



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 11:32 PM GMT

PDB ID : 5CRX  
Title : ASYMMETRIC DNA-BENDING IN THE CRE-LOXP SITE-SPECIFIC RE-COMBINATION SYNAPSE  
Authors : Guo, F.; Gopaul, D.N.; Van Duyne, G.D.  
Deposited on : 1999-04-21  
Resolution : 2.70 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

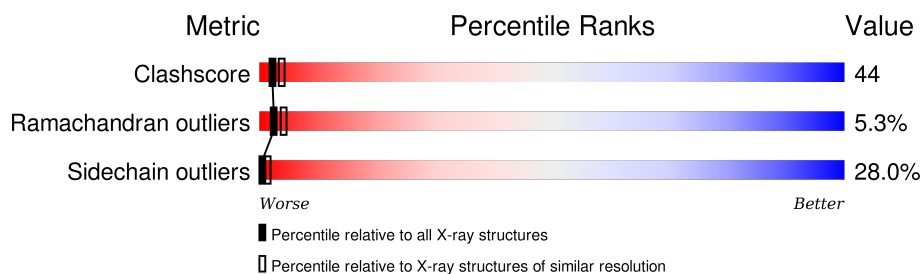
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)

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  $\geq 3$ , 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	C	35	
1	D	35	
2	A	343	
2	B	343	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6364 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 (35-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	33	Total	C	N	O	P	0	0	0
			677	325	122	197	33			
1	D	33	Total	C	N	O	P	0	0	0
			677	325	122	197	33			

- Molecule 2 is a protein called PROTEIN (BACTERIOPHAGE P1 CRE GENE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	297	Total	C	N	O	S	0	0	0
			2359	1462	452	431	14			
2	B	296	Total	C	N	O	S	0	0	0
			2337	1451	449	424	13			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	324	PHE	TYR	ENGINEERED	UNP P06956
B	324	PHE	TYR	ENGINEERED	UNP P06956

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	89	Total	O	0	0
			89	89		
3	B	135	Total	O	0	0
			135	135		
3	C	34	Total	O	0	0
			34	34		
3	D	56	Total	O	0	0
			56	56		

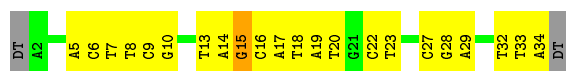
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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.

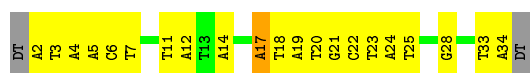
- Molecule 1: DNA (35-MER)

Chain C: 




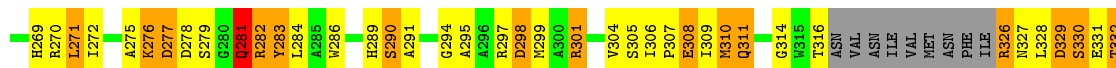
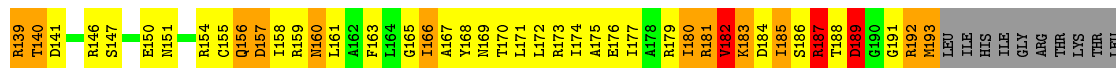
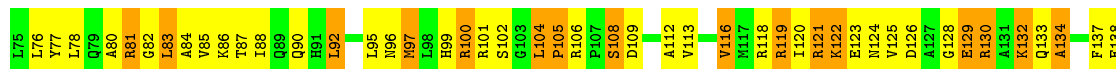
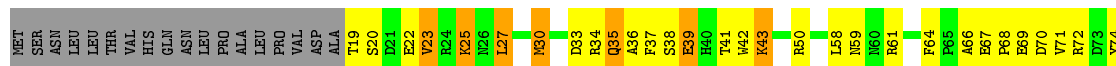
- Molecule 1: DNA (35-MER)

Chain D: 

