



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2018 – 07:57 pm GMT

PDB ID : 3C0X
Title : I-SceI in complex with a top nicked DNA substrate
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Deposited on : 2008-01-21
Resolution : 2.30 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	trunk30967
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac	:	5.8.0158
CCP4	:	7.0 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk30967

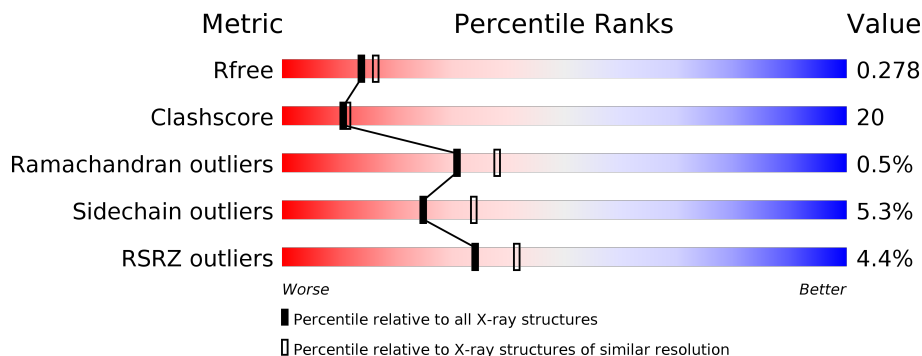
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	111664	4477 (2.30-2.30)
Clashscore	122126	5072 (2.30-2.30)
Ramachandran outliers	120053	5022 (2.30-2.30)
Sidechain outliers	120020	5021 (2.30-2.30)
RSRZ outliers	108989	4374 (2.30-2.30)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	B	14	<div> <div>43%</div> <div>50%</div> <div>7%</div> </div>
2	C	11	<div> <div>36%</div> <div>55%</div> <div>9%</div> </div>
3	D	25	<div> <div>28%</div> <div>64%</div> <div>• •</div> </div>
4	A	235	<div> <div>5%</div> <div>61%</div> <div>31%</div> <div>• 5%</div> </div>

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 2900 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 (5'-D(*DC*DAP*DCP*DGP*DCP*DTP*DAP*DCP*DGP*DGP*DAP*DTP*DAP*DA)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	13	Total	C	N	O	P	0	0	0
			268	128	55	73	12			

- Molecule 2 is a DNA chain called DNA (5'-D(P*DCP*DAP*DGP*DGP*DGP*DTP*DAP*DAP*DTP*DAP*DC)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	11	Total	C	N	O	P	0	0	0
			229	108	45	65	11			

- Molecule 3 is a DNA chain called DNA (5'-D(*DG*DGP*DTP*DAP*DTP*DTP*DAP*DCP*DCP*DCP*DTP*DGP*DTP*DTP*DAP*DTP*DCP*DCP*DCP*DTP*DAP*DGP*DCP*DGP*DT)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	24	Total	C	N	O	P	0	0	0
			482	233	79	147	23			

- Molecule 4 is a protein called Intron-encoded endonuclease I-SceI.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	A	223	Total	C	N	O	S	0	2	0
			1860	1211	309	329	11			

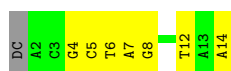
- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total	Ca	0	0
			2	2		
5	C	1	Total	Ca	0	0
			1	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	6	Total 6	O 6	0	0
6	C	6	Total 6	O 6	0	0
6	D	11	Total 11	O 11	0	0
6	A	35	Total 35	O 35	0	0

- Molecule 1: DNA (5'-D(*DC*DAP*DCP*DGP*DCP*DTP*DAP*DGP*DGP*DGP*DAP*DT
P*DAP*DA)-3')



C15	A16	G17	T20	A21	A22	T23	A24	C25
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DG
G2
T3
A4
T5
T6
A7
C8
C9
C10
T11
G12
T13
T14
A15
T16
C17
C18
C19
T20
A21
T25

