



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 12:47 PM UTC

PDB ID : 4CGY / pdb_00004cgy
Title : Crystal structure of the human topoisomerase III alpha-RMI1 complex
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Deposited on : 2013-11-27
Resolution : 2.85 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
Xtriage (Phenix)	:	2.0
EDS	:	3.0
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

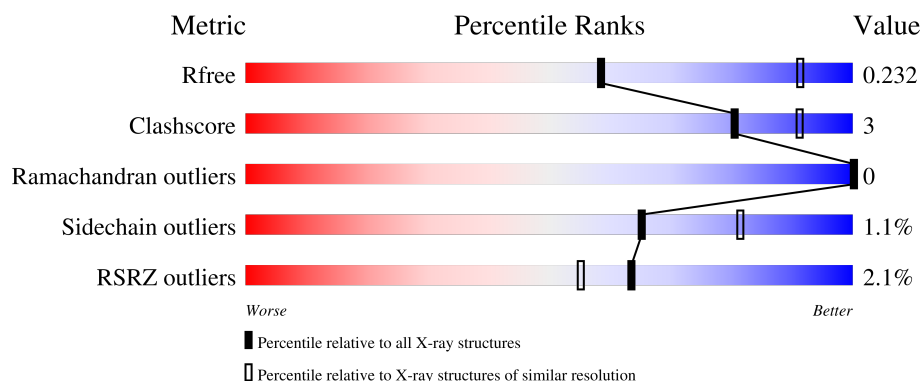
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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	1407 (2.88-2.84)
Clashscore	190562	1446 (2.88-2.84)
Ramachandran outliers	187476	1406 (2.88-2.84)
Sidechain outliers	187428	1407 (2.88-2.84)
RSRZ outliers	180081	1408 (2.88-2.84)

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	754	74% 8% 18%
2	B	219	3% 84% 9% 6%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6602 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 DNA TOPOISOMERASE 3-ALPHA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	619	Total	C	N	O	S	0	0	0
			4946	3134	874	910	28			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP Q13472
A	1	ARG	-	expression tag	UNP Q13472

- Molecule 2 is a protein called RECQ-MEDIATED GENOME INSTABILITY PROTEIN 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	205	Total	C	N	O	S	0	0	0
			1611	1037	268	300	6			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	39	Total	O	0	0
			39	39		
4	B	5	Total	O	0	0
			5	5		

4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	94.01Å 94.01Å 381.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	65.49 – 2.85 65.49 – 2.85	Depositor EDS
% Data completeness (in resolution range)	100.0 (65.49-2.85) 99.9 (65.49-2.85)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.67 (at 2.69Å)	Xtriage
Refinement program	BUSTER 2.11.4	Depositor
R, R_{free}	0.197 , 0.231 0.203 , 0.232	Depositor DCC
R_{free} test set	2432 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	72.6	Xtriage
Anisotropy	0.374	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 48.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6602	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.44% 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: MG

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	0.81	0/5052	1.31	23/6836 (0.3%)
2	B	0.83	0/1643	1.30	1/2240 (0.0%)
All	All	0.81	0/6695	1.31	24/9076 (0.3%)

There are no bond length outliers.

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	556	ASP	CA-C-N	8.84	137.61	121.70
1	A	556	ASP	C-N-CA	8.84	137.61	121.70
1	A	411	ASP	CA-CB-CG	7.31	119.91	112.60
1	A	522	ASP	CA-CB-CG	7.04	119.64	112.60
1	A	328	ASP	CA-CB-CG	6.53	119.13	112.60
1	A	556	ASP	N-CA-C	5.99	118.76	111.82
1	A	582	PRO	CA-C-N	5.49	127.90	120.38
1	A	582	PRO	C-N-CA	5.49	127.90	120.38
2	B	141	ASP	CA-CB-CG	5.23	117.83	112.60
1	A	556	ASP	CA-C-O	-5.21	113.98	119.97
1	A	546	LYS	CA-C-N	5.20	127.24	120.28
1	A	546	LYS	C-N-CA	5.20	127.24	120.28
1	A	258	ALA	CA-C-N	5.18	127.19	120.56
1	A	258	ALA	C-N-CA	5.18	127.19	120.56
1	A	555	PRO	CA-C-N	5.17	128.17	120.31
1	A	555	PRO	C-N-CA	5.17	128.17	120.31
1	A	528	GLU	CA-C-N	5.17	127.46	120.38
1	A	528	GLU	C-N-CA	5.17	127.46	120.38
1	A	539	ALA	CA-C-N	5.08	127.08	120.28
1	A	539	ALA	C-N-CA	5.08	127.08	120.28
1	A	355	TYR	CA-C-N	5.07	127.08	120.28
1	A	355	TYR	C-N-CA	5.07	127.08	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	241	TYR	CA-C-N	5.06	125.09	121.65
1	A	241	TYR	C-N-CA	5.06	125.09	121.65

