



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:03 AM UTC

PDB ID : 3TAM / pdb_00003tam
Title : Crystal structure of HIV-1 reverse transcriptase (K103N mutant) in complex with inhibitor M06
Authors : Yan, Y.
Deposited on : 2011-08-04
Resolution : 2.51 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

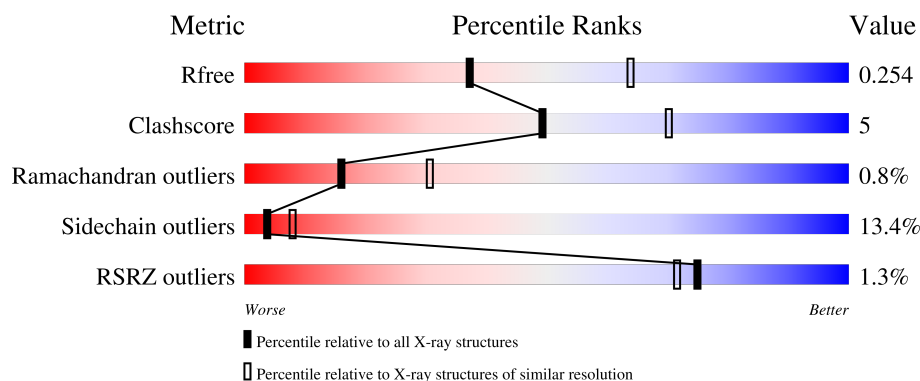
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.51 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	73%22% . .
2	B	443	2% 67%19% . . 9%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8227 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	553	Total	C	N	O	S	0	0	0
			4503	2910	753	832	8			

There are 6 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
A	1	PRO	-	expression tag	UNP P04585
A	2	ILE	-	expression tag	UNP P04585
A	103	ASN	LYS	engineered mutation	UNP P04585

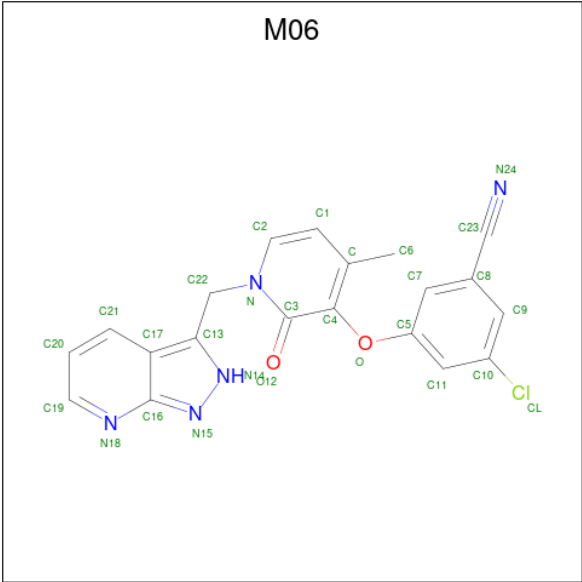
- Molecule 2 is a protein called p51 RT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	403	Total	C	N	O	S	0	0	0
			3334	2170	552	606	6			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	MET	-	expression tag	UNP P04585
B	-1	ASN	-	expression tag	UNP P04585
B	0	SER	-	expression tag	UNP P04585
B	103	ASN	LYS	engineered mutation	UNP P04585

- Molecule 3 is 3-chloro-5-([4-methyl-2-oxo-1-(2H-pyrazolo[3,4-b]pyridin-3-ylmethyl)-1,2-dihydro-3-yl]oxy)benzonitrile (CCD ID: M06) (formula: C₂₀H₁₄ClN₅O₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	Cl	N	O	0	0
			28	20	1	5	2		

