



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:08 PM UTC

PDB ID : 2YNG / pdb_00002yng
Title : HIV-1 Reverse Transcriptase in complex with inhibitor GSK560
Authors : Chong, P.; Sebahar, P.; Youngman, M.; Garrido, D.; Zhang, H.; Stewart, E.L.; Nolte, R.T.; Wang, L.; Ferris, R.G.; Edelstein, M.; Weaver, K.; Mathis, A.; Peat, A.
Deposited on : 2012-10-14
Resolution : 2.12 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

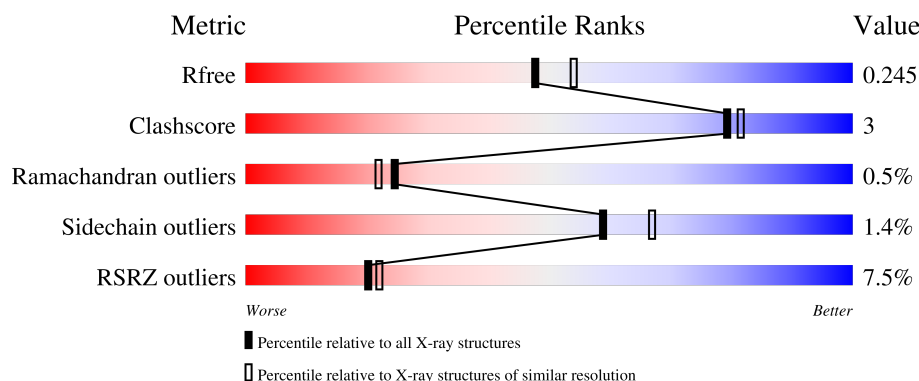
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

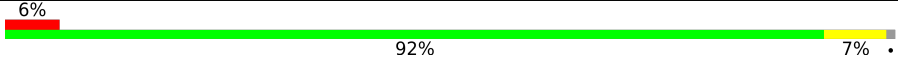
The reported resolution of this entry is 2.12 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	8290 (2.14-2.10)
Clashscore	190562	8817 (2.14-2.10)
Ramachandran outliers	187476	8738 (2.14-2.10)
Sidechain outliers	187428	8739 (2.14-2.10)
RSRZ outliers	180081	8294 (2.14-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	563	
2	B	447	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	MG	A	1561	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8582 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called REVERSE TRANSCRIPTASE/RIBONUCLEASE H.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	560	Total	C	N	O	S	0	5	0
			4520	2919	751	842	8			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	MET	-	expression tag	UNP P04585
A	-1	ASN	-	expression tag	UNP P04585
A	0	SER	-	expression tag	UNP P04585

- Molecule 2 is a protein called P51 RT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	411	Total	C	N	O	S	0	3	0
			3360	2197	547	608	8			

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	MET	-	expression tag	UNP P04585
B	-17	ALA	-	expression tag	UNP P04585
B	-16	GLY	-	expression tag	UNP P04585
B	-15	HIS	-	expression tag	UNP P04585
B	-14	HIS	-	expression tag	UNP P04585
B	-13	HIS	-	expression tag	UNP P04585
B	-12	HIS	-	expression tag	UNP P04585
B	-11	HIS	-	expression tag	UNP P04585
B	-10	HIS	-	expression tag	UNP P04585
B	-9	GLY	-	expression tag	UNP P04585
B	-8	SER	-	expression tag	UNP P04585
B	-7	ALA	-	expression tag	UNP P04585
B	-6	GLU	-	expression tag	UNP P04585

