

Gaussian 16 Features at a Glance

Features introduced since Gaussian 09 Rev A are in **blue**. Existing features enhanced in Gaussian 16 are in green.

Fundamental Algorithms

- Calculation of one- & two-electron integrals over any contracted gaussian functions
- Conventional, direct, semi-direct and in-core algorithms
- Linearized computational cost via automated fast multipole methods (FMM) and sparse matrix techniques
- Harris initial guess
- Initial guess generated from fragment guesses or fragment SCF solutions
- Density fitting and Coulomb engine for pure DFT calculations, including automated generation of fitting basis sets
- + $\mathcal{O}(N)$ exact exchange for HF and hybrid DFT
- 1D, 2D, 3D periodic boundary conditions (PBC) energies & gradients (HF & DFT)
- Shared-memory (SMP), cluster/network and GPU-based parallel execution

Model Chemistries

Molecular Mechanics

- Amber, DREIDING and UFF energies, gradients and frequencies * Custom force fields
- Standalone MM program

Ground State Semi-Empirical

- CNDO/2, INDO, MINDO3 and MNDO energies and gradients
 AM1, PM3, PM3MM, PM6 and PDDG energies, gradients and
- reimplemented (analytic) frequencies • PM7: original and modified for continuous potential energy
- surfaces
 Custom semi-empirical parameters (Gaussian and MOPAC
- External formats) • DFTB and DFTBA methods

Self Consistent Field (SCF)

- SCF restricted and unrestricted energies, gradients and frequencies, and RO energies and gradients
- EDIIS+CDIIS default algorithm; optional Quadratic Convergent SCF

• SCF procedure enhancements for very large calculations

- Complete Active Space SCF (CASSCF) energies, gradients & frequencies
- * Active spaces of up to 16 orbitals
- Restricted Active Space SCF (RASSCF) energies and gradients
- Generalized Valence Bond-Perfect Pairing energies and gradients
- Wavefunction stability analysis (HF & DFT)

Density Functional Theory

Closed and open shell energies, gradients & frequencies, and RO energies & gradients are available for all DFT methods.

- EXCHANGE FUNCTIONALS: Slater, Xα, Becke 88, Perdew-Wang 91, Barone-modified PW91, Gill 96, PBE, OPTX, TPSS, revised TPSS, BRx, PKZB, ωPBEh/HSE, PBEh
- CORRELATION FUNCTIONALS: VWN, VWN5, LYP, Perdew 81, Perdew 86, Perdew-Wang 91, PBE, B95, TPSS, revised TPSS, KCIS, BRC, PKZB, VP86, V5LYP
- HYBRID METHODS: B3LYP, B3P86, P3PW91, B1 and variations, B98, B97-1, B97-2, PBE1PBE, HSEh1PBE and variations, O3LYP, TPSSh, τHCTH hybrid, BMK, AFD, M05, M05-2X, M06, M06-HF, M062-X, M08-HX, PW6B95, PW6B95D3, M11, SOGGA11-X, N12, N12-SX, MN12-SX, MN15, HISSbPBE, X3LYP, BHandHLYP; user-configurable hybrid methods
- DOUBLE HYBRID: B2PLYP & mPW2PLYP and variations with dispersion, DSDPBEP86, PBE0DH, PBEQIDH (see also below in "Electron Correlation")

- ◆ EMPIRICAL DISPERSION: PFD, GD2, GD3, GD3BJ
- FUNCTIONALS INCLUDING DISPERSION: APFD, B97D3, B2PLYPD3
 LONG RANGE-CORRECTED: LC-ωPBE, CAM-B3LYP, ωB97XD and variations, Hirao's general LC correction
- Larger numerical integrations grids

Electron Correlation:

All methods/job types are available for both closed and open shell systems and may use frozen core orbitals; restricted open shell calculations are available for MP2, MP3, MP4 and CCSD/CCSD(T) energies.

