



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 16, 2021 – 09:37 PM EDT

PDB ID : 1SX8
Title : EcoRV bound to cognate DNA and Mn²⁺
Authors : Horton, N.C.; Perona, J.J.
Deposited on : 2004-03-30
Resolution : 2.15 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
Xtrriage (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) : 2.23.2

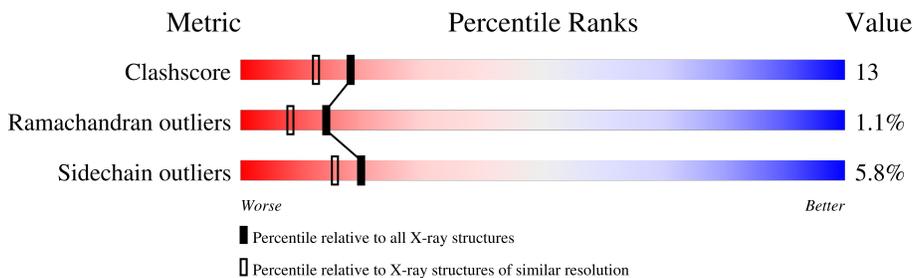
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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))
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	C	11	36% (green), 18% (yellow), 18% (orange), 18% (red), 9% (grey)
1	D	11	18% (green), 55% (yellow), 9% (orange), 9% (red), 9% (grey)
2	A	244	61% (green), 33% (yellow), 5% (orange), 1% (red), 1% (grey)
2	B	244	55% (green), 36% (yellow), 5% (orange), 1% (red), 1% (grey)

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4379 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 5'-D(*C*AP*AP*GP*AP*TP*AP*TP*CP*TP*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	C	10	202	99	36	58	9	0	0	0
1	D	10	201	98	37	57	9	0	0	0

- Molecule 2 is a protein called Type II restriction enzyme EcoRV.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	A	241	1930	1245	318	366	1	0	0	0
2	B	235	1888	1218	310	359	1	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	92	ALA	LYS	engineered mutation	UNP P04390
B	92	ALA	LYS	engineered mutation	UNP P04390

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mn		
3	A	3	3	3	0	0
3	B	3	3	3	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	12	Total	O	0	0
			12	12		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	8	Total 8	O 8	0	0
4	A	79	Total 79	O 79	0	0
4	B	53	Total 53	O 53	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: 5'-D(*C*AP*AP*GP*AP*TP*AP*TP*CP*TP*T)-3'

Chain C: 



- Molecule 1: 5'-D(*C*AP*AP*GP*AP*TP*AP*TP*CP*TP*T)-3'

Chain D: 



- Molecule 2: Type II restriction enzyme EcoRV

Chain A: 



- Molecule 2: Type II restriction enzyme EcoRV

Chain B: 





4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	47.80Å 49.10Å 63.70Å 96.90° 108.90° 107.10°	Depositor
Resolution (Å)	20.00 – 2.15	Depositor
% Data completeness (in resolution range)	91.2 (20.00-2.15)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.213 , 0.254	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	4379	wwPDB-VP
Average B, all atoms (Å ²)	24.0	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: MN

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	C	2.17	10/226 (4.4%)	1.57	2/347 (0.6%)
1	D	2.14	6/225 (2.7%)	1.50	1/345 (0.3%)
2	A	1.74	26/1980 (1.3%)	1.32	14/2692 (0.5%)
2	B	1.75	35/1936 (1.8%)	1.30	10/2631 (0.4%)
All	All	1.79	77/4367 (1.8%)	1.34	27/6015 (0.4%)

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	C	0	2
1	D	0	2
2	B	0	2
All	All	0	6

The worst 5 of 77 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	6	DT	C2-N3	11.02	1.46	1.37
2	A	125	PHE	CE2-CZ	9.04	1.54	1.37
2	B	230	TYR	CE2-CZ	8.87	1.50	1.38
2	A	206	PHE	CD2-CE2	8.67	1.56	1.39
2	B	72	TYR	CD1-CE1	8.62	1.52	1.39

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	164	LYS	C-N-CA	-9.96	101.38	122.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	49	ARG	NE-CZ-NH2	-8.57	116.01	120.30
2	A	217	ARG	NE-CZ-NH2	-7.58	116.51	120.30
2	B	43	ILE	CG1-CB-CG2	-7.17	95.63	111.40
2	A	237	ARG	NE-CZ-NH1	-6.91	116.84	120.30

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	78	TYR	Sidechain
1	C	2	DA	Sidechain
1	C	6	DT	Sidechain
1	D	10	DT	Sidechain
1	D	6	DT	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	C	202	0	116	6	0
1	D	201	0	115	5	0
2	A	1930	0	1814	56	0
2	B	1888	0	1778	58	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
4	A	79	0	0	2	0
4	B	53	0	0	2	0
4	C	12	0	0	1	0
4	D	8	0	0	0	0
All	All	4379	0	3823	108	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 13.

The worst 5 of 108 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:A:23:ILE:HG22	2:B:23:ILE:HG22	1.39	1.04
2:B:62:ILE:HD11	2:B:80:PRO:HG3	1.47	0.94
2:A:82:GLU:HG3	2:A:85:LYS:HB2	1.52	0.90
2:B:11:LEU:HD23	2:B:51:ILE:HD12	1.56	0.84
2:A:110:TYR:HA	2:A:114:ILE:HG21	1.64	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	
2	A	237/244 (97%)	222 (94%)	12 (5%)	3 (1%)	12	6
2	B	229/244 (94%)	212 (93%)	15 (7%)	2 (1%)	17	11
All	All	466/488 (96%)	434 (93%)	27 (6%)	5 (1%)	14	8

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	117	ASN
2	B	117	ASN
2	A	162	PRO
2	A	187	THR
2	B	187	THR

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	
2	A	199/219 (91%)	189 (95%)	10 (5%)	24	21
2	B	196/219 (90%)	183 (93%)	13 (7%)	16	11
All	All	395/438 (90%)	372 (94%)	23 (6%)	20	15

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	71	HIS
2	B	97	ASN
2	B	90	ASP
2	B	118	THR
2	A	114	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	69	GLN
2	B	16	GLN
2	B	53	ASN
2	B	84	ASN
2	B	193	HIS

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 6 ligands modelled in this entry, 6 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

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 [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.