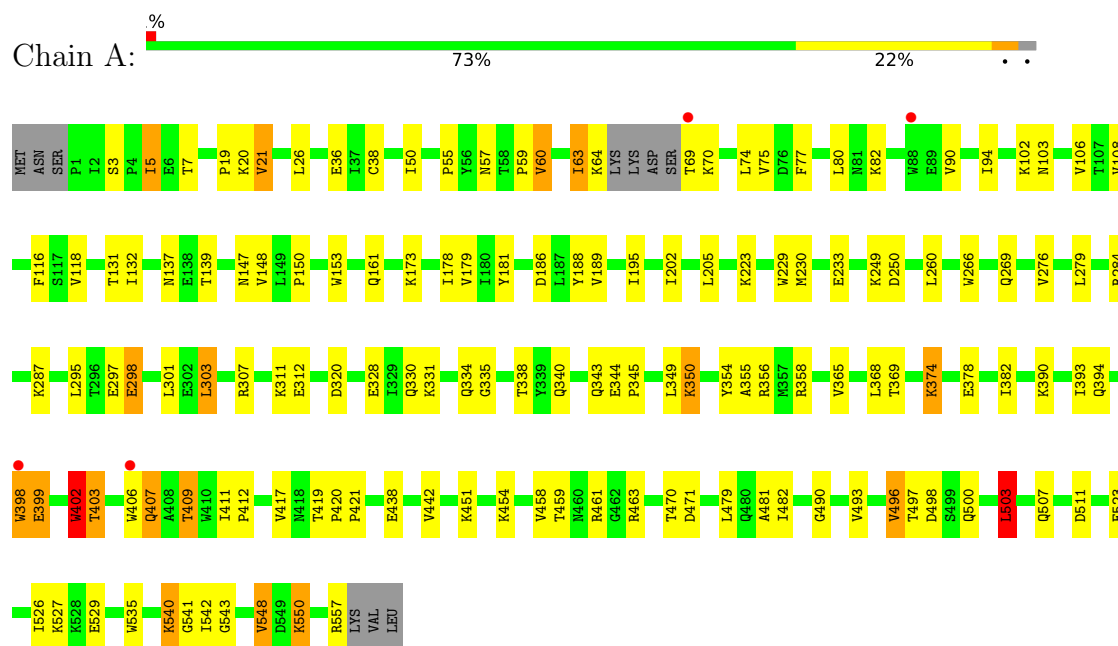
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	214	Total	O	0	0
			214	214		
4	B	148	Total	O	0	0
			148	148		

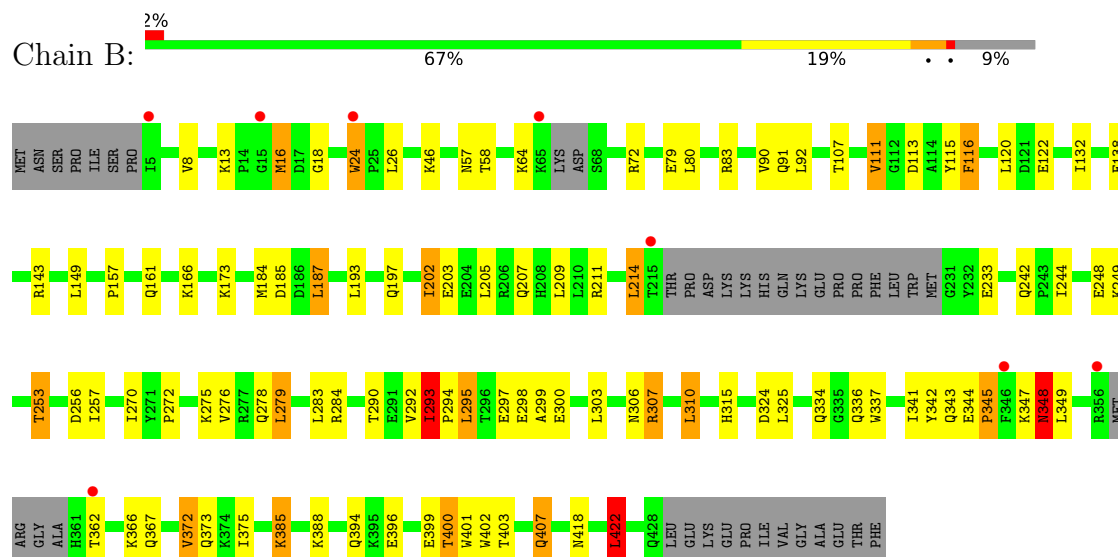
3 Residue-property plots

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	117.91Å 153.90Å 155.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	16.58 – 2.51 16.58 – 2.51	Depositor EDS
% Data completeness (in resolution range)	87.5 (16.58-2.51) 87.1 (16.58-2.51)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.46 (at 2.52Å)	Xtriage
Refinement program	BUSTER 2.9.4	Depositor
R, R_{free}	0.193 , 0.249 0.194 , 0.254	Depositor DCC
R_{free} test set	2150 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	54.9	Xtriage
Anisotropy	0.214	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 51.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8227	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.96% 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: M06

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	0.84	0/4619	1.35	27/6277 (0.4%)
2	B	0.83	0/3427	1.35	21/4657 (0.5%)
All	All	0.83	0/8046	1.35	48/10934 (0.4%)

There are no bond length outliers.