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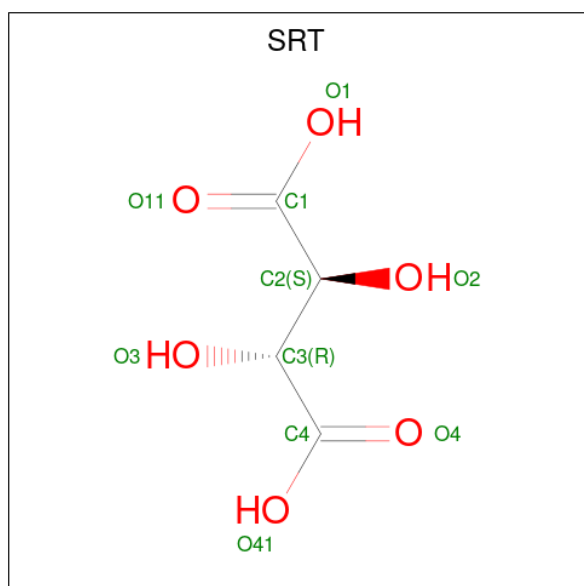
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Chain	Residue	Modelled	Actual	Comment	Reference
B	-5	ASN	-	expression tag	UNP P04585
B	-4	LEU	-	expression tag	UNP P04585
B	-3	TYR	-	expression tag	UNP P04585
B	-2	PHE	-	expression tag	UNP P04585
B	-1	GLN	-	expression tag	UNP P04585
B	0	GLY	-	expression tag	UNP P04585

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

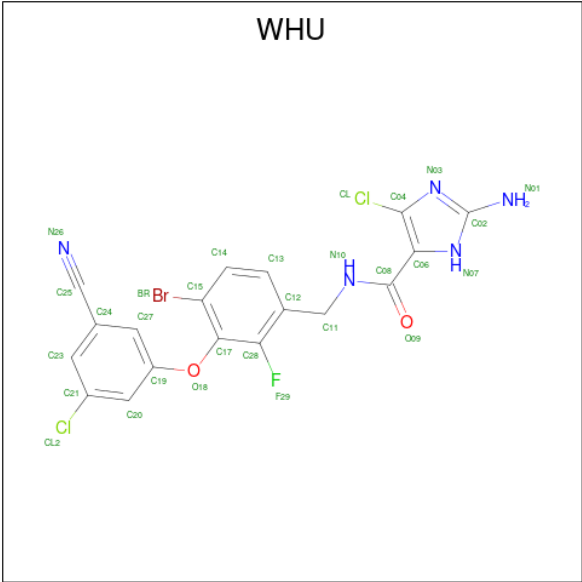
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	3	Total Mg 3 3	0	0

- Molecule 4 is S,R MESO-TARTARIC ACID (CCD ID: SRT) (formula: C₄H₆O₆).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 10 4 6	0	0

- Molecule 5 is 2-azanyl-N-[[4-bromanyl-3-(3-chloranyl-5-cyano-phenoxy)-2-fluoranyl-phenyl]methyl]-4-chloranyl-1H-imidazole-5-carboxamide (CCD ID: WHU) (formula: C₁₈H₁₁BrCl₂FN₅O₂).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
			Total	Br	C	Cl	F	N	O		
5	A	1	29	1	18	2	1	5	2	0	0

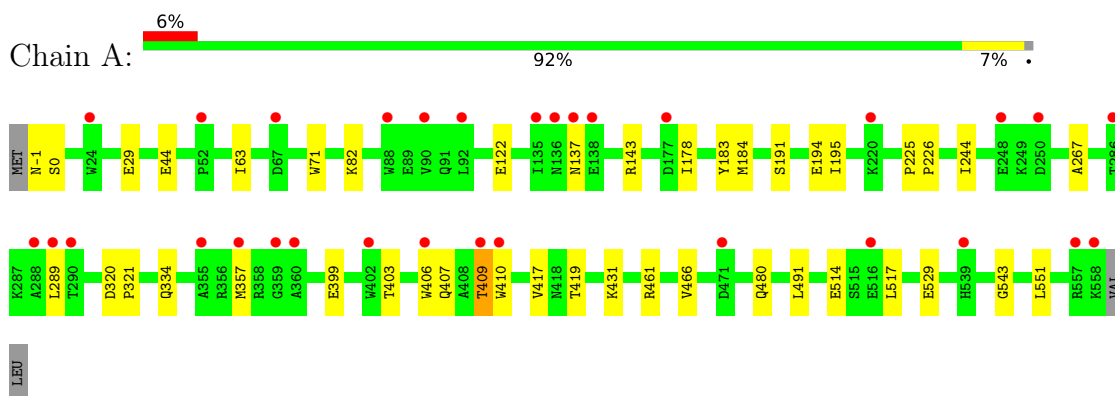
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	394	Total	O	0	0
			394	394		
6	B	266	Total	O	0	0
			266	266		

