



wwPDB X-ray Structure Validation Summary Report

Feb 26, 2014 – 10:49 PM GMT

PDB ID : 2EX5
Title : Group I Intron-encoded Homing Endonuclease I-CeuI Complexed With DNA
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Deposited on : 2005-11-07
Resolution : 2.20 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

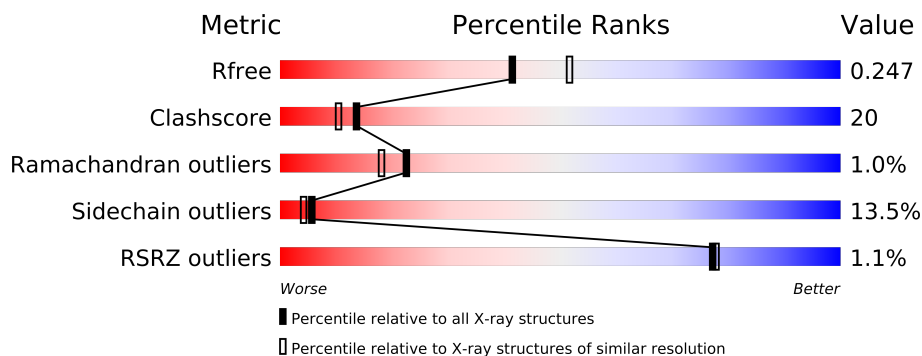
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.20 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}	66092	2938 (2.20-2.20)
Clashscore	79885	3751 (2.20-2.20)
Ramachandran outliers	78287	3681 (2.20-2.20)
Sidechain outliers	78261	3682 (2.20-2.20)
RSRZ outliers	66119	2939 (2.20-2.20)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	X	26	
2	Y	26	
3	A	207	
3	B	207	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4664 atoms, of which 0 are hydrogen and 0 are deuterium.

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 I-CeuI DNA target site.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	X	26	Total	C	N	O	P	0	0	0
			535	254	106	150	25			

- Molecule 2 is a DNA chain called I-CeuI DNA target site, complimentary strand.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	Y	26	Total	C	N	O	P	0	0	0
			525	252	90	158	25			

- Molecule 3 is a protein called DNA endonuclease I-CeuI.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	207	Total	C	N	O	S	0	0	0
			1669	1071	286	311	1			
3	B	207	Total	C	N	O	S	0	0	0
			1669	1071	286	311	1			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	93	ARG	GLN	ENGINEERED	UNP P32761
B	93	ARG	GLN	ENGINEERED	UNP P32761

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	X	1	Total	Ca	0	0
			1	1		
4	B	1	Total	Ca	0	0
			1	1		
4	A	1	Total	Ca	0	0
			1	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	118	Total 118	O 118	0	0
5	B	78	Total 78	O 78	0	0
5	X	27	Total 27	O 27	0	0
5	Y	40	Total 40	O 40	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	50.23Å 69.18Å 169.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.20 19.83 – 2.20	Depositor EDS
% Data completeness (in resolution range)	96.0 (20.00-2.20) 96.4 (19.83-2.20)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.10 (at 2.21Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.219 , 0.231 0.237 , 0.247	Depositor DCC
R_{free} test set	2959 reflections (10.00%)	DCC
Wilson B-factor (Å ²)	37.7	Xtriage
Anisotropy	0.445	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 42.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 30529 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4664	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.70% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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	X	2.23	24/602 (4.0%)	3.33	122/928 (13.1%)
2	Y	2.41	29/586 (4.9%)	3.54	135/902 (15.0%)
3	A	1.46	12/1697 (0.7%)	1.21	9/2283 (0.4%)
3	B	1.24	4/1697 (0.2%)	1.15	9/2283 (0.4%)
All	All	1.66	69/4582 (1.5%)	2.09	275/6396 (4.3%)

The worst 5 of 69 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	X	606	DA	N7-C5	9.68	1.45	1.39
2	Y	714	DA	N3-C4	9.52	1.40	1.34
1	X	609	DG	C6-N1	8.65	1.45	1.39
2	Y	701	DG	C8-N7	8.27	1.35	1.30
1	X	618	DT	N1-C6	8.00	1.43	1.38

The worst 5 of 275 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Y	708	DT	C6-C5-C7	-16.84	112.80	122.90
1	X	607	DC	O4'-C1'-N1	16.67	119.67	108.00
1	X	601	DC	O4'-C1'-N1	-15.76	96.97	108.00
2	Y	704	DT	O4'-C1'-N1	12.31	116.62	108.00
1	X	603	DA	O4'-C1'-N9	12.20	116.54	108.00

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	X	535	0	292	20	0
2	Y	525	0	295	30	1
3	A	1669	0	1717	58	0
3	B	1669	0	1717	73	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	X	1	0	0	0	0
5	A	118	0	0	11	0
5	B	78	0	0	11	0
5	X	27	0	0	2	0
5	Y	40	0	0	6	1
All	All	4664	0	4021	166	1

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 20.

The worst 5 of 166 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:B:22:LYS:HD3	5:B:1213:HOH:O	1.40	1.20
2:Y:721:DT:H2''	2:Y:722:DT:H5'	1.21	1.11
3:B:73:THR:HG22	3:B:85:VAL:HG22	1.40	1.01
2:Y:722:DT:O4	5:Y:1236:HOH:O	1.84	0.95
3:B:53:SER:O	3:B:57:LEU:HD22	1.70	0.92

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:Y:701:DG:O5'	5:Y:1234:HOH:O[2_674]	1.80	0.40

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	
3	A	205/207 (99%)	198 (97%)	7 (3%)	0	100	100
3	B	205/207 (99%)	185 (90%)	16 (8%)	4 (2%)	11	6
All	All	410/414 (99%)	383 (93%)	23 (6%)	4 (1%)	22	18

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	B	204	GLU
3	B	203	LEU
3	B	96	ASN
3	B	184	PRO

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	
3	A	185/185 (100%)	159 (86%)	26 (14%)	5	4
3	B	185/185 (100%)	161 (87%)	24 (13%)	6	5
All	All	370/370 (100%)	320 (86%)	50 (14%)	6	4

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	175	LEU
3	B	14	GLN
3	B	166	LEU
3	A	183	LEU
3	A	197	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
3	A	192	GLN
3	A	197	ASN
3	B	180	ASN
3	A	177	GLN
3	B	195	GLN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	X	26/26 (100%)	-0.17	0 100 100	38, 48, 71, 86	0
2	Y	26/26 (100%)	-0.18	0 100 100	28, 49, 61, 62	0
3	A	207/207 (100%)	-0.26	2 (0%) 79 80	21, 34, 53, 62	0
3	B	207/207 (100%)	0.04	3 (1%) 72 72	20, 44, 72, 77	0
All	All	466/466 (100%)	-0.12	5 (1%) 77 78	20, 40, 66, 86	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	B	204	GLU	2.5
3	A	49	VAL	2.5
3	A	50	GLN	2.1
3	B	14	GLN	2.0
3	B	50	GLN	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains.

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	CA	B	803	1/1	0.10	-0.55	51,51,51,51	0
4	CA	X	802	1/1	0.06	-2.55	36,36,36,36	0
4	CA	A	801	1/1	0.05	-3.23	34,34,34,34	0

6.5 Other polymers ⓘ

There are no such residues in this entry.