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	372	VAL	N-CA-CB	7.89	121.27	110.54
2	B	348	ASN	CA-C-N	7.57	131.04	120.29
2	B	348	ASN	C-N-CA	7.57	131.04	120.29
2	B	401	TRP	N-CA-C	7.55	122.79	112.90
1	A	153	TRP	CA-C-N	7.54	130.71	120.38
1	A	153	TRP	C-N-CA	7.54	130.71	120.38
2	B	343	GLN	N-CA-C	-6.81	104.85	113.43
1	A	420	PRO	N-CA-C	6.76	116.96	110.47
1	A	349	LEU	N-CA-C	-6.59	103.35	111.40
2	B	345	PRO	N-CA-C	6.46	125.78	112.47
2	B	233	GLU	N-CA-C	6.39	120.21	107.62
2	B	348	ASN	CA-CB-CG	6.33	118.93	112.60
1	A	496	VAL	N-CA-CB	6.28	119.37	111.46
2	B	307	ARG	CA-C-N	6.16	128.54	120.28
2	B	307	ARG	C-N-CA	6.16	128.54	120.28
1	A	334	GLN	N-CA-C	6.12	118.16	108.67
2	B	348	ASN	N-CA-C	6.06	118.61	108.73
1	A	186	ASP	CA-CB-CG	6.04	118.64	112.60
1	A	250	ASP	CA-CB-CG	5.94	118.54	112.60
1	A	511	ASP	CA-CB-CG	5.92	118.52	112.60
1	A	526	ILE	CA-C-N	5.90	128.18	120.28
1	A	526	ILE	C-N-CA	5.90	128.18	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	382	ILE	N-CA-C	5.83	116.61	110.72
1	A	498	ASP	CA-CB-CG	5.75	118.35	112.60
2	B	132	ILE	N-CA-C	-5.74	101.96	107.76
2	B	249	LYS	N-CA-C	5.71	117.86	109.24
1	A	132	ILE	N-CA-C	-5.67	102.40	107.56
2	B	185	ASP	CA-CB-CG	5.65	118.25	112.60
2	B	92	LEU	N-CA-C	-5.49	102.06	110.14
1	A	132	ILE	N-CA-CB	5.43	117.23	111.20
2	B	298	GLU	N-CA-C	-5.41	105.99	113.18
2	B	293	ILE	CB-CA-C	5.40	116.15	110.37
1	A	147	ASN	N-CA-C	-5.39	107.08	113.97
1	A	409	THR	CB-CA-C	5.37	119.98	109.35
2	B	402	TRP	N-CA-C	5.37	117.82	111.33
1	A	470	THR	N-CA-C	5.30	119.75	113.12
1	A	179	VAL	N-CA-CB	5.28	116.47	110.72
1	A	402	TRP	CA-C-N	5.24	127.62	120.54
1	A	402	TRP	C-N-CA	5.24	127.62	120.54
1	A	503	LEU	CA-C-N	5.20	125.87	119.99
1	A	503	LEU	C-N-CA	5.20	125.87	119.99
1	A	540	LYS	N-CA-C	-5.17	100.87	109.46
1	A	38	CYS	N-CA-C	5.15	116.89	111.28
2	B	161	GLN	CA-C-N	5.09	127.11	120.28
2	B	161	GLN	C-N-CA	5.09	127.11	120.28
1	A	550	LYS	CA-C-N	5.04	127.03	120.28
1	A	550	LYS	C-N-CA	5.04	127.03	120.28
2	B	422	LEU	N-CA-C	5.03	118.57	112.23

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	4503	0	4547	48	0
2	B	3334	0	3355	41	0
3	A	28	0	14	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	214	0	0	1	0
4	B	148	0	0	0	0
All	All	8227	0	7916	85	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 5.