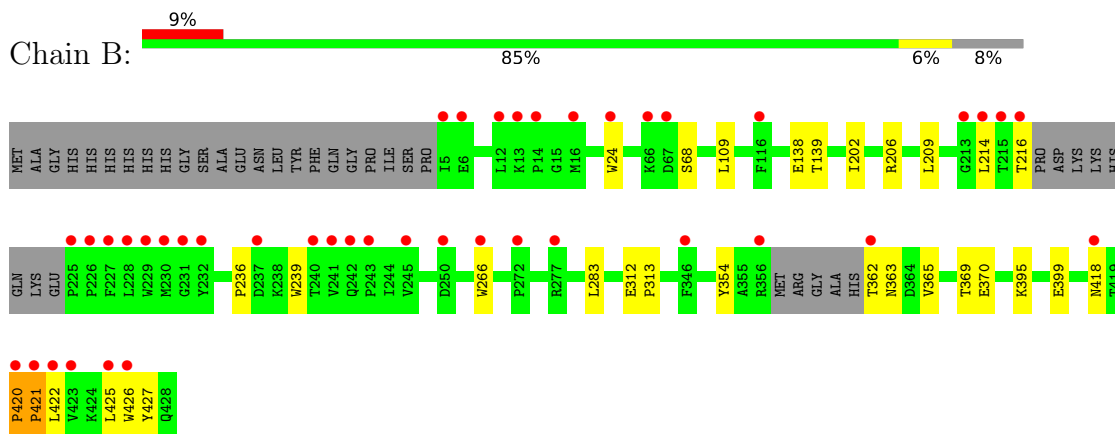
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: REVERSE TRANSCRIPTASE/RIBONUCLEASE H



• Molecule 2: P51 RT



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	118.88Å 154.63Å 156.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	78.57 – 2.12 78.57 – 2.12	Depositor EDS
% Data completeness (in resolution range)	99.9 (78.57-2.12) 99.9 (78.57-2.12)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.92 (at 2.12Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.196 , 0.241 0.200 , 0.245	Depositor DCC
R_{free} test set	2455 reflections (3.00%)	wwPDB-VP
Wilson B-factor (Å ²)	33.5	Xtriage
Anisotropy	0.158	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 48.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8582	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.02% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: WHU, MG, SRT

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.79	0/4640	0.79	0/6317
2	B	0.78	0/3466	0.78	0/4726
All	All	0.78	0/8106	0.78	0/11043