- MP2 energies, gradients, and frequencies
- Double hybrid DFT energies, gradients and frequencies, with optional empirical dispersion (see list in "Density Functional Theory" above)
- CASSCF calculations with MP2 correlation for any specified set of states
- MP3 and MP4(SDQ) energies and gradients
- MP4(SDTQ) and MP5 energies
- Configuration Interaction (CISD) energies & gradients
- Quadratic CI energies & gradients; QCISD(TQ) energies
- Coupled Cluster methods: restartable CCD, CCSD energies & gradients, CCSD(T) energies; optionally input amplitudes computed with smaller basis set
- * Optimized memory algorithm to avoid I/O during CCSD iterations
- Brueckner Doubles (BD) energies and gradients, BD(T) energies; optionally input amplitudes & orbitals computed with a smaller basis set
- Enhanced Outer Valence Green's Function (OVGF) methods for ionization potentials & electron affinities
- Complete Basis Set (CBS) MP2 Extrapolation
- Douglas-Kroll-Hess scalar relativistic Hamiltonians

Automated High Accuracy Energies

- G1, G2, G3, G4 and variations
- CBS-4, CBS-q, CBS-QB3, ROCBS-QB3, CBS-Q, CBS-APNO
- W1U, W1BD, W1RO (enhanced core correlation energy calculation)

Basis Sets and DFT Fitting Sets

- STO-3G, 3-21G, 6-21G, 4-31G, 6-31G, 6-31G†, 6-311G, D95, D95V, SHC, CEP-nG, LanL2DZ, cc-pV{D,T,Q,5,6}Z, original and def2- versions of SV, SVP, TZV & QZVP, EPR-II, EPR-III, Midi!, UGBS*, MTSmall, DG{D,T}ZVP, CBSB7
 - * Augmented cc-pV*Z schemes: Aug- prefix, spAug-, dAug-, Truhlar calendar basis sets (original and regularized)
- Effective Core Potentials (through second derivatives): LanL2DZ, CEP through Rn, Stuttgart/Dresden
- Support for basis functions and ECPs of arbitrary angular momentum
- DFT FITTING SETS: DGA1, DGA1, W06, older sets designed for SVP and TZVP basis sets; auto-generated fitting sets; optional default enabling of density fitting

Geometry Optimizations and Reaction Modeling

- Geometry optimizations for equilibrium structures, transition structures, and higher order saddle points, in redundant internal, internal (Z-matrix), Cartesian, or mixed internal and Cartesian coordinates
- GEDIIS optimization algorithm
- Redundant internal coordinate algorithm designed for large system, semi-empirical optimizations
- Newton-Raphson and Synchronous Transit-Guided Quasi-Newton (QST2/3) methods for locating transition structures
- IRCMax transition structure searches
- Relaxed and unrelaxed potential energy surface scans

- Implementation of intrinsic reaction path following (IRC), applicable to ONIOM QM:MM with thousands of atoms
- Reaction path optimization
- BOMD molecular dynamics (all analytic gradient methods); ADMP molecular dynamics: HF, DFT, ONIOM(MO:MM)
- Optimization of conical intersections via state-averaged CASSCF
- Generalized internal coordinates for complex optimization constraints

Vibrational Frequency Analysis

- Vibrational frequencies and normal modes (harmonic and anharmonic), including display/output limiting to specified atoms/ residues/modes (optional mode sorting)
- Restartable analytic HF and DFT frequencies
- MO:MM ONIOM frequencies including electronic embedding
- Analytic Infrared and static and dynamic Raman intensities (HF & DFT; MP2 for IR)
- Pre-resonance Raman spectra (HF and DFT)
- Projected frequencies perpendicular to a reaction path
- NMR shielding tensors & GIAO magnetic susceptibilities (HF, DFT, MP2) and enhanced spin-spin coupling (HF, DFT)
- Vibrational circular dichroism (VCD) rotational strengths (HF and DFT; harmonic and anharmonic)
- Dynamic Raman Optical Activity (ROA) intensities (harmonic and anharmonic)
- Raman and ROA intensities calculated separately from force constants in order to use a larger basis set
- Harmonic vibration-rotation coupling
- Enhanced anharmonic vibrational analysis, including IR intensities, DCPT2 & HDCPT2 method for resonance-free computations of anharmonic frequencies
- Anharmonic vibration-rotation coupling via perturbation theory
- Hindered rotor analysis