All (85) 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)
2:B:79:GLU:HG3	2:B:83:ARG:HE	1.49	0.76
1:A:298:GLU:CD	1:A:298:GLU:H	1.91	0.74
2:B:396:GLU:O	2:B:400:THR:HG22	1.87	0.74
1:A:330:GLN:HE22	1:A:340:GLN:HE22	1.36	0.71
2:B:214:LEU:HD23	2:B:214:LEU:H	1.56	0.70
1:A:103:ASN:H	3:A:561:M06:HN14	1.37	0.70
1:A:406:TRP:CH2	2:B:418:ASN:HA	2.26	0.69
2:B:337:TRP:HE1	2:B:367:GLN:HE21	1.38	0.69
2:B:207:GLN:HE21	2:B:211:ARG:HH12	1.40	0.68
1:A:298:GLU:N	1:A:298:GLU:OE2	2.29	0.65
2:B:207:GLN:NE2	2:B:211:ARG:HH12	1.94	0.65
2:B:13:LYS:HB2	2:B:16:MET:HE1	1.80	0.63
1:A:63:ILE:HG21	1:A:74:LEU:HD12	1.80	0.63
1:A:297:GLU:HB3	1:A:298:GLU:OE2	2.01	0.60
1:A:57:ASN:ND2	1:A:131:THR:OG1	2.35	0.59
1:A:181:TYR:HB2	1:A:188:TYR:HB2	1.87	0.56
1:A:354:TYR:HD1	1:A:374:LYS:HD3	1.71	0.55
1:A:298:GLU:CD	1:A:298:GLU:N	2.64	0.55
2:B:295:LEU:HD23	2:B:300:GLU:HG3	1.90	0.54
1:A:330:GLN:HE22	1:A:340:GLN:NE2	2.05	0.54
1:A:328:GLU:HG2	1:A:390:LYS:HB2	1.88	0.54
2:B:275:LYS:H	2:B:306:ASN:HD21	1.54	0.54
1:A:21:VAL:HG22	1:A:59:PRO:HD3	1.90	0.54
1:A:330:GLN:NE2	1:A:340:GLN:HE22	2.07	0.53
1:A:369:THR:HG22	1:A:411:ILE:HD11	1.90	0.52
2:B:362:THR:CG2	2:B:367:GLN:HG3	2.39	0.52
1:A:438:GLU:HG3	1:A:461:ARG:HG2	1.91	0.52
1:A:442:VAL:HB	1:A:481:ALA:HB1	1.91	0.52
2:B:362:THR:HG22	2:B:367:GLN:HG3	1.92	0.52
1:A:399:GLU:O	1:A:403:THR:HB	2.11	0.51
1:A:320:ASP:O	1:A:343:GLN:NE2	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:SER:OG	1:A:5:ILE:HG13	2.12	0.50
1:A:399:GLU:HA	1:A:402:TRP:HE3	1.77	0.49
1:A:417:VAL:HG22	1:A:419:THR:HG23	1.95	0.49
2:B:244:ILE:HB	2:B:310:LEU:HG	1.95	0.49
1:A:298:GLU:HA	1:A:301:LEU:HD12	1.94	0.48
1:A:181:TYR:CD1	2:B:138:GLU:HA	2.48	0.48
1:A:19:PRO:HG3	1:A:80:LEU:HB2	1.95	0.48
1:A:458:VAL:HG22	1:A:548:VAL:HG22	1.96	0.48
1:A:229:TRP:CE2	1:A:230:MET:HG2	2.49	0.48
2:B:253:THR:HG22	2:B:256:ASP:H	1.79	0.48
2:B:325:LEU:HD12	2:B:385:LYS:HB3	1.96	0.47
2:B:279:LEU:HD22	2:B:299:ALA:HB1	1.95	0.47
2:B:344:GLU:HB3	2:B:347:LYS:HE2	1.96	0.47
