



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 07:13 AM UTC

PDB ID : 2VRC / pdb_00002vrc
Title : Crystal structure of the *Citrobacter* sp. triphenylmethane reductase complexed with NADP(H)
Authors : Kim, Y.; Park, H.J.; Kwak, S.N.; Lee, J.S.; Oh, T.K.; Kim, M.H.
Deposited on : 2008-03-31
Resolution : 2.50 Å (reported)

This is a wwPDB X-ray Structure Validation Summary 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
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

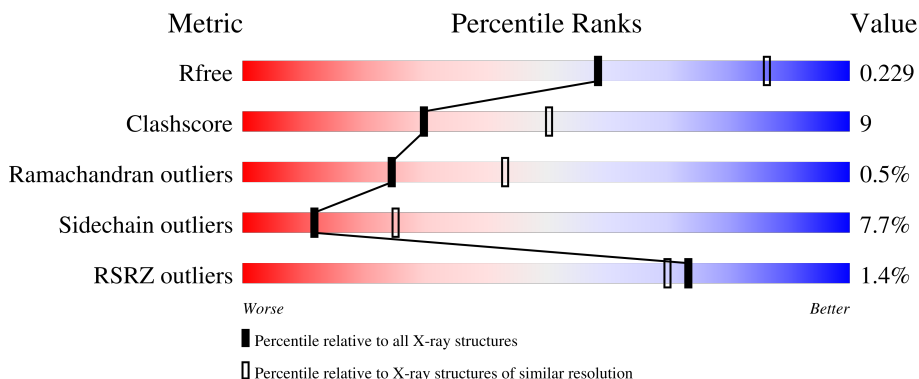
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	287	 85% 11% ..
1	B	287	 81% 16% ..
1	C	287	 3% 74% 21% ..
2	D	287	 78% 17% ..

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8912 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 TRIPHENYLMETHANE REDUCTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	Se			
1	A	285	2170	1379	367	422	2	0	1	0
1	B	285	2168	1376	367	423	2	0	1	0
1	C	285	2162	1373	366	421	2	0	0	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	PHE	MET	conflict	UNP Q2TNI4
A	21	MSE	LEU	engineered mutation	UNP Q2TNI4
A	22	ALA	LYS	engineered mutation	UNP Q2TNI4
A	23	ALA	LYS	engineered mutation	UNP Q2TNI4
A	156	THR	ILE	conflict	UNP Q2TNI4
A	235	MSE	LEU	engineered mutation	UNP Q2TNI4
B	1	PHE	MET	conflict	UNP Q2TNI4
B	21	MSE	LEU	engineered mutation	UNP Q2TNI4
B	22	ALA	LYS	engineered mutation	UNP Q2TNI4
B	23	ALA	LYS	engineered mutation	UNP Q2TNI4
B	156	THR	ILE	conflict	UNP Q2TNI4
B	235	MSE	LEU	engineered mutation	UNP Q2TNI4
C	1	PHE	MET	conflict	UNP Q2TNI4
C	21	MSE	LEU	engineered mutation	UNP Q2TNI4
C	22	ALA	LYS	engineered mutation	UNP Q2TNI4
C	23	ALA	LYS	engineered mutation	UNP Q2TNI4
C	156	THR	ILE	conflict	UNP Q2TNI4
C	235	MSE	LEU	engineered mutation	UNP Q2TNI4

- Molecule 2 is a protein called TRIPHENYLMETHANE REDUCTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	Se			
2	D	285	2170	1376	368	424	2	0	1	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1	PHE	MET	conflict	UNP Q2TNI4
D	21	MSE	LEU	engineered mutation	UNP Q2TNI4
D	22	ALA	LYS	engineered mutation	UNP Q2TNI4
D	23	ALA	LYS	engineered mutation	UNP Q2TNI4
D	128	THR	ILE	conflict	UNP Q2TNI4
D	156	THR	ILE	conflict	UNP Q2TNI4
D	235	MSE	LEU	engineered mutation	UNP Q2TNI4