Molecular Properties

- Population analysis, including per-orbital analysis for specified orbitals: Mulliken, Hirshfeld/CM5
- Computed atomic charges can be saved for use in a later MM calculation
- Electrostatic potential, electron density, density gradient, Laplacian, and magnetic shielding & induced current densities over an automatically generated grid
- Multipole moments through hexadecapole
- Biorthogonalization of MOs (producing corresponding orbitals)
- Electrostatic potential-derived charges (Merz-Singh-Kollman, CHelp, CHelpG, Hu-Lu-Yang)
- Natural orbital analysis and natural transition orbitals
- Natural Bond Orbital (NBO) analysis, including orbitals for CAS jobs. Integrated support for NBO3, **external interface to NBO6**
- Static and frequency-dependent analytic polarizabilities and hyperpolarizabilities (HF and DFT); numeric 2nd hyperpolarizabilities (HF; DFT w/ analytic 3rd derivs.)
- Approx. CAS spin orbit coupling between states
- Enhanced optical rotations and optical rotary dispersion (ORD)
- Hyperfine spectra components: electronic g tensors, Fermi contact terms, anisotropic Fermi contact terms, rotational constants, dipole hyperfine terms, quartic centrifugal distortion, electronic spin rotation tensors, nuclear electric quadrupole constants, nuclear spin rotation tensors
- ONIOM integration of electric and magnetic properties

ONIOM Calculations

- Enhanced 2 and 3 layer ONIOM energies, gradients and frequencies using any available method for any layer
- Optional electronic embedding for MO:MM energies, gradients and frequencies implemented so as to include all effects of the MM environment without neglecting terms in its coupling with the QM region
- Enhanced MO:MM ONIOM optimizations to minima and transition structures via microiterations including electronic embedding
- Support for IRC calculations
- ONIOM integration of electric and magnetic properties

Excited States

- ZINDO energies
- CI-Singles energies, gradients, & freqs.
- Restartable time-dependent (TD) HF & DFT energies, gradients and frequencies. TD-DFT can use the Tamm-Dancoff approximation.
- SAC-CI energies and gradients
- EOM-CCSD energies and **gradients** (restartable); optionally input amplitudes computed with a smaller basis set
- Franck-Condon, Herzberg-Teller and FCHT analyses
- Vibronic spectra including electronic circular dichroism (ECD) rotational strengths (HF and DFT)
- Resonance Raman spectra
- Ciofini's excited state charge transfer diagnostic (D_{CT})
- Caricato's EOMCC solvation interaction models
- CI-Singles and TD-DFT in solution
- State-specific excitations and de-excitations in solution
- An energy range for excitations can be specified for CIS and TD excitation energies

Self-Consistent Reaction Field Solvation Models

- New implementation of the Polarized Continuum Model (PCM) facility for energies, gradients and frequencies
- Solvent effects on vibrational spectra, NMR, and other properties
- Solvent effects for ADMP trajectory calcs.
- Solvent effects for ONIOM calculations
- Enhanced solvent effects for excited states
- SMD model for ΔG of solvation
- Other SCRF solvent models (HF & DFT): Onsager energies, gradients and freqs., Isodensity Surface PCM (I-PCM) energies and Self-Consistent Isodensity Surface PCM (SCI-PCM) energies and gradients

Ease-of-Use Features

- Automated counterpoise calculations
- Automated optimization followed by frequency or single point energy
- Ability to easily add, remove, freeze, differentiate redundant internal coords.
- Simplified isotope substitution and temperature/pressure specification in the route section
- Optimizations:
 - * Retrieve the *n*th geometry from a checkpoint file
 - * Recompute the force constants every nth step of a geometry optimization
 - * Reduce the maximum number of allowed steps, including across restarts
- *180° flips detected and suppressed for better visualization
- Freezing by fragment for ONIOM optimizations
- Simplified fragment definitions on molecule specifications
- Many more restartable job types
- Atom freezing in optimizations by type, fragment, ONIOM layer and/ or residue
- QST2/QST3 automated transition structure optimizations
- Saving and reading normal modes
- %OldChk Link 0 command specifies read-only checkpoint file for data retrieval
- Default.Route file for setting calculation defaults
- Enhanced set of equivalent Default.Route directives, Link 0 commands, command line options and environment variables

Integration with External Programs

- NBO 6
- COSMO/RS
- AIMPAC WfnX files
- Antechamber
- ACID
 - Pickett's program
 - DFTB input files
 - General external interface script-based automation, results postprocessing, interchanging data/calculation results with other programs, and so on:
 - * Interface routines in Fortran, Python and Perl (open source)
 - *Keyword and Link 0 command support

GaussView 6 Features at a Glance

Features new to GaussView 6 are in blue; features enhanced in GaussView 6 are in green.

