

wwPDB X-ray Structure Validation Summary Report (i)

Aug 8, 2023 – 09:54 AM EDT

PDB ID : 1QX0

Title : CONJUGATIVE RELAXASE TRWC IN COMPLEX WITH ORIT DNA.

METAL-BOUND STRUCTURE

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Deposited on : 2003-09-04

Resolution : 2.26 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 (i) 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 (i)) were used in the production of this report:

MolProbity: 4.02b-467

Mogul : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : NOT EXECUTED EDS : NOT EXECUTED

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

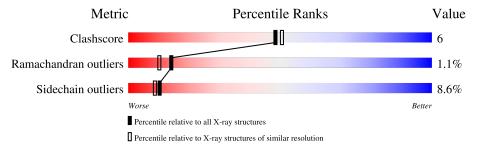
Validation Pipeline (wwPDB-VP) : 2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 2.26 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	Similar resolution		
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{resolution range}(ext{Å}))$		
Clashscore	141614	1487 (2.26-2.26)		
Ramachandran outliers	138981	1449 (2.26-2.26)		
Sidechain outliers	138945	1450 (2.26-2.26)		

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain						
1	В	25	28%	60%		12%			
2	A	293		79%	15%	5% •			



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 2984 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 DNA chain called DNA OLIGONUCLEOTIDE.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	В	25	Total 512	C 244	N 95	O 149	P 24	9	0	0

• Molecule 2 is a protein called trwC protein.

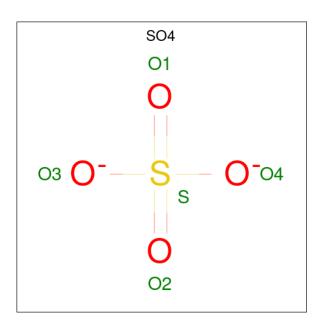
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	A	289	Total 2288	C 1411	N 431	O 442	Se 4	16	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	modified residue	UNP Q47673
A	5	MSE	MET	modified residue	UNP Q47673
A	70	MSE	MET	modified residue	UNP Q47673
A	169	MSE	MET	modified residue	UNP Q47673

• Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	В	1	Total 5	O 4	S 1	0	0

• Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

\mathbf{N}	/Iol	Chain	Residues	Ator	ns	ZeroOcc	AltConf
	4	A	1	Total 1	Zn 1	0	0

• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	В	42	Total O 42 42	0	0
5	A	136	Total O 136 136	0	0

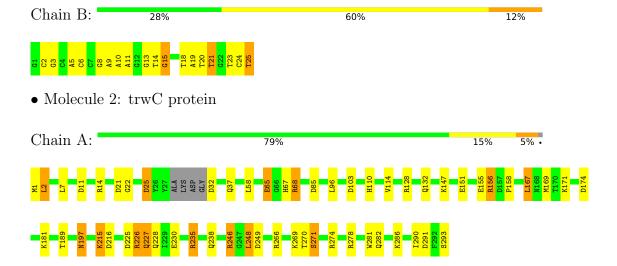


3 Residue-property plots (i)

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. 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. 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.

Note EDS was not executed.

• Molecule 1: DNA OLIGONUCLEOTIDE





4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source	
Space group	P 61 2 2	Depositor	
Cell constants	91.19Å 91.19Å 205.03Å	Danagitan	
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor	
Resolution (Å)	43.00 - 2.26	Depositor	
% Data completeness	99.2 (43.00-2.26)	Depositor	
(in resolution range)	33.2 (43.00-2.20)		
R_{merge}	0.12	Depositor	
R_{sym}	(Not available)	Depositor	
Refinement program	REFMAC 5.1.24	Depositor	
R, R_{free}	0.234 , 0.281	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	2984	wwPDB-VP	
Average B, all atoms (Å ²)	27.0	wwPDB-VP	



5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, SO4

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		nd lengths	Bond angles		
MIOI		RMSZ	# Z > 5	RMSZ	# Z > 5	
1	В	1.16	1/574~(0.2%)	1.79	16/885 (1.8%)	
2	A	0.61	0/2317	0.86	13/3104 (0.4%)	
All	All	0.75	1/2891 (0.0%)	1.13	$29/3989 \ (0.7\%)$	

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	$Ideal(\AA)$
1	В	24	DC	C3'-O3'	-6.74	1.35	1.44

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	${f Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	В	21	DT	O4'-C1'-N1	11.95	116.37	108.00
1	В	2	DC	O4'-C1'-N1	-8.06	102.36	108.00
2	A	21	ASP	CB-CG-OD2	7.90	125.41	118.30
2	A	103	ASP	CB-CG-OD2	6.69	124.32	118.30
2	A	85	ASP	CB-CG-OD2	6.67	124.31	118.30

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	В	512	0	283	9	0
2	A	2288	0	2268	26	0
3	В	5	0	0	0	0
4	A	1	0	0	0	0
5	A	136	0	0	2	0
5	В	42	0	0	2	0
All	All	2984	0	2551	32	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 6.

The worst 5 of 32 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap $(Å)$	
1:B:8:DG:H21	1:B:10:DA:H2	1.06	1.01	
1:B:25:DT:OP2	5:B:221:HOH:O	1.98	0.80	
1:B:25:DT:P	5:B:221:HOH:O	2.41	0.78	
2:A:2:LEU:HD13	2:A:189:THR:HG23	1.76	0.68	
2:A:2:LEU:CD1	2:A:189:THR:HG23	2.34	0.57	

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	
2	A	285/293 (97%)	276 (97%)	6 (2%)	3 (1%)	14 10	

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	215	LYS
2	A	22	GLY

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Mol	Chain	Res	Type
2	A	65	GLU

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	nalysed Rotameric Outliers		
2	A	232/230 (101%)	212 (91%)	20 (9%)	10 9

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	246	ARG
2	A	271	SER
2	A	278	ARG
2	A	274	ARG
2	A	96	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
2	A	227	GLN
2	A	238	GLN
2	A	132	GLN
2	A	197	ASN
2	A	205	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	Type	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Res	Link	B	ond leng	$_{ m gths}$	В	ond ang	gles
	Type		i ites .	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2								
3	SO4	В	182	-	4,4,4	0.12	0	6,6,6	0.28	0								

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 (i)

There are no chain breaks in this entry.



6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