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4520	0	4484	24	0
2	B	3360	0	3302	21	0
3	A	3	0	0	0	0
4	A	10	0	4	1	0
5	A	29	0	11	0	0
6	A	394	0	0	2	0
6	B	266	0	0	2	0
All	All	8582	0	7801	42	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (42) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:466:VAL:CG2	1:A:551:LEU:HG	2.17	0.74
1:A:183:TYR:OH	1:A:184:MET:HE3	1.87	0.73
1:A:466:VAL:HG21	1:A:551:LEU:HG	1.77	0.66
1:A:409:THR:HG21	6:A:2278:HOH:O	1.94	0.66
2:B:202:ILE:O	2:B:206[A]:ARG:HG2	1.99	0.62
1:A:244:ILE:HD13	1:A:267:ALA:HB2	1.84	0.60
2:B:365:VAL:O	2:B:369:THR:HG23	2.03	0.59
1:A:461:ARG:NH2	4:A:1562:SRT:O4	2.36	0.55
2:B:24[C]:TRP:HB2	6:B:2017:HOH:O	2.05	0.55
2:B:266:TRP:HH2	2:B:427:TYR:CZ	2.25	0.55
1:A:410:TRP:CE3	2:B:363:ASN:HB2	2.42	0.55
1:A:-1:ASN:HB2	1:A:44:GLU:HG2	1.90	0.54
1:A:491:LEU:HB3	1:A:529:GLU:HG3	1.89	0.53
2:B:266:TRP:CH2	2:B:427:TYR:CZ	2.97	0.52
2:B:216:THR:CB	6:B:2179:HOH:O	2.58	0.52
2:B:109:LEU:HD22	2:B:206[A]:ARG:NH1	2.25	0.51
2:B:395:LYS:NZ	2:B:399:GLU:OE2	2.44	0.51
2:B:354:TYR:OH	2:B:370:GLU:OE1	2.20	0.51
1:A:357:MET:HE2	1:A:514:GLU:HG3	1.92	0.51
2:B:312:GLU:HG3	2:B:313:PRO:HD2	1.94	0.49
1:A:406:TRP:CE3	1:A:407:GLN:HG2	2.48	0.48
2:B:109:LEU:HD22	2:B:206[A]:ARG:HH11	1.78	0.47
1:A:-1:ASN:HB2	1:A:44:GLU:CG	2.45	0.46
1:A:195:ILE:HD12	1:A:195:ILE:H	1.81	0.46
2:B:138:GLU:HG2	2:B:139:THR:HG23	1.98	0.45
1:A:183:TYR:CZ	1:A:184:MET:HE3	2.52	0.43
1:A:480:GLN:HG2	1:A:517:LEU:HD21	2.00	0.43
2:B:312:GLU:HG3	2:B:313:PRO:CD	2.49	0.43
1:A:178:ILE:HD12	1:A:191:SER:HB3	2.01	0.43
1:A:29:GLU:HG2	1:A:71:TRP:CZ2	2.55	0.42
1:A:122:GLU:HG3	6:A:2012:HOH:O	2.19	0.42
1:A:417:VAL:HG22	1:A:419:THR:HG23	2.01	0.42
1:A:410:TRP:CE3	2:B:363:ASN:CB	3.03	0.41
2:B:266:TRP:CG	2:B:426:TRP:CE3	3.08	0.41
2:B:420:PRO:HB2	2:B:421:PRO:CA	2.50	0.41
1:A:225:PRO:HA	1:A:226:PRO:C	2.44	0.41
2:B:209:LEU:HD22	2:B:214:LEU:HD23	2.02	0.41
1:A:320:ASP:HA	1:A:321:PRO:HD2	1.96	0.41
1:A:543:GLY:HA3	2:B:283:LEU:O	2.20	0.41
2:B:236:PRO:HA	2:B:239:TRP:CD2	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:266:TRP:CZ3	2:B:426:TRP:HB3	2.56	0.40
1:A:399:GLU:O	1:A:403:THR:HG23	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	563/563 (100%)	543 (96%)	16 (3%)	4 (1%)	18	15
2	B	408/447 (91%)	393 (96%)	13 (3%)	2 (0%)	24	22
All	All	971/1010 (96%)	936 (96%)	29 (3%)	6 (1%)	24	18

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	137	ASN
1	A	334[A]	GLN
1	A	334[B]	GLN
2	B	421	PRO
1	A	289	LEU
2	B	420	PRO

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	484/503 (96%)	477 (99%)	7 (1%)	59	67
2	B	358/404 (89%)	353 (99%)	5 (1%)	59	67
All	All	842/907 (93%)	830 (99%)	12 (1%)	59	67

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	0	SER
1	A	63	ILE
1	A	82	LYS
1	A	143	ARG
1	A	194	GLU
1	A	409	THR
1	A	431	LYS
2	B	68	SER
2	B	362	THR
2	B	418	ASN
2	B	422	LEU
2	B	425	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	137	ASN
1	A	315	HIS
1	A	336	GLN
2	B	265	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	SRT	A	1562	-	9,9,9	1.18	0	12,12,12	1.33	2 (16%)
5	WHU	A	1563	-	31,31,31	1.10	2 (6%)	37,44,44	1.65	8 (21%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	SRT	A	1562	-	-	7/12/12/12	-
5	WHU	A	1563	-	-	0/15/15/15	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1563	WHU	C08-N10	3.10	1.38	1.33
5	A	1563	WHU	C02-N01	2.30	1.39	1.34

