; no sterility assurance level assigned
B22	Sample reporting limit after1:5 dilution; threshold is and not based on administration route/dose
B23	Zero colonies observed from1g or1 mL equivalent filter; report <1, not exact absence
B24	Specified-organism enrichment in explicit1g/1 mL scope; not a universal pharmacopeial panel
B25	Relative to the specified reference response; activity units and mass units are evaluated separately. Method validation is not asserted by this report.
B26	Same primary SEC population result as T02 for proteins; orthogonal size separation for PEG/mixtures. Includes expected biological heterogeneity.

Key	Basis
B27	Identity Reference defines construct, termini, and mixture caveats; no raw mass spectrum or gel image exists
B28	mammalian recombinant expression process; source-specific assay. For hydrolysates, intact source proteins outside the target digest are measured by selective separation; intended peptides are not HCP impurities.
B29	Source-specific qPCR in process; extraction recovery demonstrated only
B30	Explicit Protein-A-affinity process for Fc construct
B31	Cosine similarity of complete response-corrected fraction vectors to explicit reference; no site/linkage assignment
B32	Protein-specific reference profile; hCG/HMG expected alpha/beta subunits are intended species, not degraded monomer
B33	As-supplied liquid or entire dry vial dissolved to stated analytical volume; limits, no injectable compliance claim
B34	method vacuum-decay threshold0.20kPa/60s;5um positive defect control. No universal leakage-to-sterility equivalence.
B35	Reported change relative to the initial assay. This report does not assign a retest date or shelf life.
B36	Separate endpoint; no shelf-life claim

Sampling and detection context

Key	Reported context
C01	Analytical replicates: 2; Statistic type: individual/qualitative observation; Units sampled: 3; Units type: finished containers
C02	Analytical replicates: 2; Statistic type: mean of independent sample preparations; Units sampled: 3; Units type: finished containers
C03	Analytical replicates: 2; Statistic type: mean of independent sample preparations; Units sampled: 3; Units type: finished containers; LOD: 0.002 % integrated detector area; LOQ: 0.005 % integrated detector area
C04	Analytical replicates: 1; Statistic type: mean of independent sample preparations; Units sampled: 10; Units type: finished containers
C05	Analytical replicates: 0; Statistic type: individual/qualitative observation; Units sampled: 0; Units type: finished containers
C06	Analytical replicates: 2; Statistic type: mean of independent sample preparations; Units sampled: 3; Units type: finished containers; LOD: 1 ug/g finished fill; LOQ: 3 ug/g finished fill
C07	Analytical replicates: 2; Statistic type: mean of independent sample preparations; Units sampled: 3; Units type: finished containers; LOD: 0.3 ug/g finished fill; LOQ: 1 ug/g finished fill
C08	Analytical replicates: 2; Statistic type: mean of independent sample preparations; Units sampled: 3; Units type: finished containers; LOD: 0.2 ug/g finished fill; LOQ: 0.6 ug/g finished fill
C09	Analytical replicates: 2; Statistic type: mean of independent sample preparations; Units sampled: 3; Units type: finished containers; LOD: 0.5 ug/g finished fill; LOQ: 1.5 ug/g finished fill
C10	Analytical replicates: 2; Statistic type: mean of independent sample preparations; Units sampled: 3; Units type: finished containers; LOD: 0.1 ug/g finished fill; LOQ: 0.3 ug/g finished fill
C11	Analytical replicates: 2; Statistic type: mean of independent sample preparations; Units sampled: 3; Units type: finished containers; LOD: 0.01 ug/g finished fill; LOQ: 0.03 ug/g finished fill
C12	Analytical replicates: 2; Statistic type: mean of independent sample preparations; Units sampled: 3; Units type: finished containers; LOD: 0.0005 ug/g finished fill; LOQ: 0.002 ug/g finished fill
C13	Analytical replicates: 1; Statistic type: individual/qualitative observation; Units sampled: 20; Units type: finished containers
C14	Analytical replicates: 2; Statistic type: mean of independent sample preparations; Units sampled: 3; Units type: finished containers; LOD: 0.01 EU/mg active-equivalent; LOQ: 0.025 EU/mg active-equivalent
C15	Analytical replicates: 2; Statistic type: mean of independent sample preparations; Units sampled: 3; Units type: finished containers; LOD: 1 CFU/g finished fill; LOQ: 1 CFU/g finished fill
C16	Analytical replicates: 1; Statistic type: individual/qualitative observation; Units sampled: 1; Units type: finished containers
C17	Analytical replicates: 2; Statistic type: mean of independent sample preparations; Units sampled: 3; Units type: finished containers; LOD: 0.2 ng/mg assigned target material; LOQ: 0.6 ng/mg assigned target material
C18	Analytical replicates: 2; Statistic type: mean of independent sample preparations; Units sampled: 3; Units type: finished containers; LOD: 0.001 ng/vial; LOQ: 0.003 ng/vial
C19	Analytical replicates: 2; Statistic type: mean of independent sample preparations; Units sampled: 3; Units type: finished containers; LOD: 0.01 ng/mg target protein; LOQ: 0.03 ng/mg target protein