Examine Molecular Structures

- Rotate, translate and zoom in 3D in any display using mouse operations and/or a precision positioning toolbar
- View numeric value for any structural parameter
- Use multiple synchronized or independent views of same structure (customizable)
- Manipulate multiple structures as an ensemble
- Display formats: wire frame, tubes, ball & stick/bond type, space fill (CPK) style
- View per-atom labels for element, serial number, NMR shielding (when available)
- Visualize depth with fog feature
- Display stereochemistry info
- Highlight, display or hide atoms based on rich selection capabilities (optionally persistent)

Build/Modify Molecules

- Convenient palettes for atoms, functional groups, rings, amino acids (central fragment, amino- or carboxyl-terminated) and nucleosides (central fragment, C3'-, C5'-terminated, free forms)
- Custom fragment libraries
- Import standard molecule file formats:
- * PDB, including ones created by AMBER. Optionally include/discard waters, apply standard residue bonding on PDB import.
- * Gaussian input (.gjf and .com), output (.log and .out), checkpoint
- (.chk and .fchk), cube (.cub), and frequency (.gfrq) files * Sybyl .mol2, .ml2; include/convert .mol2 lone pairs
- * MDL files: .mol, .rxn, .sdf
- * Crystallographic Information files: .cif
- Optionally include intermediate structures from optimizations, scans, etc.
- Accurately add hydrogens automatically or manually to an entire molecule or a selection
- An advanced open dialog, allowing options to be customized and retained across sessions:
 - * Reading intermediate geometries
 - * Using the bond table and weak bond inclusion
 - * Gaussian input & log file load orders
 - * PDB and .mol2 file settings
- * Saving the formatted checkpoint file
- Modify bond type/length, bond angles, dihedral angles
- Rationalize structures with an advanced clean function
- Recompute bonding on demand
- Increase or decrease symmetry of molecular structure; constrain structure to specific point group
- Mirror invert structure
- Invert structure about selected atom
- Place atom/fragment at centroid of selected atoms
- Define named groups of atoms via:
- *Click, marquee & brush selection modes
- * Complex filters combining atom type, number, MM settings, ONIOM layer
- * Select by PDB residue and/or secondary structure (e.g., helix, chain) * Expand selections by bond or proximity
- * Use groups for display purposes and in Gaussian input
- Specify nonstandard isotopes
- Customize fragment placement behavior
- Specify custom bonding parameters

Graphical Setup for Specific Calculations

- Specify input for complex calculations via simple mouse/spreadsheet operations:
- Build unit cells for polymers, 2D surfaces and crystals (periodic boundary conditions)
- \ast Constrain to specific space group symmetry
- Assign atoms to ONIOM layers by
- *Direct selection
- * Bond proximity to specified atom
- * Absolute distance from specified atom
- * PDB file residue, secondary structure

- *Complex selection criteria
- View/specify MM atom types and charges
- Add/redefine redundant internal coordinates
- Specify frozen atoms/coordinates during optimizations
- Set atom equivalences for QST2/QST3 TS optimizations
- Manipulate MOs: Select, rearrange/reoccupy orbitals for CASSCF, etc.
 Define fragments for fragment guess/counterpoise calculations
- Define fragments for fragment guess/counterpoise calculation * Assign fragment-specific charges & spin multiplicities
 Include PDB data in molecule specification
- Include PDB data in molecule specification
 Select normal modes for frequency calculations
- Select normal modes for frequency calculations
 Specify atoms for NMR spin-spin coupling
- Specify atoms for NMR spin-spin coupling
 Search for conformations using the GMMX add-on
- Full AMPAC integration if software is installed