2:B:342:TYR:HB3	2:B:348:ASN:HB3	1.97	0.47
1:A:365:VAL:O	1:A:369:THR:HG23	2.15	0.47
1:A:77:PHE:CE2	1:A:150:PRO:HB2	2.49	0.46
1:A:331:LYS:HB3	1:A:421:PRO:HG2	1.98	0.46
2:B:107:THR:HG21	2:B:202:ILE:HD13	1.98	0.46
2:B:116:PHE:HD2	2:B:116:PHE:C	2.24	0.46
2:B:24:TRP:N	2:B:24:TRP:CD1	2.83	0.45
2:B:373:GLN:HE22	2:B:407:GLN:H	1.63	0.45
1:A:303:LEU:O	1:A:307:ARG:HG3	2.16	0.44
1:A:20:LYS:HE2	1:A:55:PRO:HB2	1.98	0.44
2:B:116:PHE:C	2:B:116:PHE:CD2	2.95	0.44
2:B:272:PRO:HG2	2:B:315:HIS:HB3	1.98	0.44
2:B:303:LEU:HD13	2:B:307:ARG:HH21	1.82	0.44
1:A:350:LYS:HE2	1:A:378:GLU:OE2	2.18	0.44
1:A:540:LYS:O	1:A:542:ILE:N	2.47	0.44
1:A:82:LYS:HD3	4:A:668:HOH:O	2.18	0.44
1:A:497:THR:O	1:A:535:TRP:HA	2.17	0.44
2:B:111:VAL:HG21	2:B:187:LEU:HD22	2.00	0.43
1:A:60:VAL:HG13	1:A:75:VAL:HG22	2.00	0.43
2:B:157:PRO:HG3	2:B:184:MET:HA	1.99	0.43
2:B:193:LEU:HB3	2:B:197:GLN:HB2	2.01	0.43
1:A:500:GLN:HG3	2:B:422:LEU:HD12	2.00	0.43
2:B:13:LYS:HB2	2:B:16:MET:CE	2.48	0.43
1:A:297:GLU:CB	1:A:298:GLU:OE2	2.67	0.42
2:B:57:ASN:OD1	2:B:143:ARG:NH1	2.52	0.42
1:A:407:GLN:HE22	2:B:394:GLN:HB2	1.83	0.42
2:B:293:ILE:HA	2:B:294:PRO:HD3	1.97	0.42
1:A:335:GLY:O	1:A:355:ALA:HA	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:266:TRP:O	1:A:269:GLN:HG2	2.20	0.41
2:B:24:TRP:CZ3	2:B:399:GLU:HG2	2.55	0.41
2:B:324:ASP:HA	2:B:385:LYS:HE2	2.02	0.41
2:B:362:THR:HG23	2:B:366:LYS:HE3	2.02	0.41
1:A:356:ARG:NH2	1:A:358:ARG:HD2	2.36	0.41
1:A:116:PHE:O	1:A:148:VAL:HG11	2.20	0.40
1:A:393:ILE:HD13	1:A:398:TRP:HD1	1.85	0.40
2:B:257:ILE:HG13	2:B:283:LEU:HD21	2.03	0.40
2:B:115:TYR:HB3	2:B:149:LEU:HB2	2.02	0.40
1:A:229:TRP:CD2	3:A:561:M06:H9	2.56	0.40
1:A:503:LEU:HD22	1:A:507:GLN:HG3	2.03	0.40
2:B:341:ILE:HD11	2:B:375:ILE:HG23	2.03	0.40
2:B:373:GLN:NE2	2:B:407:GLN:H	2.20	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	549/563 (98%)	520 (95%)	23 (4%)	6 (1%)	11	22
2	B	395/443 (89%)	378 (96%)	15 (4%)	2 (0%)	24	43
All	All	944/1006 (94%)	898 (95%)	38 (4%)	8 (1%)	16	31

