

# Full wwPDB X-ray Structure Validation Report (i)

Apr 25, 2022 – 01:17 pm BST

PDB ID : 7OC3

Title : Crystal structure of the third tudor domain of Qin

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Deposited on : 2021-04-25

Resolution : 2.25 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity : 4.02b-467

Mogul : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.28

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

Refmac: 5.8.0267

CCP4 : 7.1.010 (Gargrove)

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

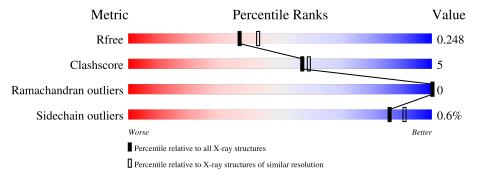
Validation Pipeline (wwPDB-VP) : 2.28

# 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 2.25 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
Medit	$(\# {\rm Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
$R_{free}$	130704	1377 (2.26-2.26)
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%

Mol	Chain	Length	Quality of chain	
1	A	212	89%	10%
1	В	212	86%	12% •



# 2 Entry composition (i)

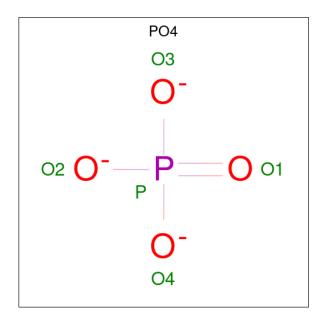
There are 3 unique types of molecules in this entry. The entry contains 3314 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Qin.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace			
1	A	212	Total 1663	C 1049	N 296	O 307	S 4	Se 7	0	0	0
1	В	209	Total 1644	C 1039		O 302	S 4	Se 7	0	0	0

• Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O P 5 4 1	0	0

• Molecule 3 is water.

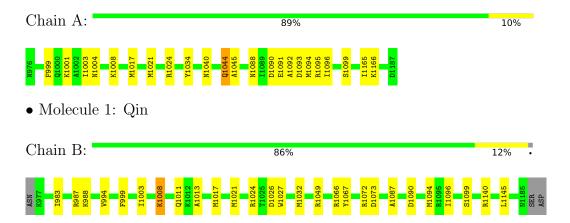
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total O 2 2	0	0



# 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.

• Molecule 1: Qin





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants	74.80Å 74.80Å 165.09Å	Donogiton
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $120.00^{\circ}$	Depositor
Resolution (Å)	37.40 - 2.25	Depositor
Resolution (A)	37.40  -  2.25	EDS
% Data completeness	99.1 (37.40-2.25)	Depositor
(in resolution range)	99.3 (37.40-2.25)	EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	3.06 (at 2.24Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
D.D.	0.208 , $0.245$	Depositor
$R, R_{free}$	0.211 , $0.248$	DCC
$R_{free}$ test set	1336 reflections $(5.15\%)$	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	54.9	Xtriage
Anisotropy	0.755	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	(Not available), (Not available)	EDS
L-test for twinning <sup>2</sup>	$< L > = 0.49, < L^2> = 0.31$	Xtriage
Estimated twinning fraction	0.032 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	3314	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.36% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $<L^2>$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: PO4

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	
IVIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	A	0.28	0/1692	0.51	0/2285
1	В	0.25	0/1673	0.49	0/2259
All	All	0.27	0/3365	0.50	0/4544

There are no bond length outliers.

There are no bond angle outliers.

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	1663	0	1641	16	0
1	В	1644	0	1628	17	0
2	A	5	0	0	0	0
3	A	2	0	0	0	0
All	All	3314	0	3269	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 5.

All (32) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



Atom-1	Atom-2	Interatomic	Clash
1:A:1044:GLN:OE1	1:A:1045:ALA:N	<u>distance (Å)</u> 2.06	overlap (Å) 0.87
1:A:1044:GLN:OE1 1:B:987:ARG:HD3	1:A:1045:ALA:N 1:B:988:LYS:HE2		
		1.68	0.74
1:B:1032:MSE:HE1	1:B:1072:ARG:HD2	1.70	0.72
1:A:1040:ASN:OD1	1:B:1066:ARG:NH1	2.27	0.61
1:B:1032:MSE:HG3	1:B:1094:MSE:SE	2.52	0.59
1:B:1003:ILE:HD12	1:B:1099:SER:HB3	1.84	0.59
1:A:1004:ASN:HB3	1:A:1008:LYS:HZ1	1.69	0.58
1:B:1017:MSE:HE1	1:B:1090:ASP:HB2	1.88	0.55
1:A:1024:ARG:NH1	1:A:1088:ASN:OD1	2.36	0.53
1:B:983:ILE:HD13	1:B:994:VAL:HG12	1.93	0.50
1:A:999:PHE:O	1:A:1003:ILE:HG12	2.12	0.50
1:A:1091:GLU:HA	1:A:1094:MSE:HE3	1.92	0.50
1:A:1003:ILE:HD12	1:A:1099:SER:HB3	1.94	0.50
1:B:1049:ARG:NH2	1:B:1096:ILE:O	2.45	0.50
1:A:1034:TYR:OH	1:A:1093:ASP:OD2	2.29	0.49
1:B:1021:MSE:SE	1:B:1087:ALA:HA	2.63	0.48
1:B:999:PHE:O	1:B:1003:ILE:HG12	2.14	0.46
1:B:1013:ALA:O	1:B:1017:MSE:HG2	2.16	0.46
1:A:1091:GLU:CG	1:A:1095:ARG:HH12	2.29	0.45
1:B:988:LYS:HE3	1:B:988:LYS:HB2	1.66	0.45
1:A:1091:GLU:HG3	1:A:1095:ARG:HH12	1.82	0.44
1:A:1165:ILE:O	1:A:1166:LYS:HD3	2.16	0.44
1:B:1049:ARG:NH1	1:B:1073:ASP:OD1	2.51	0.44
1:B:1024:ARG:HE	1:B:1026:ASP:HB3	1.83	0.44
1:B:1027:TRP:HB2	1:B:1067:TYR:CE2	2.53	0.43
1:B:1008:LYS:HA	1:B:1011:GLN:HG2	2.01	0.43
1:A:1021:MSE:HE3	1:A:1088:ASN:ND2	2.34	0.43
1:A:1092:ALA:O	1:A:1096:ILE:HG13	2.19	0.42
1:A:1091:GLU:HG3	1:A:1095:ARG:NH1	2.35	0.42
1:A:1001:LYS:HE3	1:A:1001:LYS:HB2	1.84	0.41
1:A:1017:MSE:HE3	1:A:1090:ASP:HB2	2.02	0.41
1:B:1140:ARG:HG3	1:B:1145:LEU:HA	2.04	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	Perce	ntiles
1	A	210/212 (99%)	206 (98%)	4 (2%)	0	100	100
1	В	$207/212 \ (98\%)$	201 (97%)	6 (3%)	0	100	100
All	All	417/424 (98%)	407 (98%)	10 (2%)	0	100	100

There are no Ramachandran outliers to report.

#### 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	Perce	ntiles
1	A	180/176 (102%)	179 (99%)	1 (1%)	86	91
1	В	178/176 (101%)	177 (99%)	1 (1%)	86	91
All	All	358/352 (102%)	356 (99%)	2 (1%)	86	91

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1044	GLN
1	В	1008	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

#### 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)

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
2	PO4	A	1201	-	4,4,4	0.91	0	6,6,6	0.39	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)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

## 6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

## 6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

