

Full wwPDB X-ray Structure Validation Report (i)

Aug 6, 2023 – 08:19 AM EDT

PDB ID : 1KT3

Title : Crystal structure of bovine holo-RBP at pH 2.0

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Deposited on : 2002-01-15

Resolution : 1.40 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity: 4.02b-467

Mogul : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : NOT EXECUTED

EDS : NOT EXECUTED

buster-report : 1.1.7 (2018)

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)

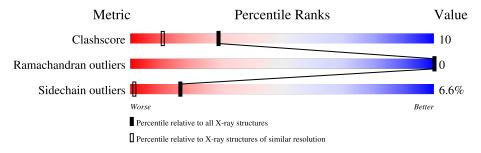
Validation Pipeline (wwPDB-VP) : 2.35

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 1.40 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	Similar resolution	
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{resolution range}(ext{Å}))$	
Clashscore	141614	1812 (1.40-1.40)	
Ramachandran outliers	138981	1763 (1.40-1.40)	
Sidechain outliers	138945	1762 (1.40-1.40)	

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain		
1	A	183	76%	14%	



2 Entry composition (i)

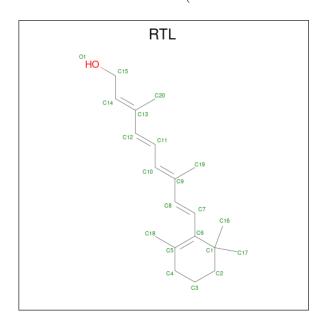
There are 3 unique types of molecules in this entry. The entry contains 1633 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 protein called Plasma retinol-binding protein.

Mo	l Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	175	Total 1418	C 893	N 246	O 269	S 10	0	0	0

• Molecule 2 is RETINOL (three-letter code: RTL) (formula: $C_{20}H_{30}O$).



ľ	Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
	2	A	1	Total 21	C 20	O 1	0	0

• Molecule 3 is water.

\mathbf{Mol}	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	194	Total O 194 194	0	0

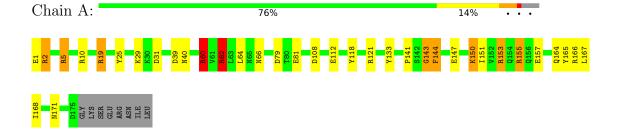


3 Residue-property plots (i)

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: Plasma retinol-binding protein





4 Data and refinement statistics (i)

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

Property	Value	Source	
Space group	P 21 21 21	Depositor	
Cell constants	46.84Å 50.20Å 77.78Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	34.25 - 1.40	Depositor	
% Data completeness	82.8 (34.25-1.40)	Depositor	
(in resolution range)	02.0 (04.20 1.40)	Беровног	
R_{merge}	0.07	Depositor	
R_{sym}	0.07	Depositor	
Refinement program	SHELXL-97	Depositor	
R, R_{free}	0.175 , 0.249	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	1633	wwPDB-VP	
Average B, all atoms (Å ²)	32.0	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: RTL

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	Bo	nd lengths	Bond angles		
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.86	$2/1452 \ (0.1\%)$	1.71	25/1961~(1.3%)	

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(A)	$\operatorname{Ideal}(ext{\AA})$
1	A	143	GLY	C-N	11.61	1.60	1.34
1	A	144	PHE	N-CA	11.46	1.69	1.46

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$Ideal(^{o})$
1	A	143	GLY	C-N-CA	-10.41	95.66	121.70
1	A	144	PHE	N-CA-CB	10.04	128.68	110.60
1	A	143	GLY	N-CA-C	8.08	133.30	113.10
1	A	108	ASP	CB-CG-OD1	8.06	125.56	118.30
1	A	60	ARG	CA-CB-CG	7.87	130.72	113.40
1	A	144	PHE	CB-CG-CD1	7.46	126.02	120.80
1	A	121	ARG	NE-CZ-NH1	7.30	123.95	120.30
1	A	5	ARG	NE-CZ-NH2	7.23	123.92	120.30
1	A	133	TYR	CA-CB-CG	7.13	126.95	113.40
1	A	5	ARG	CD-NE-CZ	6.88	133.24	123.60
1	A	153	ARG	CD-NE-CZ	6.67	132.94	123.60
1	A	118	TYR	CB-CG-CD2	6.38	124.83	121.00
1	A	166	ARG	CD-NE-CZ	6.26	132.37	123.60
1	A	31	ASP	CB-CG-OD2	6.04	123.73	118.30
1	A	166	ARG	NE-CZ-NH1	-5.96	117.32	120.30
1	A	19	ARG	NE-CZ-NH2	-5.76	117.42	120.30
1	A	25	TYR	CB-CG-CD2	5.70	124.42	121.00
1	A	165	TYR	CB-CG-CD1	5.68	124.41	121.00
1	A	155	ARG	NE-CZ-NH1	-5.64	117.48	120.30

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Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	60	ARG	NE-CZ-NH1	5.59	123.09	120.30
1	A	79	ASP	CB-CG-OD1	5.51	123.26	118.30
1	A	62	ARG	CD-NE-CZ	5.45	131.23	123.60
1	A	118	TYR	CA-CB-CG	5.31	123.49	113.40
1	A	141	PRO	C-N-CA	5.26	134.84	121.70
1	A	164	GLN	O-C-N	-5.18	114.41	122.70

There are no chirality outliers.

There are no planarity outliers.

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	A	1418	0	1337	26	0
2	A	21	0	30	1	0
3	A	194	0	0	11	0
All	All	1633	0	1367	27	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 10.