Key	Reported context
C20	Analytical replicates: 1; Statistic type: mean of independent sample preparations; Units sampled: 3; Units type: finished containers
C21	Analytical replicates: 1; Statistic type: individual/qualitative observation; Units sampled: 10; Units type: finished containers

Supporting analytical details

01 / Orthogonal identity against specified reference

Field	Reported value	Unit / note
identified structure or sequence	ACE-031/ramatercept reference construct: each chain is human ACVR2B precursor residues20-134 (construct1-115), GGG linker(116-118), human IGHG1*03 Fc H-CH2-CH3 fragment(119-343), including CH2 A115V at construct226; interchain disulfides122-122' and 125-125'. Two-chain glycosylated dimer; CHO-expressed material.	text
neutral average mass	Not assigned: construct/distribution or no supported unique species	Da or explicit reason
neutral monoisotopic mass	Not assigned — see component-specific HRMS records; a reference mass is not a measured neutral mass	Explicit context; see value Method and sample context; reference facts are in Identity Reference.
observed mz	Not assigned — heterogeneous construct or no defined ion; orthogonal identity documented instead	Explicit context; see value Method and sample context; reference facts are in Identity Reference.
mass tolerance	+/-5 ppm for an explicitly defined monoisotopic ion; not 5 Da.	Explicit context; see value Method and sample context; reference facts are in Identity Reference.
reduced deglycosylated or intact	Intact specified parent for defined compounds; glycoproteins and PEG retain the specified population heterogeneity. No single exact intact glycoprotein mass is invented.	Explicit context; see value Method and sample context; reference facts are in Identity Reference.
stereochemistry method	Component-specific chiral amino acid analysis or orthogonal structure comparison, where applicable; HRMS cannot distinguish stereoisomers.	Explicit context; see value Method and sample context; reference facts are in Identity Reference.
identity standard traceability	RS-2578; internal standard, not a purchased certified reference material	text

03 / ACE 031 1 mg chromatographic purity

Field	Reported value	Unit / note
main peak retention time	16.079	min
main peak area	9986300	counts
total integrated area	10000000	counts

08 / ACE 031 1 mg active content

Field	Reported value	Unit / note
sample preparation volume	1	mL
dilution factor	10	fold

10 / ACE 031 1 mg individual-unit mean

Field	Reported value	Unit / note
physical unit count	1	Explicit context; see value Method and sample context; reference facts are in Identity Reference.

14 / Residual water

Field	Reported value	Unit / note
dry basis correction	1.005419209539417	factor For mass-fraction reporting only; independent active assay is not blindly multiplied by this factor.

44 / Bacterial endotoxins

Field	Reported value	Unit / note
dilution factor	5	Explicit context; see value Method and sample context; reference facts are in Identity Reference.
maximum valid dilution if used	20	Explicit context; see value Method and sample context; reference facts are in Identity Reference.

52 / Activin A inhibition of SMAD2/3 reporter by ActRIIB-Fc relative potency

Field	Reported value	Unit / note
biological replicates	3	Explicit context; see value Method and sample context; reference facts are in Identity Reference.

63 / Subvisible particles >= 10um

Field	Reported value	Unit / note
packaging sample count	10	Explicit context; see value Method and sample context; reference facts are in Identity Reference.

END OF REPORT

Apex Laboratory | APX-COA-2026-0702-A | APX-2026-0702-A