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	90	VAL
1	A	412	PRO
1	A	541	GLY
1	A	543	GLY
2	B	345	PRO

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Mol	Chain	Res	Type
1	A	345	PRO
1	A	490	GLY
2	B	18	GLY

5.3.2 Protein sidechains ⓘ

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	493/503 (98%)	427 (87%)	66 (13%)	4	8
2	B	367/403 (91%)	318 (87%)	49 (13%)	4	8
All	All	860/906 (95%)	745 (87%)	115 (13%)	4	8

All (115) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	ILE
1	A	7	THR
1	A	21	VAL
1	A	26	LEU
1	A	36	GLU
1	A	50	ILE
1	A	60	VAL
1	A	63	ILE
1	A	64	LYS
1	A	69	THR
1	A	70	LYS
1	A	94	ILE
1	A	102	LYS
1	A	106	VAL
1	A	108	VAL
1	A	118	VAL
1	A	137	ASN
1	A	139	THR
1	A	161	GLN
1	A	173	LYS

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Mol	Chain	Res	Type
1	A	178	ILE
1	A	189	VAL
1	A	195	ILE
1	A	202	ILE
1	A	205	LEU
1	A	223	LYS
1	A	233	GLU
1	A	249	LYS
1	A	260	LEU
1	A	276	VAL
1	A	279	LEU
1	A	284	ARG
1	A	287	LYS
1	A	295	LEU
1	A	298	GLU
1	A	303	LEU
1	A	311	LYS
1	A	312	GLU
1	A	338	THR
1	A	344	GLU
1	A	350	LYS
1	A	368	LEU
1	A	374	LYS
1	A	394	GLN
1	A	398	TRP
1	A	399	GLU
1	A	402	TRP
1	A	403	THR
1	A	407	GLN
1	A	409	THR
1	A	451	LYS
1	A	454	LYS
1	A	459	THR
1	A	463	ARG
1	A	471	ASP
1	A	479	LEU
1	A	482	ILE
1	A	493	VAL
1	A	496	VAL
1	A	503	LEU
1	A	523	GLU
1	A	527	LYS

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Mol	Chain	Res	Type
1	A	529	GLU
1	A	548	VAL
1	A	550	LYS
1	A	557	ARG
2	B	8	VAL
2	B	16	MET
2	B	24	TRP
2	B	26	LEU
2	B	46	LYS
2	B	58	THR
2	B	64	LYS
2	B	72	ARG
2	B	80	LEU
2	B	90	VAL
2	B	91	GLN
2	B	111	VAL
2	B	113	ASP
2	B	116	PHE
2	B	120	LEU
2	B	122	GLU
2	B	166	LYS
2	B	173	LYS
2	B	187	LEU
2	B	202	ILE
2	B	203	GLU
2	B	205	LEU
2	B	209	LEU
2	B	214	LEU
2	B	242	GLN
2	B	248	GLU
2	B	253	THR
2	B	270	ILE
2	B	276	VAL
2	B	278	GLN
2	B	279	LEU
2	B	284	ARG
2	B	290	THR
2	B	292	VAL
2	B	293	ILE
2	B	295	LEU
2	B	297	GLU
2	B	310	LEU

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Mol	Chain	Res	Type
2	B	334	GLN
2	B	336	GLN
2	B	348	ASN
2	B	349	LEU
2	B	372	VAL
2	B	385	LYS
2	B	388	LYS
2	B	400	THR
2	B	403	THR
2	B	407	GLN
2	B	422	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	ASN
1	A	137	ASN
1	A	161	GLN
1	A	198	HIS
1	A	222	GLN
1	A	258	GLN
1	A	330	GLN
1	A	334	GLN
1	A	394	GLN
1	A	407	GLN
1	A	418	ASN
1	A	480	GLN
1	A	500	GLN
1	A	509	GLN
1	A	519	ASN
1	A	547	GLN
2	B	147	ASN
2	B	151	GLN
2	B	175	ASN
2	B	182	GLN
2	B	207	GLN
2	B	208	HIS
2	B	242	GLN
2	B	255	ASN
2	B	258	GLN
2	B	278	GLN
2	B	306	ASN

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Mol	Chain	Res	Type
2	B	367	GLN
2	B	373	GLN
2	B	394	GLN
2	B	407	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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	$\# Z > 2$
3	M06	A	561	-	28,31,31	1.92	10 (35%)	29,44,44	2.41	10 (34%)

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
3	M06	A	561	-	-	1/10/10/10	0/4/4/4

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	561	M06	C4-C3	4.34	1.55	1.43
3	A	561	M06	C13-N14	3.54	1.38	1.35
3	A	561	M06	C9-C10	3.23	1.43	1.38
3	A	561	M06	C19-N18	3.06	1.41	1.34
3	A	561	M06	C9-C8	2.94	1.44	1.39
3	A	561	M06	C22-N	2.62	1.49	1.46
3	A	561	M06	O-C5	-2.39	1.36	1.41
3	A	561	M06	C8-C23	-2.29	1.39	1.44
3	A	561	M06	C11-C10	2.10	1.41	1.38
3	A	561	M06	C3-N	2.06	1.43	1.39