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1563	WHU	C12-C11-N10	-6.37	100.31	113.15
5	A	1563	WHU	C19-O18-C17	3.44	123.83	118.40
4	A	1562	SRT	O41-C4-C3	2.65	120.67	113.31
5	A	1563	WHU	F29-C28-C17	-2.38	115.78	119.39
5	A	1563	WHU	C06-C04-CL	2.23	127.78	126.37
4	A	1562	SRT	O1-C1-C2	2.20	119.42	113.31
5	A	1563	WHU	C27-C24-C25	-2.14	116.66	119.55
5	A	1563	WHU	C17-C28-C12	2.05	124.45	121.33
5	A	1563	WHU	C20-C21-CL2	2.03	121.72	119.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1563	WHU	C27-C24-C23	2.03	122.84	119.70

There are no chirality outliers.

All (7) torsion outliers are listed below:

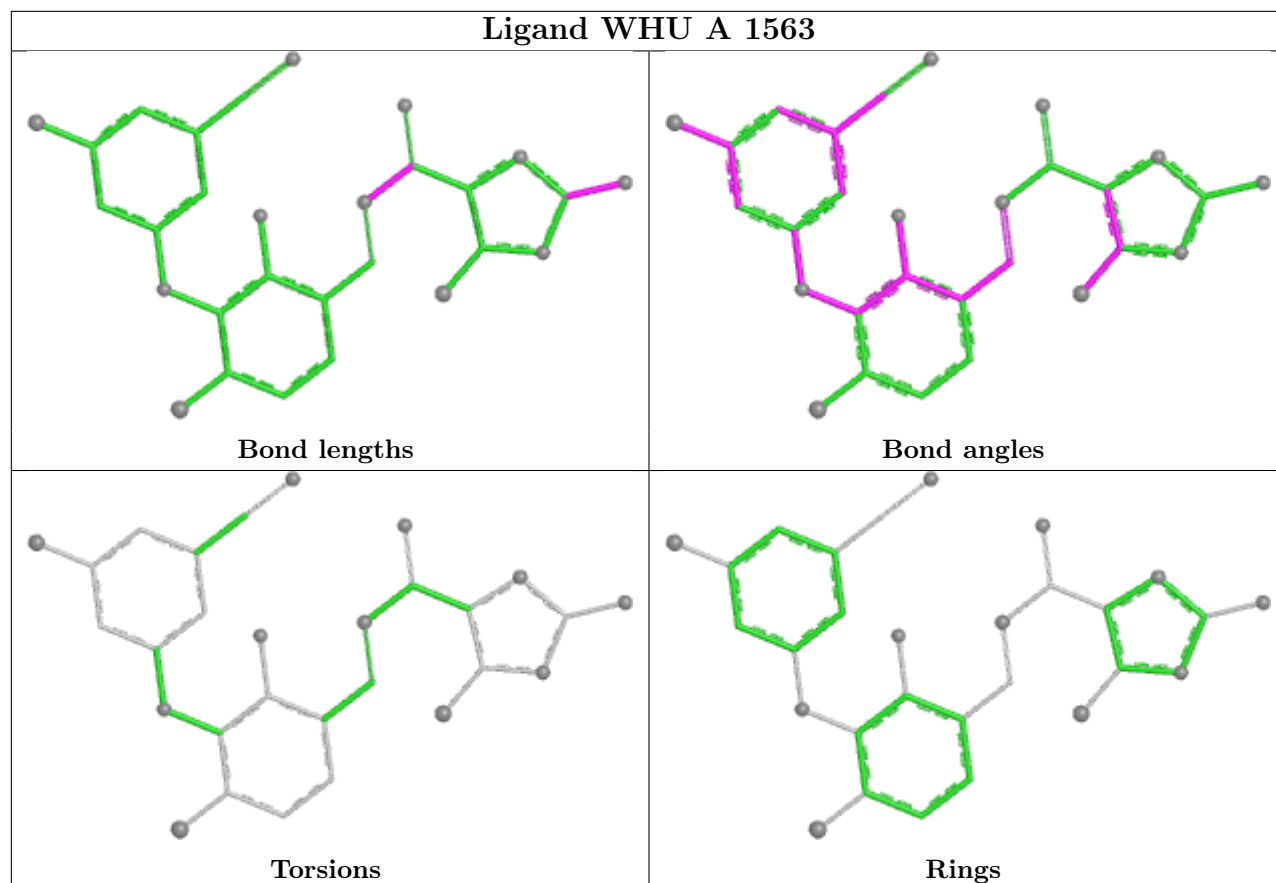
Mol	Chain	Res	Type	Atoms
4	A	1562	SRT	O1-C1-C2-O2
4	A	1562	SRT	O11-C1-C2-O2
4	A	1562	SRT	O3-C3-C4-O4
4	A	1562	SRT	O3-C3-C4-O41
4	A	1562	SRT	O2-C2-C3-O3
4	A	1562	SRT	O2-C2-C3-C4
4	A	1562	SRT	O1-C1-C2-C3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1562	SRT	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	560/563 (99%)	0.29	31 (5%)	30 33	18, 41, 74, 104	12 (2%)
2	B	411/447 (91%)	0.46	42 (10%)	12 13	19, 40, 88, 158	6 (1%)
All	All	971/1010 (96%)	0.36	73 (7%)	20 22	18, 41, 78, 158	18 (1%)