K193	V89	NET
P196	N90	N3
I197	H91	I4
I198	L92	K5
S202	G93	
	N94	Q8
	L95	
L206	V96	L12
	T97	
K213	T98	
P214	N99	S16
Y215	Q107	K17
L216	A108	L18
I217	F109	L19
P218	N110	K20
Q219	K111	E21
M220	L112	Y22
P225	L115	L26
ASN		L27
THR	N119	E28
ILE	N120	I31
SER	K121	E32
SER		Q33
THR	P125	F34
GLU	N126	
PHE	N127	G37
LEU	L128	I38
LYS	V129	
	M143	Q43
	D144	Y46
	D145	I47
		R48
	Y151	S49
	N152	R50
	K153	D51
	N154	
	K158	Y56
	S159	G57
	I160	M58
	V161	
	L162	W62
	N163	
	T164	K65
	Q165	M68
	S166	D69
	F169	C72
	V172	Y75
		D76
	G178	Q77
	L179	
	R180	H84
	I191	E87
	N192	E92

4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	80.68Å 80.68Å 128.32Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.08 – 2.30 36.08 – 2.29	Depositor EDS
% Data completeness (in resolution range)	96.8 (36.08-2.30) 96.4 (36.08-2.29)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.83 (at 2.29Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.255 , 0.288 0.251 , 0.278	Depositor DCC
R_{free} test set	945 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	48.5	Xtriage
Anisotropy	0.141	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 38.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2900	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.22% 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: CA

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	B	0.49	0/302	0.69	0/465
2	C	0.72	1/257 (0.4%)	0.77	0/393
3	D	0.50	0/537	0.80	0/826
4	A	0.41	0/1919	0.63	0/2593
All	All	0.47	1/3015 (0.0%)	0.69	0/4277

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
3	D	0	3
All	All	0	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	15	DC	OP3-P	-7.80	1.51	1.61

There are no bond angle outliers.

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	14	DA	Sidechain
3	D	15	DA	Sidechain
3	D	21	DA	Sidechain

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Mol	Chain	Res	Type	Group
3	D	7	DA	Sidechain

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	B	268	0	147	12	0
2	C	229	0	124	6	0
3	D	482	0	275	22	0
4	A	1860	0	1874	70	0
5	A	2	0	0	0	0
5	C	1	0	0	0	0
6	A	35	0	0	2	0
6	B	6	0	0	0	0
6	C	6	0	0	0	0
6	D	11	0	0	0	0
All	All	2900	0	2420	103	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 20.

The worst 5 of 103 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)
2:C:16:DA:H2''	2:C:17:DG:H5''	1.24	1.18
3:D:17:DC:H2''	3:D:18:DC:H5''	1.47	0.95
3:D:12:DG:H2''	3:D:13:DT:H5'	1.52	0.89
2:C:16:DA:H2''	2:C:17:DG:C5'	2.04	0.86
3:D:14:DT:H2''	3:D:15:DA:C5	2.17	0.79

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	
4	A	223/235 (95%)	210 (94%)	12 (5%)	1 (0%)	36	45

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	219	GLN

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	
4	A	208/218 (95%)	197 (95%)	11 (5%)	25	34

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	A	91	HIS
4	A	127	ASN
4	A	216	LEU
4	A	77	GLN
4	A	206	LEU

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

Mol	Chain	Res	Type
4	A	94	ASN
4	A	219	GLN
4	A	127	ASN
4	A	84	HIS
4	A	114	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are 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 [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	B	13/14 (92%)	0.01	0 100 100	36, 53, 70, 71	0
2	C	11/11 (100%)	-0.42	0 100 100	37, 55, 59, 60	0
3	D	24/25 (96%)	-0.09	0 100 100	39, 48, 66, 68	0
4	A	223/235 (94%)	0.31	12 (5%) 26 33	29, 44, 63, 80	2 (0%)
All	All	271/285 (95%)	0.23	12 (4%) 34 41	29, 45, 66, 80	2 (0%)

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	A	98[A]	THR	7.7
4	A	180[A]	ARG	6.2
4	A	119	ASN	4.3
4	A	153	LYS	3.2
4	A	89	VAL	3.0

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 carbohydrates 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(\AA^2)	Q<0.9
5	CA	A	301	1/1	0.95	0.13	34,34,34,34	0
5	CA	C	302	1/1	0.96	0.04	48,48,48,48	0
5	CA	A	303	1/1	0.97	0.05	41,41,41,41	0

6.5 Other polymers [i](#)

There are no such residues in this entry.