



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 02:07 AM GMT

PDB ID : 2FO1  
Title : Crystal Structure of the CSL-Notch-Mastermind ternary complex bound to DNA  
Authors : Wilson, J.J.; Kovall, R.A.  
Deposited on : 2006-01-12  
Resolution : 3.12 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) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

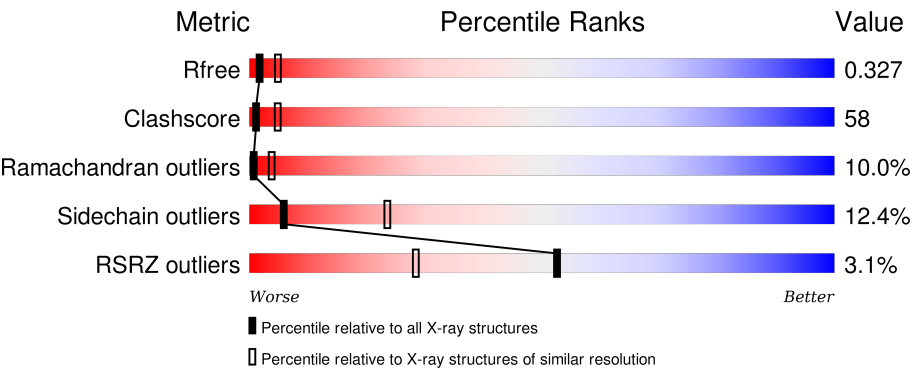
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.12 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 <sub>free</sub>	91344	1112 (3.16-3.08)
Clashscore	102246	1218 (3.16-3.08)
Ramachandran outliers	100387	1175 (3.16-3.08)
Sidechain outliers	100360	1175 (3.16-3.08)
RSRZ outliers	91569	1114 (3.16-3.08)

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.

Mol	Chain	Length	Quality of chain
1	B	15	<div><div></div><div><div></div><div></div><div></div><div></div></div><div>33%60%7%</div></div>
2	C	15	<div><div></div><div><div></div><div></div><div></div><div></div></div><div>33%60%7%</div></div>
3	A	477	<div><div>4%</div><div></div><div><div></div><div></div><div></div><div></div></div><div>34%48%10%8%</div></div>
4	D	85	<div><div></div><div><div></div><div></div><div></div><div></div></div><div>21%44%8%26%</div></div>
5	E	373	<div><div>2%</div><div></div><div><div></div><div></div><div></div><div></div></div><div>16%46%16%20%</div></div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6939 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(\*TP\*TP\*AP\*CP\*TP\*GP\*TP\*GP\*GP\*GP\*AP\*A P\*AP\*GP\*A)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	15	Total	C	N	O	P	0	0	0
			311	149	61	87	14			

- Molecule 2 is a DNA chain called 5'-D(\*AP\*AP\*TP\*CP\*TP\*TP\*TP\*CP\*CP\*CP\*AP\*CP \*AP\*GP\*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	15	Total	C	N	O	P	0	0	0
			298	145	50	89	14			

- Molecule 3 is a protein called Lin-12 and glp-1 phenotype protein 1, isoform b.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	439	Total	C	N	O	S	0	0	0
			3497	2218	608	654	17			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	187	GLY	-	CLONING ARTIFACT	GB 22532887
A	188	PRO	-	CLONING ARTIFACT	GB 22532887
A	189	LEU	-	CLONING ARTIFACT	GB 22532887
A	190	GLY	-	CLONING ARTIFACT	GB 22532887
A	191	SER	-	CLONING ARTIFACT	GB 22532887

- Molecule 4 is a protein called Protein lag-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	63	Total	C	N	O	S	0	0	0
			524	316	102	105	1			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	48	SER	-	CLONING ARTIFACT	UNP Q09260

