



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 7B06 / pdb_00007b06
Title : TgoT_RT521 apo
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Deposited on : 2020-11-18
Resolution : 2.35 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

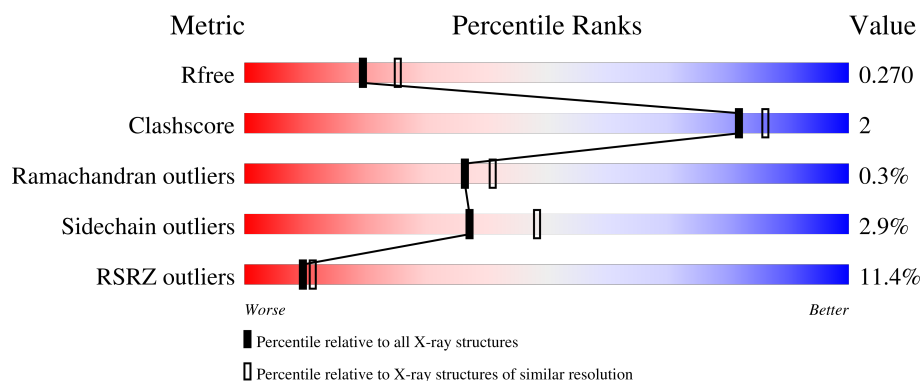
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	3031 (2.36-2.32)
Clashscore	190562	3127 (2.36-2.32)
Ramachandran outliers	187476	3095 (2.36-2.32)
Sidechain outliers	187428	3095 (2.36-2.32)
RSRZ outliers	180081	3033 (2.36-2.32)

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	773	10% 81% 7% 11%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5759 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 polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	685	Total	C	N	O	S	0	0	0
			5641	3641	937	1050	13			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	93	GLN	VAL	conflict	UNP P56689
A	141	ALA	ASP	conflict	UNP P56689
A	143	ALA	GLU	conflict	UNP P56689
A	485	LEU	ALA	conflict	UNP P56689
A	521	LEU	ILE	conflict	UNP P56689
A	664	LYS	GLU	conflict	UNP P56689

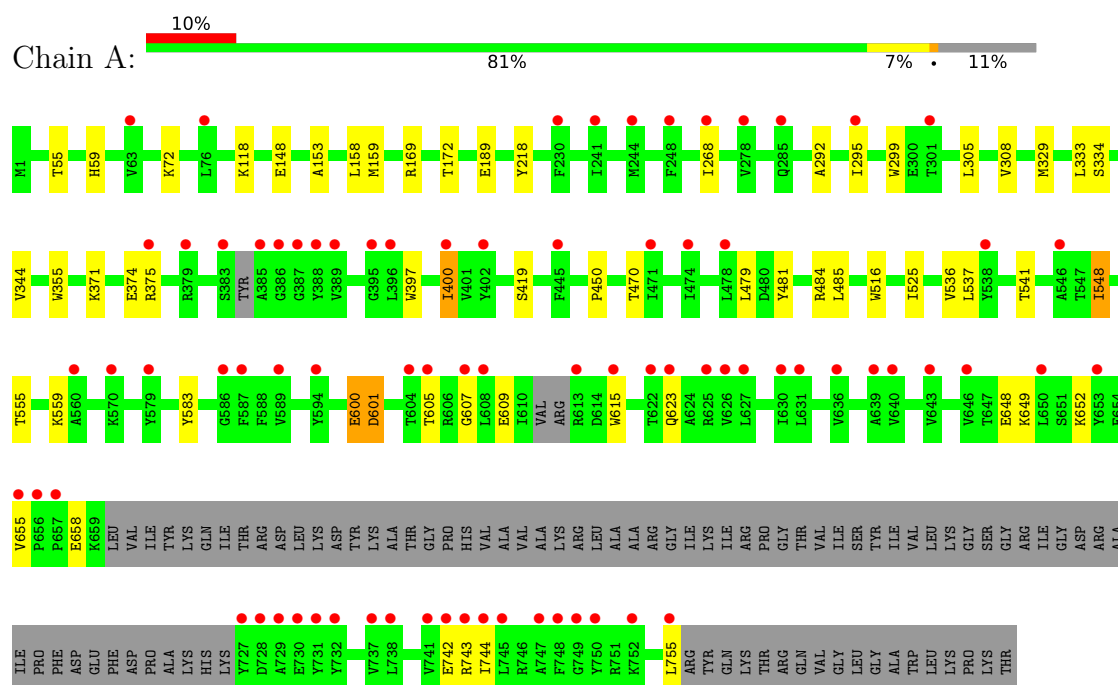
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	118	Total	O	0	0
			118	118		

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: DNA polymerase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	70.53Å 109.85Å 111.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.69 – 2.35 43.69 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.3 (43.69-2.35) 99.2 (43.69-2.35)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.29 (at 2.34Å)	Xtriage
Refinement program	BUSTER 2.10.3 (20-MAY-2020)	Depositor
R, R_{free}	0.225 , 0.247 0.248 , 0.270	Depositor DCC
R_{free} test set	1825 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	56.6	Xtriage
Anisotropy	0.522	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 53.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.003 for -h,l,k	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5759	wwPDB-VP
Average B, all atoms (Å ²)	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.00% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.54	0/5766	0.90	1/7772 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	148	GLU	N-CA-C	5.41	117.60	111.11

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	5641	0	5639	28	0
2	A	118	0	0	0	0
All	All	5759	0	5639	28	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 2.