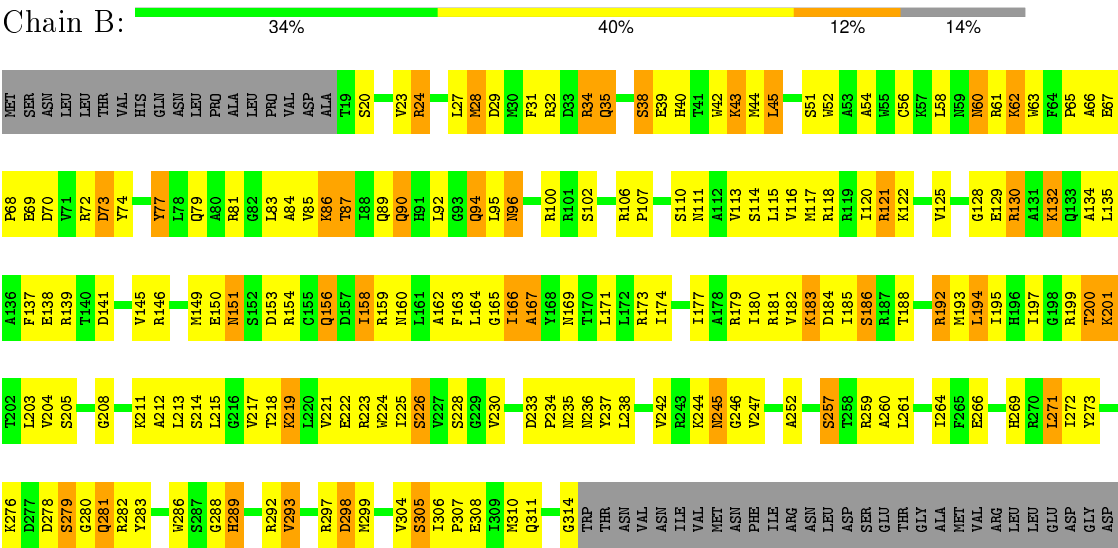


- Molecule 2: PROTEIN (BACTERIOPHAGE P1 CRE GENE)

Chain A: 



- Molecule 2: PROTEIN (BACTERIOPHAGE P1 CRE GENE)



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	107.10Å 123.10Å 180.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.00 – 2.70	Depositor
% Data completeness (in resolution range)	96.1 (48.00-2.70)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, $R_{free}$	0.227 , 0.304	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6364	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	50.0	wwPDB-VP

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	0.64	0/759	0.84	0/1169
1	D	0.62	0/759	0.83	0/1169
2	A	0.47	0/2396	0.66	0/3224
2	B	0.48	0/2375	0.68	0/3199
All	All	0.52	0/6289	0.72	0/8761

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	1
1	D	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	15	DG	Sidechain
1	D	17	DA	Sidechain

### 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	C	677	0	375	41	0
1	D	677	0	375	67	0
2	A	2359	0	2364	275	4
2	B	2337	0	2362	175	4
3	A	89	0	0	17	0
3	B	135	0	0	19	0
3	C	34	0	0	4	0
3	D	56	0	0	8	0
All	All	6364	0	5476	508	4

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 44.

The worst 5 of 508 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)
1:D:5:DA:H1'	1:D:6:DC:H5'	1.23	1.14
2:B:181:ARG:HA	3:B:439:HOH:O	1.50	1.11
1:C:17:DA:H2''	1:C:18:DT:C5'	1.82	1.09
1:D:19:DA:H2''	1:D:20:DT:C5'	1.86	1.04
1:D:6:DC:H5''	3:D:64:HOH:O	1.56	1.03

All (4) 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	Interatomic distance (Å)	Clash overlap (Å)
2:A:332:THR:CG2	2:B:212:ALA:CB[4_566]	1.81	0.39
2:A:337:ARG:NH1	2:B:308:GLU:OE2[4_566]	2.04	0.16
2:A:122:LYS:CD	2:B:35:GLN:O[4_566]	2.06	0.14
2:A:327:ASN:ND2	2:B:194:LEU:CD2[4_566]	2.10	0.10

## 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	
2	A	291/343 (85%)	216 (74%)	49 (17%)	26 (9%)	1	1
2	B	294/343 (86%)	261 (89%)	28 (10%)	5 (2%)	11	29
All	All	585/686 (85%)	477 (82%)	77 (13%)	31 (5%)	2	4

5 of 31 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	134	ALA
2	A	214	SER
2	A	232	ASP
2	A	248	ALA
2	A	249	ALA

### 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	
2	A	247/287 (86%)	163 (66%)	84 (34%)	0	0
2	B	245/287 (85%)	191 (78%)	54 (22%)	1	3
All	All	492/574 (86%)	354 (72%)	138 (28%)	0	1

5 of 138 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	255	GLN
2	A	316	THR
2	B	245	ASN
2	A	258	THR
2	A	282	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
2	A	281	GLN

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Mol	Chain	Res	Type
2	A	311	GLN
2	B	94	GLN
2	A	235	ASN
2	A	245	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](#)

There are no ligands in this entry.

### 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 will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.