



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2014 – 02:02 AM GMT

PDB ID : 2CBR  
Title : CELLULAR RETINOIC ACID BINDING PROTEIN I IN COMPLEX WITH  
A RETINO BENZOIC ACID (AM80)  
Authors : Chaudhuri, B.; Kleywegt, G.J.; Bergfors, T.; Jones, T.A.  
Deposited on : 1999-02-22  
Resolution : 2.80 Å(reported)

This is a full wwPDB validation 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/ValidationPDFNotes.html>

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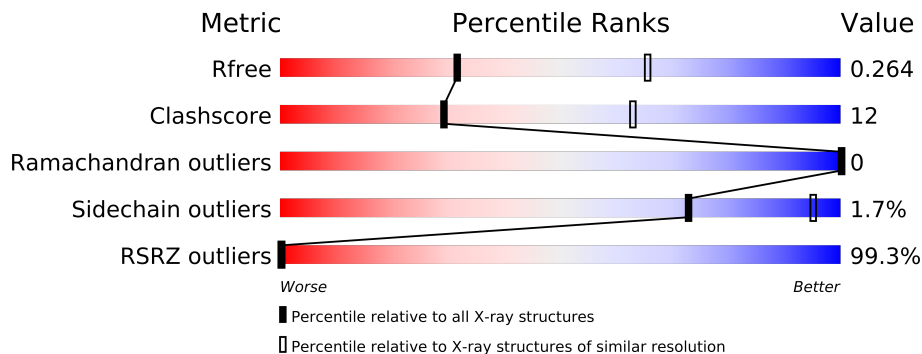
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 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 2.80 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	1799 (2.80-2.80)
Clashscore	79885	2295 (2.80-2.80)
Ramachandran outliers	78287	2252 (2.80-2.80)
Sidechain outliers	78261	2254 (2.80-2.80)
RSRZ outliers	66119	1802 (2.80-2.80)

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. 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	A	136	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	A80	A	201	-	X

## 2 Entry composition i

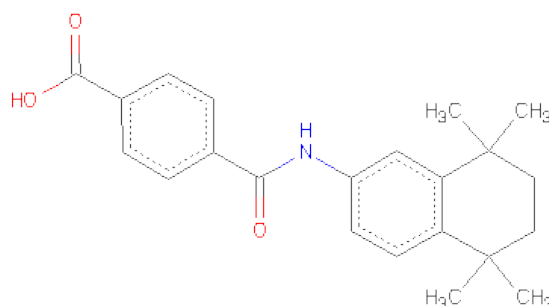
There are 3 unique types of molecules in this entry. The entry contains 1121 atoms, of which 0 are hydrogen and 0 are deuterium.

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 protein called PROTEIN (CRABP-I).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	136	Total	C	N	O	S	0	0	0
			1087	680	189	213	5			

- Molecule 2 is 4-[(5,5,8,8-TETRAMETHYL-5,6,7,8-TETRAHYDRONAPHTHALEN-2-YL) CARBAMOYL]BENZOICACID (three-letter code: A80) (formula: C<sub>22</sub>H<sub>25</sub>NO<sub>3</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			26	22	1	3		

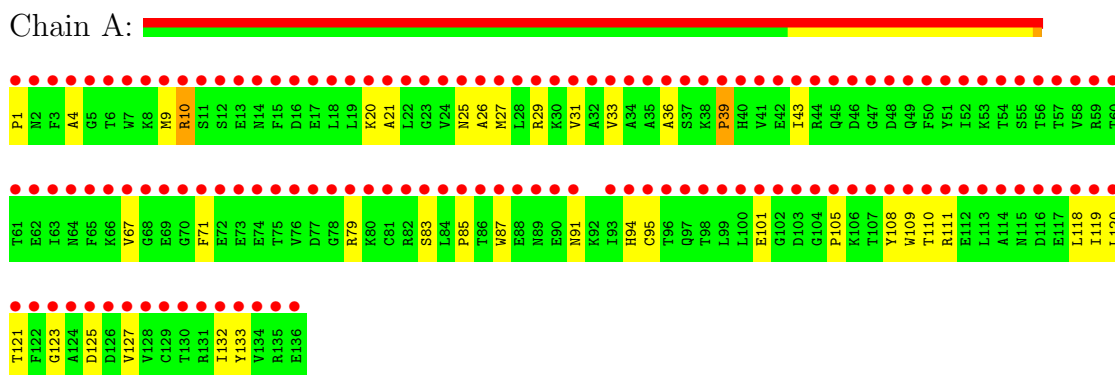
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	8	Total	O	0	0
			8	8		

### 3 Residue-property plots

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.