- Molecule 5 is a protein called Lin-12 protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
5	E	297	Total	C	N	O	S	Se	0	0	0
			2309	1420	427	445	3	14			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	929	GLY	-	CLONING ARTIFACT	UNP P14585
E	930	SER	-	CLONING ARTIFACT	UNP P14585
E	939	MSE	MET	MODIFIED RESIDUE	UNP P14585
E	946	MSE	MET	MODIFIED RESIDUE	UNP P14585
E	949	MSE	MET	MODIFIED RESIDUE	UNP P14585
E	1090	MSE	MET	MODIFIED RESIDUE	UNP P14585
E	1099	MSE	MET	MODIFIED RESIDUE	UNP P14585
E	1114	MSE	MET	MODIFIED RESIDUE	UNP P14585
E	1142	MSE	MET	MODIFIED RESIDUE	UNP P14585
E	1143	MSE	MET	MODIFIED RESIDUE	UNP P14585
E	1146	MSE	MET	MODIFIED RESIDUE	UNP P14585
E	1164	MSE	MET	MODIFIED RESIDUE	UNP P14585
E	1168	MSE	MET	MODIFIED RESIDUE	UNP P14585
E	1220	MSE	MET	MODIFIED RESIDUE	UNP P14585
E	1246	MSE	MET	MODIFIED RESIDUE	UNP P14585
E	1258	MSE	MET	MODIFIED RESIDUE	UNP P14585

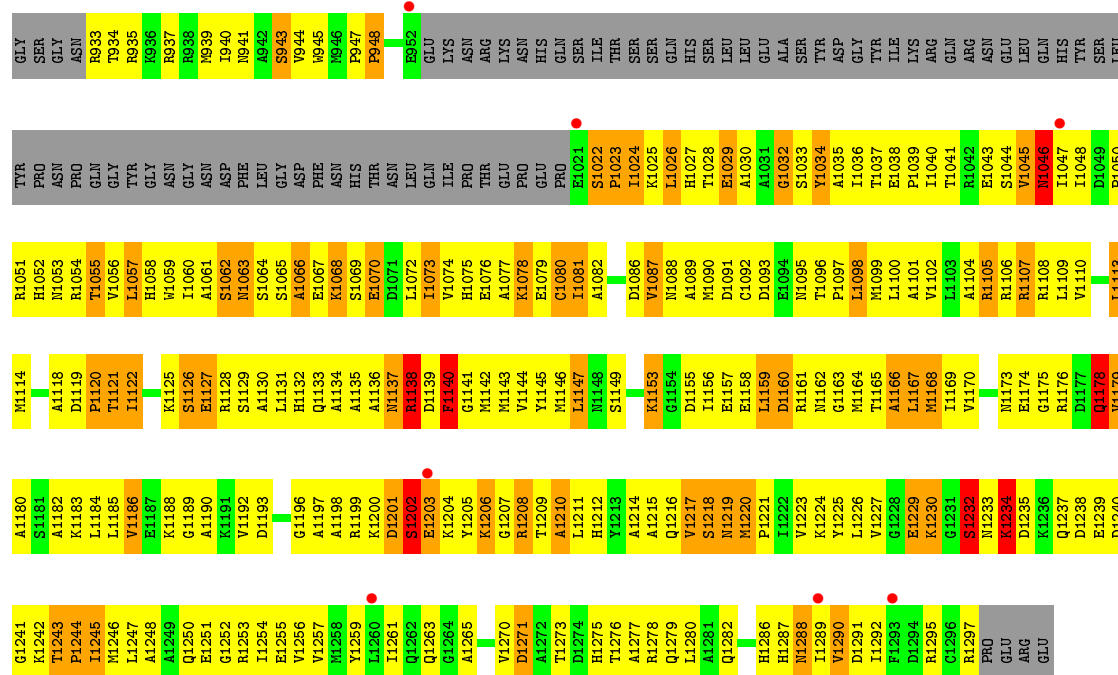
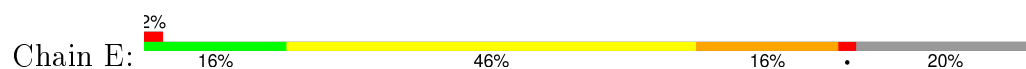