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	213	GLY	8.6
2	B	215	THR	6.7
2	B	214	LEU	6.4
2	B	422	LEU	5.5
1	A	136	ASN	5.3
2	B	216	THR	5.1
2	B	266	TRP	5.1
2	B	421	PRO	4.8
2	B	228	LEU	4.6
2	B	227	PHE	4.4
2	B	225	PRO	4.3
1	A	558	LYS	4.3
2	B	66	LYS	4.3
2	B	14	PRO	4.2
2	B	24[A]	TRP	4.0
2	B	425	LEU	4.0
1	A	406	TRP	4.0
2	B	426	TRP	3.9
2	B	420	PRO	3.9
2	B	16[A]	MET	3.8
1	A	357	MET	3.8
2	B	5	ILE	3.6
2	B	67	ASP	3.6
1	A	289	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	288	ALA	3.5
1	A	360	ALA	3.4
2	B	116	PHE	3.4
1	A	24	TRP	3.3
1	A	410	TRP	3.3
2	B	423	VAL	3.3
2	B	229	TRP	3.3
2	B	356	ARG	3.2
1	A	137	ASN	3.2
2	B	241	VAL	3.2
2	B	362	THR	3.2
2	B	243	PRO	3.2
2	B	242	GLN	3.2
1	A	250	ASP	3.1
2	B	245	VAL	3.0
1	A	359	GLY	2.9
1	A	135	ILE	2.8
1	A	138	GLU	2.8
1	A	290	THR	2.8
2	B	231	GLY	2.8
1	A	67	ASP	2.7
1	A	52	PRO	2.7
2	B	418	ASN	2.7
1	A	402	TRP	2.7
2	B	226	PRO	2.7
2	B	6	GLU	2.6
2	B	230	MET	2.6
1	A	88	TRP	2.6
2	B	272	PRO	2.5
1	A	248	GLU	2.5
1	A	286	THR	2.5
1	A	557	ARG	2.5
1	A	92	LEU	2.4
2	B	346	PHE	2.4
2	B	12	LEU	2.4
1	A	90	VAL	2.4
2	B	13	LYS	2.3
1	A	539	HIS	2.3
2	B	250	ASP	2.2
1	A	409	THR	2.2
1	A	471	ASP	2.2
2	B	237	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	355	ALA	2.1
1	A	177[A]	ASP	2.1
2	B	232	TYR	2.1
2	B	240	THR	2.1
2	B	277	ARG	2.0
1	A	516	GLU	2.0
1	A	220	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