• Molecule 1: PROTEIN (CRABP-I)



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	133.50Å 133.50Å 40.57Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.80 38.28 – 2.80	Depositor EDS
% Data completeness (in resolution range)	97.0 (30.00-2.80) 97.0 (38.28-2.80)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.15 (at 2.81Å)	Xtriage
Refinement program	CNS 0.3	Depositor
R, $R_{free}$	0.230 , 0.268 0.227 , 0.264	Depositor DCC
$R_{free}$ test set	820 reflections (8.81%)	DCC
Wilson B-factor (Å <sup>2</sup> )	36.7	Xtriage
Anisotropy	0.075	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 14.6	EDS
Estimated twinning fraction	0.046 for -h,-k,l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 10128 reflections	Xtriage
$F_o, F_c$ correlation	0.55	EDS
Total number of atoms	1121	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.21% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities 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: A80

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	A	0.38	0/1107	0.75	2/1495 (0.1%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	10	ARG	NE-CZ-NH2	6.71	123.65	120.30
1	A	9	MET	CG-SD-CE	5.59	109.15	100.20

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	A	1087	0	1065	26	1
2	A	26	0	24	2	0
3	A	8	0	0	0	0
All	All	1121	0	1089	27	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 12.

All (27) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:25:ASN:HD21	1:A:27:MET:HB2	1.58	0.69
1:A:108:TYR:CE1	1:A:123:GLY:HA3	2.35	0.61
1:A:36:ALA:O	1:A:39:PRO:HD3	2.02	0.59
1:A:20:LYS:HG2	1:A:29:ARG:NH1	2.18	0.58
1:A:105:PRO:HB3	1:A:125:ASP:OD2	2.05	0.57
1:A:133:TYR:OH	2:A:201:A80:O26	2.23	0.55
1:A:20:LYS:CG	1:A:29:ARG:NH1	2.71	0.54
1:A:26:ALA:HA	1:A:29:ARG:HE	1.75	0.52
1:A:1:PRO:HG3	1:A:91:ASN:HA	1.91	0.52
2:A:201:A80:H7	2:A:201:A80:O24	2.10	0.51
1:A:27:MET:O	1:A:31:VAL:HG23	2.11	0.50
1:A:25:ASN:ND2	1:A:27:MET:HB2	2.27	0.50
1:A:21:ALA:HB2	1:A:127:VAL:HG21	1.95	0.49
1:A:118:LEU:HB3	1:A:133:TYR:HB2	1.95	0.48
1:A:71:PHE:HE1	1:A:85:PRO:HD3	1.79	0.48
1:A:4:ALA:HA	1:A:43:ILE:O	2.14	0.47
1:A:109:TRP:HA	1:A:121:THR:O	2.14	0.47
1:A:71:PHE:CE1	1:A:85:PRO:HD3	2.50	0.47
1:A:10:ARG:HH11	1:A:10:ARG:HG2	1.81	0.46
1:A:10:ARG:NH2	1:A:132:ILE:HG21	2.31	0.46
1:A:119:ILE:HD12	1:A:119:ILE:N	2.32	0.44
1:A:10:ARG:HH21	1:A:132:ILE:HG21	1.83	0.43
1:A:94:HIS:HA	1:A:110:THR:HG22	2.01	0.43
1:A:111:ARG:HG2	1:A:120:LEU:HD13	2.01	0.42
1:A:29:ARG:O	1:A:33:VAL:HG23	2.19	0.42
1:A:83:SER:HB3	1:A:95:CYS:SG	2.61	0.41
1:A:67:VAL:HG11	1:A:87:TRP:CD1	2.56	0.41

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)
1:A:101:GLU:OE1	1:A:101:GLU:OE1[4_555]	1.93	0.27

## 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	
1	A	134/136 (98%)	131 (98%)	3 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	
1	A	118/118 (100%)	116 (98%)	2 (2%)	73	95

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	PRO
1	A	79	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	ASN

### 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 ⓘ

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	A80	A	201	-	28,28,28	1.75	7 (25%)	43,43,43	0.84	1 (2%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	A80	A	201	-	-	0/12/31/31	0/1/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	201	A80	C10-C5	5.11	1.50	1.40
2	A	201	A80	C4-C5	3.02	1.58	1.53
2	A	201	A80	C1-C10	2.54	1.57	1.53
2	A	201	A80	C7-C8	2.44	1.43	1.39
2	A	201	A80	C16-C19	-2.32	1.44	1.49
2	A	201	A80	C18-C13	2.27	1.43	1.39
2	A	201	A80	C9-C10	2.12	1.43	1.39

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	201	A80	C13-C12-N11	2.11	119.88	115.86

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, 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	A	136/136 (100%)	11.31	135 (99%) 0 0	12, 34, 81, 98	0