All (28) 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:158:LEU:HD22	1:A:299:TRP:CD2	2.20	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:555:THR:HG22	1:A:559:LYS:HE2	1.77	0.65
1:A:623:GLN:HE21	1:A:744:ILE:HD11	1.63	0.64
1:A:158:LEU:HD22	1:A:299:TRP:CE2	2.33	0.64
1:A:548:ILE:HG13	1:A:559:LYS:HE3	1.82	0.60
1:A:118:LYS:HZ3	1:A:355:TRP:HZ2	1.50	0.60
1:A:555:THR:O	1:A:559:LYS:HG2	2.01	0.59
1:A:609:GLU:H	1:A:623:GLN:HE22	1.51	0.57
1:A:605:THR:HG22	1:A:607:GLY:H	1.71	0.56
1:A:400:ILE:HG13	1:A:583:TYR:HB2	1.88	0.54
1:A:648:GLU:HG2	1:A:652:LYS:HE2	1.90	0.54
1:A:305:LEU:HA	1:A:308:VAL:HG12	1.89	0.53
1:A:419:SER:HB3	1:A:450:PRO:HD3	1.92	0.51
1:A:397:TRP:CE2	1:A:537:LEU:HD22	2.47	0.50
1:A:159:MET:HE1	1:A:308:VAL:HG22	1.95	0.49
1:A:159:MET:HG2	1:A:172:THR:HB	1.95	0.48
1:A:525:ILE:HG23	1:A:536:VAL:HG21	1.97	0.46
1:A:481:TYR:HD1	1:A:484:ARG:HH21	1.62	0.45
1:A:333:LEU:HD13	1:A:485:LEU:HD22	1.99	0.44
1:A:615:TRP:HH2	1:A:743:ARG:HH22	1.65	0.44
1:A:470:THR:HG21	1:A:479:LEU:HD12	2.00	0.43
1:A:118:LYS:NZ	1:A:355:TRP:HZ2	2.17	0.42
1:A:334:SER:HA	1:A:344:VAL:HG21	2.01	0.42
1:A:649:LYS:HB3	1:A:655:VAL:HG23	2.02	0.41
1:A:153:ALA:HA	1:A:218:TYR:CZ	2.56	0.41
1:A:292:ALA:O	1:A:295:ILE:HG12	2.20	0.40
1:A:600:GLU:O	1:A:601:ASP:HB2	2.21	0.40
1:A:292:ALA:HA	1:A:295:ILE:HG12	2.04	0.40

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	677/773 (88%)	655 (97%)	20 (3%)	2 (0%)	36	41

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	601	ASP
1	A	541	THR

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	596/669 (89%)	579 (97%)	17 (3%)	37	48

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	55	THR
1	A	59	HIS
1	A	72	LYS
1	A	169	ARG
1	A	189	GLU
1	A	268	ILE
1	A	329	MET
1	A	371	LYS
1	A	374	GLU
1	A	375	ARG
1	A	400	ILE
1	A	516	TRP
1	A	548	ILE
1	A	600	GLU
1	A	658	GLU
1	A	742	GLU
1	A	755	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	103	HIS
1	A	399	ASN
1	A	461	GLN
1	A	623	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](#)

There are no ligands in this entry.

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	685/773 (88%)	0.77	78 (11%)	10 11	55, 86, 173, 190	0

All (78) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	755	LEU	5.8
1	A	744	ILE	5.6
1	A	737	VAL	5.0
1	A	747	ALA	4.8
1	A	627	LEU	4.7
1	A	395	GLY	4.4
1	A	748	PHE	4.2
1	A	389	VAL	3.9
1	A	657	PRO	3.9
1	A	383	SER	3.8
1	A	643	VAL	3.7
1	A	750	TYR	3.7
1	A	589	VAL	3.5
1	A	388	TYR	3.5
1	A	727	TYR	3.5
1	A	387	GLY	3.5
1	A	560	ALA	3.5
1	A	400	ILE	3.4
1	A	385	ALA	3.3
1	A	587	PHE	3.3
1	A	650	LEU	3.3
1	A	608	LEU	3.2
1	A	656	PRO	3.2
1	A	653	TYR	3.1
1	A	738	LEU	3.1
1	A	295	ILE	3.1
1	A	741	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	396	LEU	3.0
1	A	613	ARG	2.9
1	A	586	GLY	2.9
1	A	623	GLN	2.8
1	A	471	ILE	2.8
1	A	631	LEU	2.8
1	A	732	TYR	2.7
1	A	607	GLY	2.7
1	A	646	VAL	2.7
1	A	729	ALA	2.6
1	A	594	TYR	2.6
1	A	630	ILE	2.6
1	A	386	GLY	2.5
1	A	445	PHE	2.5
1	A	731	TYR	2.5
1	A	745	LEU	2.5
1	A	301	THR	2.5
1	A	622	THR	2.5
1	A	579	TYR	2.5
1	A	743	ARG	2.4
1	A	230	PHE	2.3
1	A	639	ALA	2.3
1	A	625	ARG	2.3
1	A	749	GLY	2.3
1	A	375	ARG	2.3
1	A	268	ILE	2.3
1	A	474	ILE	2.3
1	A	63	VAL	2.3
1	A	752	LYS	2.2
1	A	605	THR	2.2
1	A	402	TYR	2.2
1	A	640	VAL	2.2
1	A	570	LYS	2.2
1	A	546	ALA	2.2
1	A	742	GLU	2.2
1	A	76	LEU	2.1
1	A	636	VAL	2.1
1	A	244	MET	2.1
1	A	730	GLU	2.1
1	A	278	VAL	2.1
1	A	655	VAL	2.1
1	A	728	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	626	VAL	2.1
1	A	615	TRP	2.1
1	A	248	PHE	2.1
1	A	604	THR	2.0
1	A	478	LEU	2.0
1	A	538	TYR	2.0
1	A	379	ARG	2.0
1	A	285	GLN	2.0
1	A	241	ILE	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.