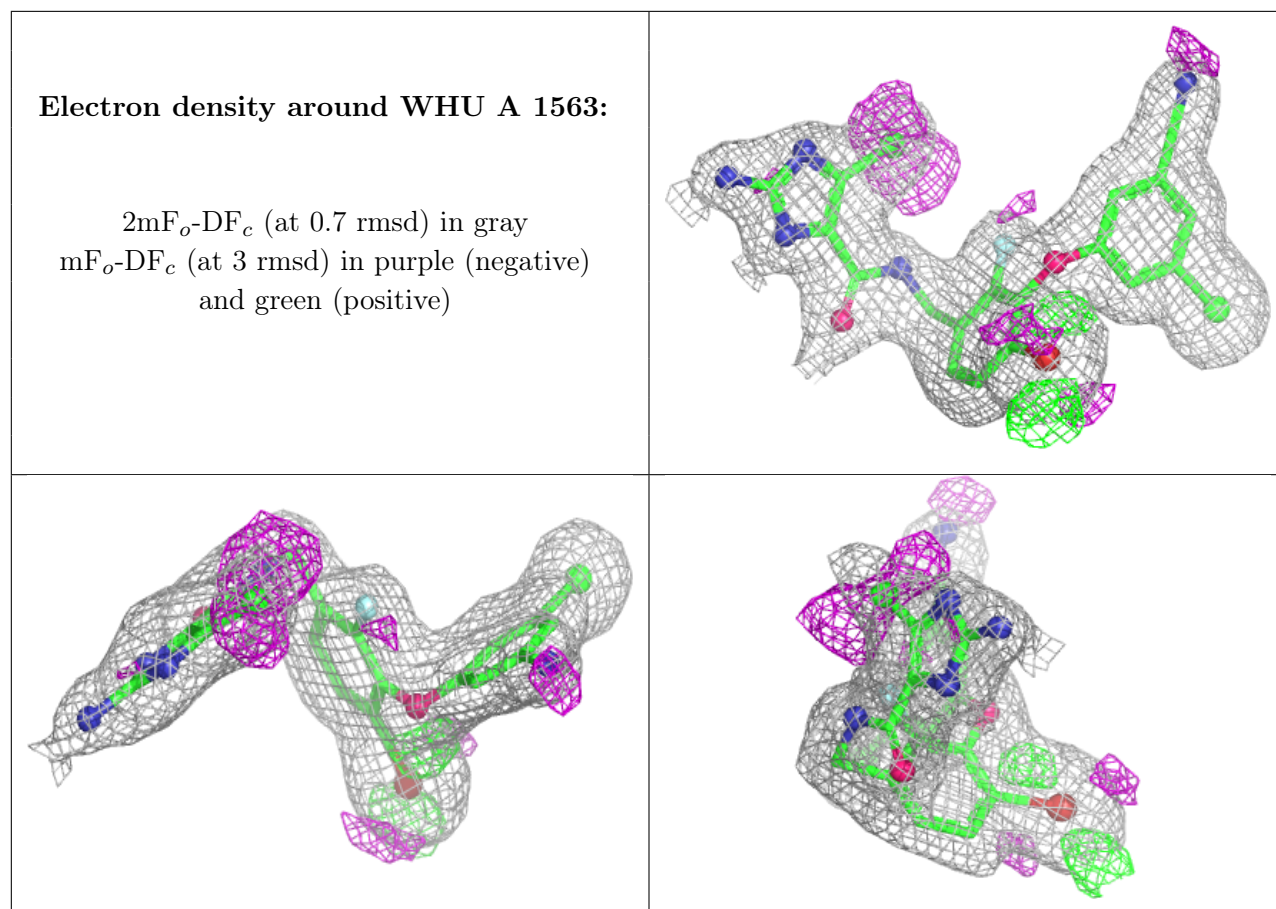
There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	MG	A	1561	1/1	0.68	0.43	45,45,45,45	1
3	MG	A	1560	1/1	0.77	0.29	40,40,40,40	1
4	SRT	A	1562	10/10	0.78	0.14	53,64,71,75	0
3	MG	A	1559	1/1	0.90	0.10	36,36,36,36	0
5	WHU	A	1563	29/29	0.97	0.07	25,29,38,48	1

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers ⓘ

There are no such residues in this entry.