All (135) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	130	THR	40.8
1	A	129	CYS	30.8
1	A	26	ALA	30.5
1	A	59	ARG	30.4
1	A	27	MET	30.1
1	A	56	THR	24.8
1	A	14	ASN	24.6
1	A	34	ALA	23.6
1	A	12	SER	23.6
1	A	11	SER	23.5
1	A	29	ARG	23.4
1	A	15	PHE	23.3
1	A	16	ASP	23.2
1	A	55	SER	22.0
1	A	60	THR	21.0
1	A	10	ARG	20.5
1	A	128	VAL	19.7
1	A	57	THR	19.0
1	A	46	ASP	18.3
1	A	28	LEU	18.2
1	A	37	SER	18.0
1	A	132	ILE	17.7
1	A	114	ALA	17.7
1	A	131	ARG	17.4
1	A	33	VAL	17.4
1	A	36	ALA	17.1
1	A	17	GLU	17.1

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Mol	Chain	Res	Type	RSRZ
1	A	126	ASP	16.9
1	A	61	THR	16.7
1	A	31	VAL	16.6
1	A	18	LEU	16.1
1	A	58	VAL	15.5
1	A	30	LYS	15.5
1	A	21	ALA	14.7
1	A	51	TYR	14.5
1	A	24	VAL	14.5
1	A	9	MET	14.4
1	A	38	LYS	13.8
1	A	116	ASP	13.7
1	A	115	ASN	13.5
1	A	127	VAL	13.4
1	A	64	ASN	13.4
1	A	74	GLU	13.3
1	A	32	ALA	13.3
1	A	77	ASP	12.9
1	A	63	ILE	12.8
1	A	78	GLY	12.7
1	A	45	GLN	12.5
1	A	19	LEU	12.4
1	A	91	ASN	12.2
1	A	39	PRO	12.2
1	A	23	GLY	12.1
1	A	25	ASN	12.1
1	A	35	ALA	11.6
1	A	2	ASN	11.3
1	A	4	ALA	11.3
1	A	89	ASN	11.2
1	A	62	GLU	11.1
1	A	47	GLY	11.1
1	A	13	GLU	10.8
1	A	134	VAL	10.7
1	A	119	ILE	10.6
1	A	117	GLU	10.6
1	A	1	PRO	10.5
1	A	52	ILE	10.2
1	A	44	ARG	10.2
1	A	5	GLY	10.2
1	A	42	GLU	10.1
1	A	113	LEU	10.0

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Mol	Chain	Res	Type	RSRZ
1	A	49	GLN	9.9
1	A	76	VAL	9.7
1	A	40	HIS	9.4
1	A	75	THR	9.3
1	A	81	CYS	9.3
1	A	118	LEU	9.3
1	A	50	PHE	9.2
1	A	6	THR	9.2
1	A	54	THR	8.8
1	A	43	ILE	8.8
1	A	20	LYS	8.7
1	A	79	ARG	8.6
1	A	22	LEU	8.5
1	A	3	PHE	8.3
1	A	72	GLU	8.2
1	A	102	GLY	7.8
1	A	65	PHE	7.8
1	A	121	THR	7.8
1	A	101	GLU	7.7
1	A	133	TYR	7.7
1	A	7	TRP	7.6
1	A	80	LYS	7.5
1	A	53	LYS	7.4
1	A	8	LYS	6.9
1	A	100	LEU	6.9
1	A	112	GLU	6.9
1	A	41	VAL	6.8
1	A	123	GLY	6.8
1	A	103	ASP	6.7
1	A	87	TRP	6.7
1	A	96	THR	6.6
1	A	122	PHE	6.2
1	A	135	ARG	6.1
1	A	120	LEU	5.9
1	A	48	ASP	5.8
1	A	99	LEU	5.7
1	A	125	ASP	5.5
1	A	124	ALA	5.0
1	A	95	CYS	4.9
1	A	73	GLU	4.9
1	A	90	GLU	4.7
1	A	107	THR	4.5

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Mol	Chain	Res	Type	RSRZ
1	A	66	LYS	4.3
1	A	68	GLY	4.2
1	A	70	GLY	4.2
1	A	97	GLN	4.1
1	A	94	HIS	4.1
1	A	69	GLU	4.0
1	A	93	ILE	3.9
1	A	105	PRO	3.9
1	A	111	ARG	3.8
1	A	67	VAL	3.4
1	A	110	THR	3.4
1	A	136	GLU	3.3
1	A	108	TYR	3.3
1	A	98	THR	3.2
1	A	71	PHE	3.2
1	A	106	LYS	3.2
1	A	84	LEU	3.0
1	A	109	TRP	2.9
1	A	85	PRO	2.8
1	A	82	ARG	2.5
1	A	104	GLY	2.4
1	A	88	GLU	2.2
1	A	83	SER	2.1
1	A	86	THR	2.1

## 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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
2	A80	A	201	26/26	1.44	0.34	24,24,24,24	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.