All (27) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
1:A:144:PHE:CA	1:A:144:PHE:N	1.69	1.54
1:A:143:GLY:C	1:A:144:PHE:CA	2.44	0.85
1:A:2:ARG:HG2	3:A:303:HOH:O	1.85	0.76
1:A:144:PHE:N	1:A:144:PHE:HA	2.00	0.73
1:A:153:ARG:HD2	3:A:375:HOH:O	1.89	0.71
1:A:62:ARG:HH21	1:A:62:ARG:HG3	1.59	0.67
1:A:29:LYS:HE3	3:A:190:HOH:O	1.95	0.66
1:A:64:LEU:HD22	1:A:64:LEU:H	1.62	0.65
1:A:168:ILE:HG12	3:A:190:HOH:O	2.00	0.61
1:A:150:LYS:HG3	1:A:151:ILE:N	2.16	0.59
1:A:147:GLU:O	1:A:150:LYS:HG2	2.02	0.59

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Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	${ m distance}({ m \AA})$	overlap (Å)
1:A:10:ARG:HD3	3:A:338:HOH:O	2.04	0.58
1:A:5:ARG:HD3	3:A:359:HOH:O	2.05	0.56
1:A:40:ASN:HD21	1:A:171:ASN:HB2	1.73	0.54
1:A:39:ASP:OD1	1:A:60:ARG:HG3	2.13	0.49
1:A:40:ASN:OD1	1:A:171:ASN:HB2	2.13	0.49
1:A:62:ARG:HG3	1:A:62:ARG:NH2	2.26	0.47
2:A:184:RTL:H151	2:A:184:RTL:H201	1.69	0.46
1:A:144:PHE:HA	3:A:276:HOH:O	2.15	0.46
1:A:39:ASP:OD1	1:A:60:ARG:NE	2.49	0.46
1:A:143:GLY:O	1:A:144:PHE:CA	2.65	0.45
1:A:155:ARG:NH1	3:A:257:HOH:O	2.49	0.45
1:A:29:LYS:NZ	3:A:356:HOH:O	2.50	0.44
1:A:10:ARG:NH1	3:A:355:HOH:O	2.50	0.43
1:A:66:ASN:ND2	3:A:195:HOH:O	2.50	0.42
1:A:40:ASN:ND2	1:A:171:ASN:HB2	2.36	0.41
1:A:64:LEU:H	1:A:64:LEU:CD2	2.33	0.40

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
1	A	173/183 (94%)	167 (96%)	6 (4%)	0	100 100

There are no Ramachandran outliers to report.

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		
1	A	151/158 (96%)	141 (93%)	10 (7%)	16 1		

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	GLU
1	A	2	ARG
1	A	19	ARG
1	A	60	ARG
1	A	62	ARG
1	A	81	GLU
1	A	112	GLU
1	A	150	LYS
1	A	157	GLU
1	A	167	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	50	ASN
1	A	52	HIS
1	A	98	GLN
1	A	156	GLN

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)

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		
IVIOI	туре	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	RTL	A	184	-	21,21,21	2.28	7 (33%)	26,28,28	2.47	13 (50%)

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	RTL	A	184	-	-	1/14/31/31	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(\text{\AA})$
2	A	184	RTL	C5-C6	6.79	1.46	1.34
2	A	184	RTL	C20-C13	3.60	1.58	1.50
2	A	184	RTL	C14-C13	3.34	1.43	1.33
2	A	184	RTL	C19-C9	2.94	1.56	1.50
2	A	184	RTL	C10-C9	2.31	1.38	1.35
2	A	184	RTL	C8-C9	-2.16	1.41	1.45
2	A	184	RTL	C12-C13	-2.14	1.41	1.45

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
2	A	184	RTL	C11-C10-C9	4.83	134.20	127.31
2	A	184	RTL	C7-C8-C9	4.39	132.88	126.23
2	A	184	RTL	C18-C5-C6	4.08	129.11	124.53
2	A	184	RTL	C20-C13-C14	-4.07	115.60	123.59
2	A	184	RTL	C8-C9-C10	3.41	124.18	118.94
2	A	184	RTL	C11-C12-C13	3.22	135.47	126.42
2	A	184	RTL	C16-C1-C6	3.14	115.39	110.30

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Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
2	A	184	RTL	C19-C9-C8	-2.93	113.45	118.08
2	A	184	RTL	C2-C1-C6	2.74	114.69	110.48
2	A	184	RTL	C19-C9-C10	-2.60	119.28	122.92
2	A	184	RTL	C1-C6-C7	2.35	122.43	115.78
2	A	184	RTL	O1-C15-C14	2.12	115.54	110.79
2	A	184	RTL	C7-C6-C5	-2.03	116.55	121.46

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	184	RTL	C11-C10-C9-C19

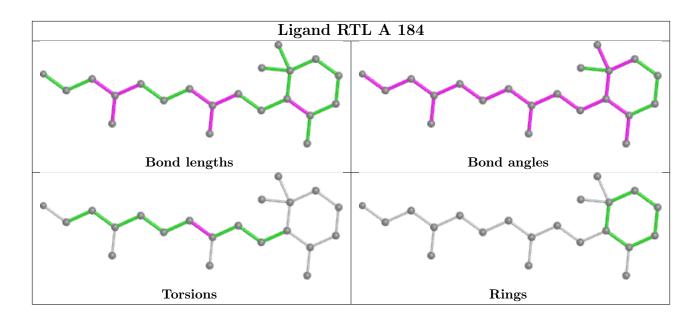
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	184	RTL	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	143:GLY	С	144:PHE	N	1.60



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.