• Molecule 4: Protein lag-3



• Molecule 5: Lin-12 protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	66.09 Å 96.78 Å 243.54 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.51 – 3.12 43.51 – 3.12	Depositor EDS
% Data completeness (in resolution range)	88.6 (43.51-3.12) 93.0 (43.51-3.12)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.67 (at 3.12 Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.273 , 0.340 0.276 , 0.327	Depositor DCC
$R_{free}$ test set	2632 reflections (9.92%)	DCC
Wilson B-factor (Å <sup>2</sup> )	94.2	Xtriage
Anisotropy	0.612	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.23 , 72.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	2 of 52029 reflections (0.004%)	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	6939	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	103.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.03% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup> Intensities estimated from amplitudes.

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

## 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	B	0.66	0/350	0.80	0/540
2	C	0.64	0/332	0.81	0/509
3	A	0.45	0/3573	0.70	0/4822
4	D	0.37	0/532	0.69	1/714 (0.1%)
5	E	0.42	0/2327	0.76	0/3113
All	All	0.46	0/7114	0.73	1/9698 (0.0%)

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	2
2	C	0	2
All	All	0	4

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	54	GLU	C-N-CD	-5.81	107.83	120.60

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	12	DA	Sidechain
1	B	2	DT	Sidechain
2	C	2	DA	Sidechain
2	C	5	DT	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	B	311	0	171	20	0
2	C	298	0	172	17	0
3	A	3497	0	3441	343	0
4	D	524	0	491	51	0
5	E	2309	0	2301	392	0
All	All	6939	0	6576	785	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 58.

The worst 5 of 785 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)
5:E:1022:SER:H	5:E:1023:PRO:HD2	1.17	1.08
5:E:1167:LEU:HD12	5:E:1167:LEU:H	1.14	1.07
3:A:283:ALA:HB1	3:A:351:CYS:HB3	1.33	1.07
5:E:935:ARG:NH1	5:E:1158:GLU:HG2	1.69	1.06
2:C:8:DC:H2''	2:C:9:DC:H5'	1.33	1.04

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
3	A	429/477 (90%)	324 (76%)	77 (18%)	28 (6%)	<b>1</b> <b>10</b>

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	D	61/85 (72%)	44 (72%)	14 (23%)	3 (5%)	3	17
5	E	293/373 (79%)	170 (58%)	76 (26%)	47 (16%)	0	0
All	All	783/935 (84%)	538 (69%)	167 (21%)	78 (10%)	1	4

5 of 78 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	299	ARG
3	A	399	ARG
3	A	400	SER
3	A	403	VAL
3	A	504	GLU

### 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	385/416 (92%)	341 (89%)	44 (11%)	7	28
4	D	54/73 (74%)	47 (87%)	7 (13%)	5	22
5	E	244/298 (82%)	210 (86%)	34 (14%)	4	19
All	All	683/787 (87%)	598 (88%)	85 (12%)	6	23

5 of 85 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	631	ARG
4	D	91	ASN
5	E	1229	GLU
3	A	644	ARG
3	A	662	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
4	D	70	HIS
4	D	114	GLN
5	E	1275	HIS
4	D	80	ASN
4	D	91	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](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	B	15/15 (100%)	-0.31	0 <span>100</span> <span>100</span>	72, 88, 113, 115	0
2	C	15/15 (100%)	-0.36	0 <span>100</span> <span>100</span>	66, 85, 113, 113	0
3	A	439/477 (92%)	0.05	18 (4%) <span>41</span> <span>19</span>	37, 97, 165, 197	0
4	D	63/85 (74%)	-0.49	0 <span>100</span> <span>100</span>	68, 123, 174, 200	0
5	E	283/373 (75%)	-0.20	7 (2%) <span>61</span> <span>39</span>	52, 94, 165, 202	0
All	All	815/965 (84%)	-0.09	25 (3%) <span>52</span> <span>28</span>	37, 98, 166, 202	0

The worst 5 of 25 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	A	400	SER	8.2
3	A	484	SER	5.4
5	E	1203	GLU	4.3
3	A	626	TRP	3.8
3	A	661	LEU	3.7

### 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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.