Prepare and Run Gaussian Calculations

- Create input files via a menu-driven interface:
 * Select job/method/basis from pop-up menus; related options appear automatically
 - * Supports all major Gaussian 16 features
- * Convenient access to commonly-used general options
- * Additional input can be entered; input sections in imported files are retained
- * Preview input file before saving/submitting
- Select solvent and specify other parameters for calculations in solution
- Specify Link 0 commands
- Specify settings for multiprocessor and cluster/network parallel jobs
- Use calculation schemes to set up jobs from templates
- "Quick launch" Gaussian jobs with a single mouse click
- Molecule specification created automatically * Optional connectivity section
- Stream log files in a text-searchable window
- Monitor/control local Gaussian and utility processes
- Integrated, customizable queuing system
- Initiate remote jobs via a script
- Generate job-specific input automatically:
 * PBC translation vector for periodic structures like polymers and crystals
 - * Orbital alterations
 - * Multiple molecule specifications for QST2/QST3 transition state searches
 - * Fragment guess and counterpoise per-fragment charge and spin multiplicity
- Apply calculation settings to a group of molecules with one click
- Save/submit identical jobs for a group of molecules in a single step, using unique file names

Examine & Visualize Gaussian Results

- Select which jobs to open from multi-step results files
- Show calculation results summary, including basic information, optimization step data and thermochemical results
- Display results tables for a molecule group
- Examine atomic charges: numerical values, color atoms by charge, dipole moment vector
- Visualize atomic properties, predicted bond lengths and predicted bond orders
- Create surfaces and contours for molecular orbitals, electron density, electrostatic potential, spin density, NMR shielding density
 - * Display formats: 3D solid, translucent or wire mesh; 2D contour
 - * Color surfaces by a separate property
 - * Specify the desired contour plane
 - * Load cubes created by Gaussian; save computed cubes for future reuse; perform operations on cubes
- Animate normal modes:

* Scale frequencies

* Indicate motion via displacement vector, dipole derivative unit vector

* Save animations as MP4 movies, with options for speed, aspect

ratio, looping, time delay between frames and frames/loop

* Save generated normal modes back to checkpoint file

* Displace structures along normal mode * Select subset of modes for display

- Display spectra: IR, Raman, NMR, VCD, ROA, UV-Visible, etc.
 - * Select Harmonic and/or Anharmonic results
 - * Customize plot displays
 - * Display multiple data sets on a single spectra plot, with optional conformational averaging
- Substitute isotopes in frequency analysis
- Specify incident light frequency for frequency-dependent calculations
- Display results from Gaussian trajectory calculations
- View energy plot of conformational search result set
- NMR Results:
 - * Report absolute NMR chemical shifts or relative to reference compound
 - * Export NMR summary data as text
- Animate structure sequences: geometry optimizations, IRC reaction paths, potential energy surface scans, BOMD and ADMP trajectories * Single play or continuous looping; play in reverse
 - * Save animations as MP4 movies, with options for speed, aspect ratio and frame & endpoint delays
 - * Plots of related data are also produced
- Display 3D surface plots for 2-variable scan calculations
- Customize plot and spectra displays by zooming, scaling, inverting, etc. * Add molecular properties to plots
- * Advanced plot customization; line color, canvas and background color, title, x- and y- axis settings, etc.
- * Mixture Editor for multiple overlaid plots
- Save any image to a file (including customizations):
 - * Produce web graphics: JPEG, PNG and other formats * Produce publication quality graphics files and printouts: TIFF, JPEG, vector graphics EPS

- * Create images at arbitrary size and resolution
- * Select full color or high quality grey scale formats
- * Specify custom colors and/or background
- Save plots as images or textual data files
- Save animations in GIF, MNG, MP4 format or as individual frames
- Display PCM solvation cavity as a surface

Customize GaussView

Set/save preferences for most aspects of GaussView functionality:

- Control building toolbars individually · Colors: per-element, molecule window background, surfaces,
- transparency
- Builder operation: atom and fragment join methods, adding hydrogens when needed, automated full or partial clean operations, etc.
- Gaussian 16 calculation settings Gaussian job execution methods
- Display modes
- Window placement and visibility
- Icon sizes
- File/directory locations
- Image capture and printing defaults
- Animation settings and movie defaults
- Clean function parameters
- Charge distribution display defaults
- Custom bonding parameters
- GaussView Tips facility
- Windows file extension associations
- Dialog-specific help system



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