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	4946	0	4896	24	0
2	B	1611	0	1632	11	0
3	A	1	0	0	0	0
4	A	39	0	0	0	0
4	B	5	0	0	0	0
All	All	6602	0	6528	34	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 (34) 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:23:ARG:O	1:A:27:GLU:HG3	1.83	0.78
2:B:92:LEU:HD13	2:B:137:LEU:HG	1.71	0.72
1:A:556:ASP:HB3	1:A:558:ARG:HG3	1.72	0.71
1:A:118:ILE:HD13	1:A:212:LEU:HD23	1.71	0.70
1:A:161:ILE:HG12	1:A:173:VAL:HG11	1.76	0.67
2:B:138:GLN:HE21	2:B:145:GLN:HE21	1.46	0.63
1:A:60:ARG:HG3	1:A:71:TYR:CE1	2.38	0.59
2:B:103:ILE:O	2:B:107:ARG:HG3	2.11	0.51
2:B:146:ILE:HD12	2:B:180:LEU:HD11	1.93	0.49
2:B:163:PRO:HD2	2:B:198:LEU:HD23	1.94	0.49
1:A:362:TYR:CE2	1:A:364:ARG:HB2	2.48	0.49
2:B:146:ILE:CD1	2:B:180:LEU:HD11	2.43	0.48
1:A:273:THR:HG22	1:A:282:GLU:HG3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:319:LYS:HB2	1:A:453:GLU:HB2	1.96	0.48
1:A:446:SER:OG	1:A:447:GLN:N	2.43	0.48
1:A:330:VAL:HG12	1:A:334:LYS:HE2	1.94	0.48
1:A:566:MET:O	1:A:570:GLU:HG2	2.14	0.48
1:A:61:ARG:HH21	1:A:72:GLU:CD	2.21	0.48
1:A:231:PRO:O	1:A:235:ALA:HB2	2.14	0.47
1:A:26:MET:HG2	1:A:78:TYR:CZ	2.49	0.47
1:A:104:LYS:HB2	1:A:107:SER:HB3	1.97	0.47
1:A:471:MET:HE3	1:A:473:LEU:HD21	1.97	0.46
1:A:363:PRO:HA	1:A:417:ILE:HG12	1.99	0.45
1:A:288:HIS:CD2	1:A:288:HIS:C	2.94	0.44
1:A:287:ARG:HD2	1:A:463:GLU:OE1	2.18	0.44
1:A:52:LEU:HD22	1:A:183:PRO:HG3	2.00	0.44
2:B:167:ILE:HG22	2:B:189:VAL:HA	2.01	0.43
1:A:299:LEU:HD21	2:B:149:MET:HE1	2.01	0.43
1:A:326:ALA:HB3	1:A:368:ASN:O	2.19	0.42
2:B:195:ASP:HA	2:B:198:LEU:HD12	2.02	0.42
1:A:554:THR:O	1:A:557:LYS:HA	2.20	0.42
2:B:168:LEU:HB3	2:B:188:LYS:HB3	2.01	0.41
1:A:272:VAL:HG23	1:A:283:PHE:HB2	2.02	0.41
2:B:169:ILE:HD12	2:B:182:LEU:HD22	2.03	0.41

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	617/754 (82%)	593 (96%)	24 (4%)	0	100	100
2	B	201/219 (92%)	198 (98%)	3 (2%)	0	100	100
All	All	818/973 (84%)	791 (97%)	27 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	530/661 (80%)	524 (99%)	6 (1%)	65	81
2	B	177/193 (92%)	175 (99%)	2 (1%)	65	81
All	All	707/854 (83%)	699 (99%)	8 (1%)	65	81

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	LEU
1	A	58	MET
1	A	112	VAL
1	A	135	ARG
1	A	486	TRP
1	A	546	LYS
2	B	165	THR
2	B	188	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	260	GLN
1	A	268	HIS
1	A	284	ASN
1	A	288	HIS
1	A	293	HIS
1	A	301	GLN
1	A	412	GLN
1	A	447	GLN
1	A	452	GLN
1	A	501	GLN
1	A	633	GLN

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Mol	Chain	Res	Type
2	B	2	ASN
2	B	82	ASN
2	B	97	GLN
2	B	102	GLN
2	B	110	ASN
2	B	113	ASN
2	B	145	GLN
2	B	147	GLN
2	B	152	GLN
2	B	203	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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	619/754 (82%)	0.01	10 (1%) 70 64	52, 74, 116, 142	0
2	B	205/219 (93%)	0.07	7 (3%) 48 38	60, 80, 122, 135	0
All	All	824/973 (84%)	0.02	17 (2%) 63 55	52, 76, 117, 142	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	21	PHE	5.4
2	B	216	LEU	5.2
2	B	120	ALA	5.1
1	A	639	THR	4.3
2	B	131	PRO	3.9
2	B	40	ASN	3.8
1	A	577	TYR	3.6
1	A	373	ASP	3.1
2	B	2	ASN	2.9
1	A	276	HIS	2.6
1	A	278	ASP	2.4
1	A	452	GLN	2.4
1	A	306	ASP	2.3
1	A	408	ASN	2.2
2	B	41	VAL	2.2
2	B	188	LYS	2.1
1	A	638	GLY	2.1

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

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	1640	1/1	0.99	0.03	62,62,62,62	0

6.5 Other polymers [i](#)

There are no such residues in this entry.