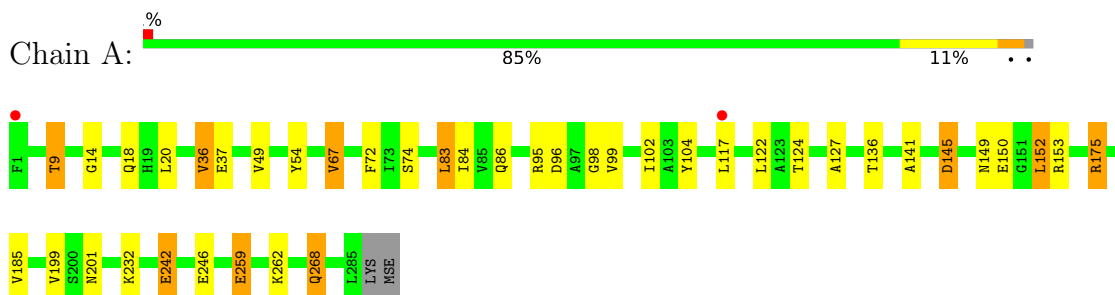
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	76	Total	O	0	0
			76	76		
3	B	80	Total	O	0	0
			80	80		
3	C	34	Total	O	0	0
			34	34		
3	D	52	Total	O	0	0
			52	52		

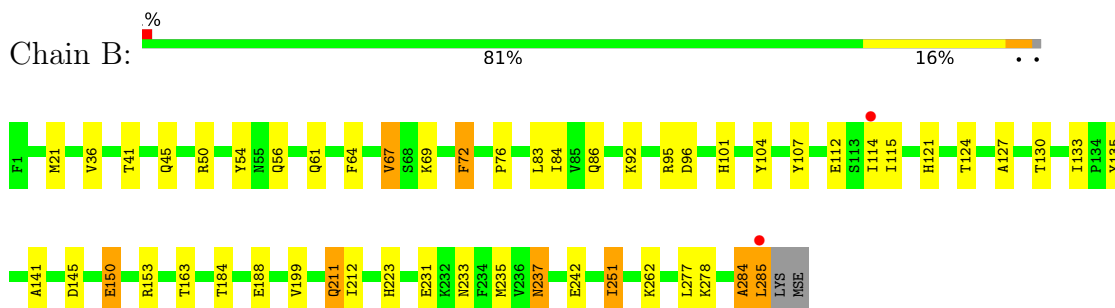
3 Residue-property plots [i](#)

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.

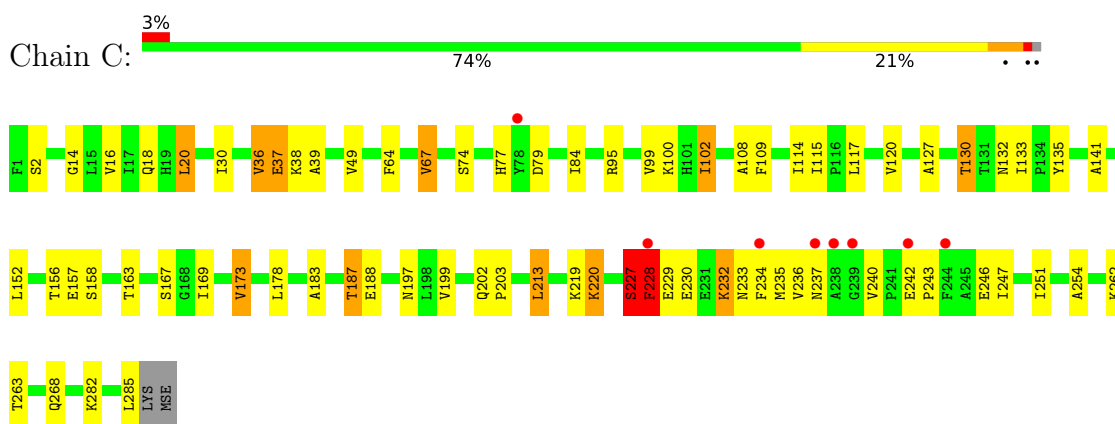
- Molecule 1: TRIPHENYLMETHANE REDUCTASE



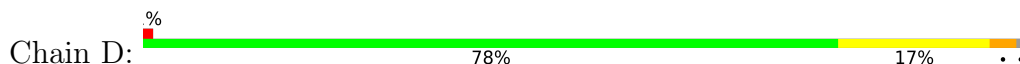
- Molecule 1: TRIPHENYLMETHANE REDUCTASE