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	561	M06	C16-N15-N14	5.72	113.76	103.03
3	A	561	M06	C22-N-C3	5.57	121.48	117.38
3	A	561	M06	C13-N14-N15	-4.74	103.93	112.64
3	A	561	M06	O12-C3-N	3.17	124.76	120.53
3	A	561	M06	C2-N-C3	-3.14	120.71	122.90
3	A	561	M06	C20-C19-N18	2.73	127.74	123.42
3	A	561	M06	C21-C20-C19	-2.52	115.28	118.92
3	A	561	M06	C19-N18-C16	-2.45	113.71	116.64
3	A	561	M06	C8-C9-C10	-2.42	116.70	118.89
3	A	561	M06	C20-C21-C17	-2.31	119.53	121.80

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	561	M06	N24-C23-C8-C9

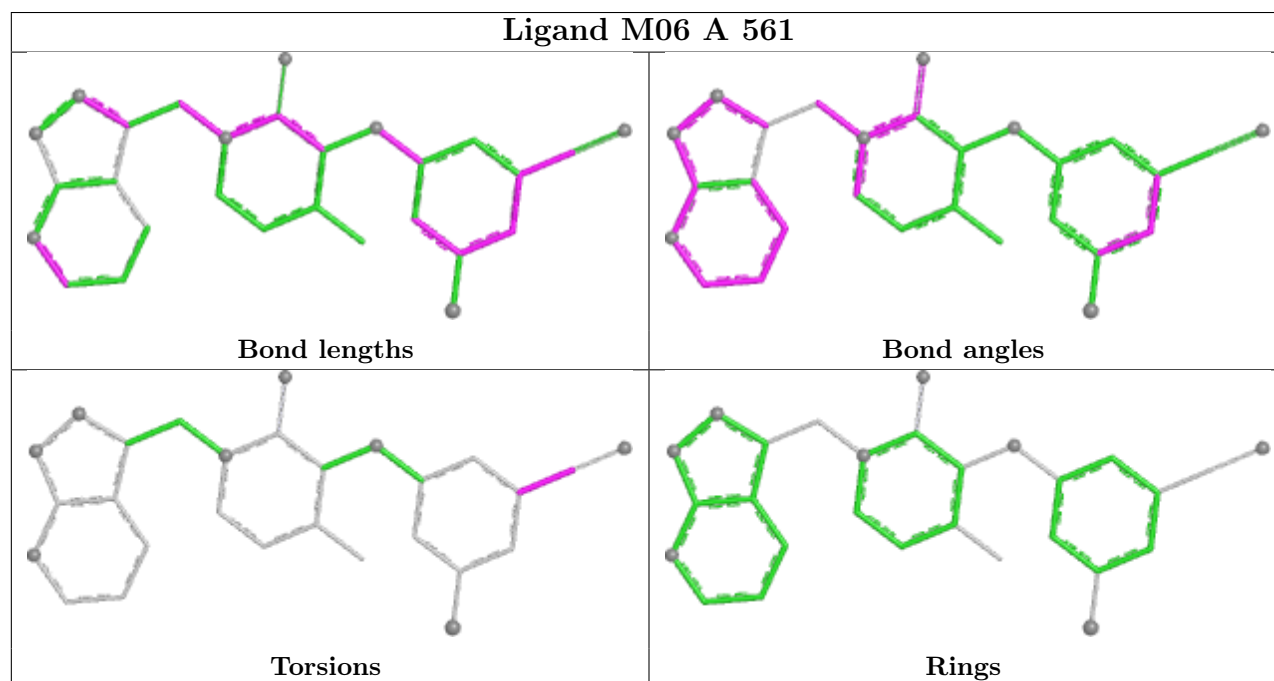
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	561	M06	2	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	553/563 (98%)	-0.24	4 (0%) 84 81	33, 59, 89, 107	0
2	B	403/443 (90%)	-0.14	8 (1%) 65 61	37, 59, 100, 117	0
All	All	956/1006 (95%)	-0.19	12 (1%) 75 71	33, 59, 95, 117	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	215	THR	3.7
2	B	362	THR	2.8
2	B	24	TRP	2.7
2	B	65	LYS	2.7
1	A	88	TRP	2.5
2	B	15	GLY	2.4
2	B	5	ILE	2.4
2	B	356	ARG	2.2
2	B	346	PHE	2.1
1	A	398	TRP	2.1
1	A	69	THR	2.0
1	A	406	TRP	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](#)