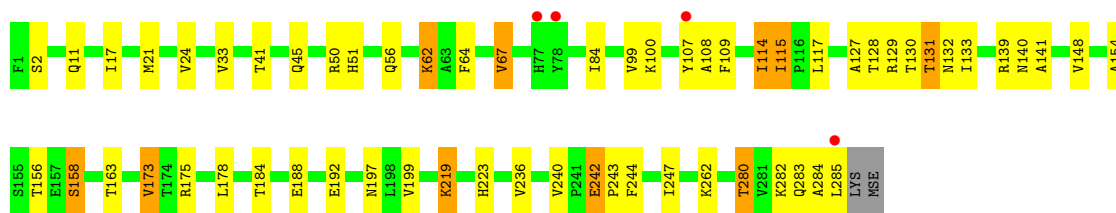


- Molecule 1: TRIPHENYLMETHANE REDUCTASE



- Molecule 2: TRIPHENYLMETHANE REDUCTASE





4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	75.96Å 76.95Å 272.83Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.36 – 2.50 29.36 – 2.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (29.36-2.50) 95.8 (29.36-2.50)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	82.19 (at 2.51Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.190 , 0.239 0.183 , 0.229	Depositor DCC
R_{free} test set	2747 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	41.6	Xtrriage
Anisotropy	0.068	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 51.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	0.033 for k,h,-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8912	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.53% 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	0.83	0/2208	1.00	2/3003 (0.1%)
1	B	0.78	0/2206	0.97	1/3000 (0.0%)
1	C	0.69	0/2200	0.98	8/2992 (0.3%)
2	D	0.72	0/2208	0.97	6/3003 (0.2%)
All	All	0.76	0/8822	0.98	17/11998 (0.1%)

There are no bond length outliers.

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	228	PHE	CB-CA-C	-13.74	83.07	110.42
1	C	202	GLN	CA-C-N	-6.73	113.78	120.98
1	C	202	GLN	C-N-CA	-6.73	113.78	120.98
1	C	227	SER	N-CA-C	6.54	118.48	111.36
1	C	229	GLU	N-CA-C	-5.78	98.49	110.80

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	2170	0	2171	25	0
1	B	2168	0	2165	43	0
1	C	2162	0	2161	50	0
2	D	2170	0	2164	43	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	76	0	0	2	0
3	B	80	0	0	4	0
3	C	34	0	0	1	0
3	D	52	0	0	2	0
All	All	8912	0	8661	148	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 9.

The worst 5 of 148 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:C:228:PHE:CD2	1:C:228:PHE:O	1.69	1.45
1:B:284:ALA:O	1:B:285:LEU:HD12	1.41	1.20
1:B:284:ALA:C	1:B:285:LEU:HD12	1.76	1.08
1:B:284:ALA:C	1:B:285:LEU:CD1	2.30	1.05
1:C:228:PHE:O	1:C:228:PHE:HD2	1.21	0.94

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	284/287 (99%)	278 (98%)	6 (2%)	0	100	100
1	B	284/287 (99%)	277 (98%)	7 (2%)	0	100	100
1	C	283/287 (99%)	264 (93%)	14 (5%)	5 (2%)	6	12
2	D	284/287 (99%)	273 (96%)	10 (4%)	1 (0%)	30	49
All	All	1135/1148 (99%)	1092 (96%)	37 (3%)	6 (0%)	24	43

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	228	PHE
1	C	156	THR
1	C	220	LYS
1	C	234	PHE
1	C	38	LYS

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	231/229 (101%)	211 (91%)	20 (9%)	9 21
1	B	231/229 (101%)	216 (94%)	15 (6%)	15 32
1	C	230/229 (100%)	210 (91%)	20 (9%)	9 21
2	D	231/229 (101%)	214 (93%)	17 (7%)	13 27
All	All	923/916 (101%)	851 (92%)	72 (8%)	12 24

5 of 72 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	50	ARG
2	D	280	THR
2	D	67	VAL
2	D	158	SER
1	B	67	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	268	GLN
2	D	197	ASN
2	D	11	GLN
2	D	55	ASN
1	B	86	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 [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	283/287 (98%)	-0.36	2 (0%) 84 81	17, 34, 50, 61	1 (0%)
1	B	283/287 (98%)	0.02	2 (0%) 84 81	17, 35, 52, 60	1 (0%)
1	C	283/287 (98%)	0.25	8 (2%) 55 50	35, 46, 77, 88	0
2	D	283/287 (98%)	0.01	4 (1%) 73 70	17, 41, 63, 67	1 (0%)
All	All	1132/1148 (98%)	-0.02	16 (1%) 73 70	17, 39, 63, 88	3 (0%)

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	78	TYR	4.2
1	C	234	PHE	3.9
1	B	285	LEU	2.9
1	C	78	TYR	2.9
1	C	244	PHE	2.9

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.