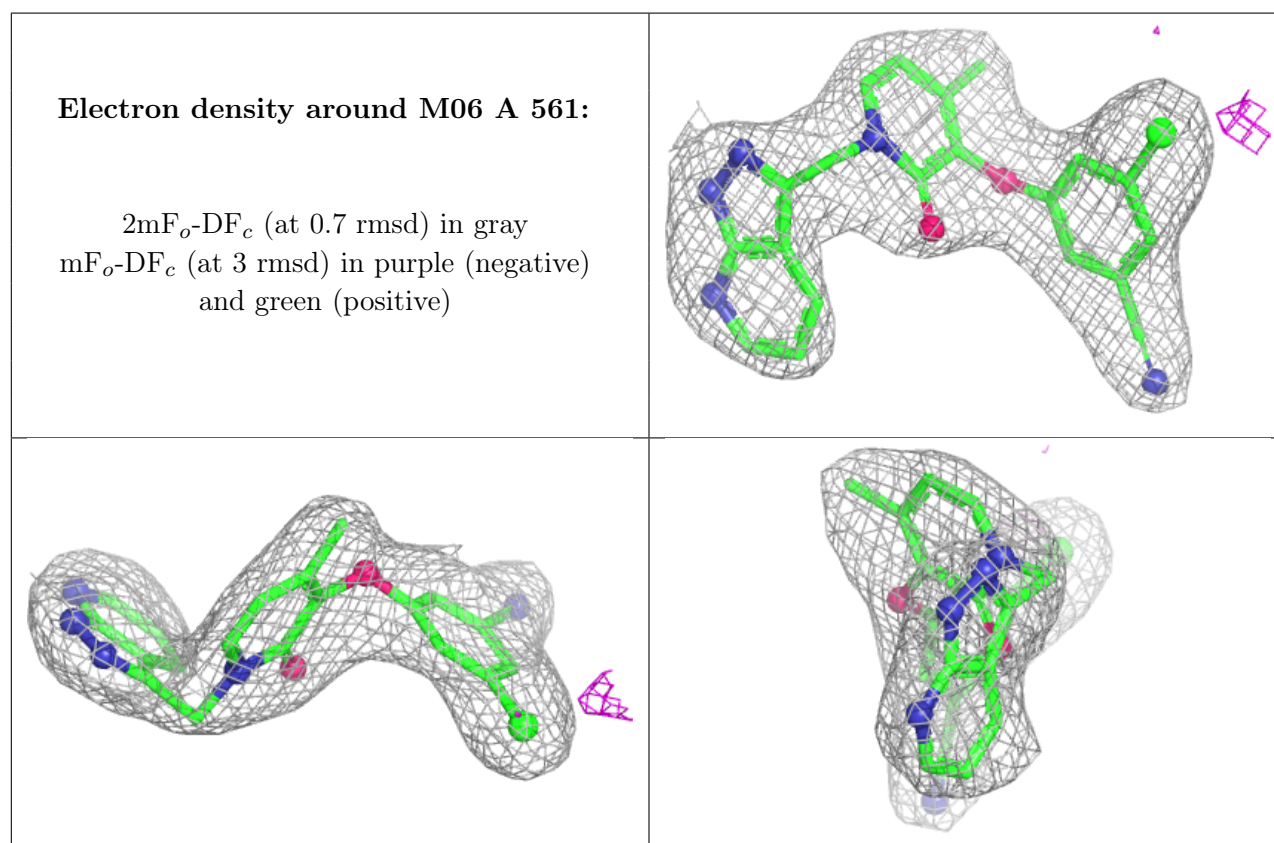
There are no oligosaccharides in this entry.

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(Å ²)	Q<0.9
3	M06	A	561	28/28	0.96	0.06	38,52,59,60	0

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 [i](#)

There are no such residues in this entry.