

# Full wwPDB X-ray Structure Validation Report (i)

#### Oct 8, 2023 – 10:52 PM EDT

PDB ID	:	6WNF
Title	:	The Crystal Structure of Apo Domain-Swapped Dimer Q108K:K40D:T53A:R
		58L:Q38F:Q4F:F57H Variant of HCRBPII
Authors	:	Ghanbarpour, A.; Geiger, J.
Deposited on	:	2020-04-22
Resolution	:	1.67  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:

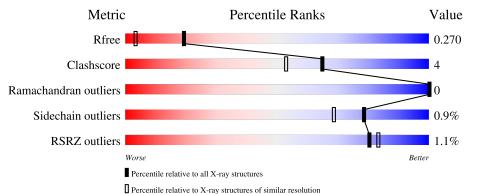
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY \, DIFFRACTION$ 

The reported resolution of this entry is 1.67 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
$R_{free}$	130704	6780 (1.70-1.66)
Clashscore	141614	7310 (1.70-1.66)
Ramachandran outliers	138981	7173 (1.70-1.66)
Sidechain outliers	138945	7172 (1.70-1.66)
RSRZ outliers	127900	6661 (1.70-1.66)

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% 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	А	133	.% <b>9</b> 5%	•	
1	В	133	89%	11%	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:



Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	ACT	В	201	-	-	Х	-



#### 6WNF

## 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2375 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.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	٨	133	Total	С	Ν	Ο	$\mathbf{S}$	0	4	0
1	A	155	1096	696	183	212	5	0	4	U
1	р	133	Total	С	Ν	0	S	0	6	0
1	D	100	1099	698	182	214	5			0

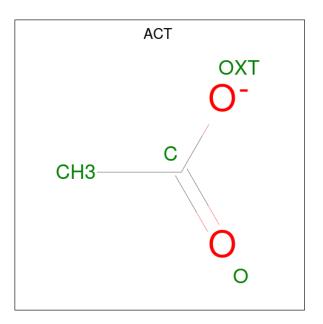
• Molecule 1 is a protein called Retinol-binding protein 2.

Chain	Residue	Modelled	Actual	Comment	Reference
А	4	PHE	GLN	engineered mutation	UNP P50120
А	38	PHE	GLN	engineered mutation	UNP P50120
А	40	ASP	LYS	engineered mutation	UNP P50120
А	53	ALA	THR	engineered mutation	UNP P50120
А	57	HIS	PHE	engineered mutation	UNP P50120
А	58	LEU	ARG	engineered mutation	UNP P50120
А	108	LYS	GLN	engineered mutation	UNP P50120
В	4	PHE	GLN	engineered mutation	UNP P50120
В	38	PHE	GLN	engineered mutation	UNP P50120
В	40	ASP	LYS	engineered mutation	UNP P50120
В	53	ALA	THR	engineered mutation	UNP P50120
В	57	HIS	PHE	engineered mutation	UNP P50120
В	58	LEU	ARG	engineered mutation	UNP P50120
В	108	LYS	GLN	engineered mutation	UNP P50120

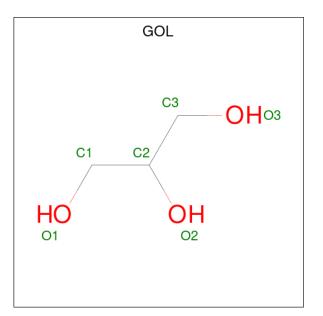
There are 14 discrepancies between the modelled and reference sequences:

• Molecule 2 is ACETATE ION (three-letter code: ACT) (formula:  $C_2H_3O_2$ ).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
2	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
2	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{C} \\ 6 & 3 & 3 \end{array}$	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 6  3  3 \end{array}$	0	0

• Molecule 4 is water.

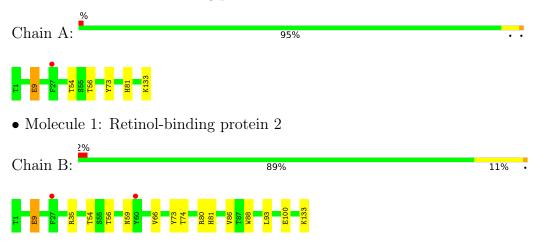
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	65	Total O 65 65	0	0
4	В	67	Total         O           67         67	0	0



# 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 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: Retinol-binding protein 2





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	60.09Å 63.85Å 72.83Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	46.35 - 1.67	Depositor
Resolution (A)	46.35 - 1.67	EDS
% Data completeness	99.6 (46.35-1.67)	Depositor
(in resolution range)	$99.6 \ (46.35 - 1.67)$	EDS
R <sub>merge</sub>	0.09	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.96 (at 1.67 Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
D D.	0.239 , $0.270$	Depositor
$R, R_{free}$	0.239 , $0.270$	DCC
$R_{free}$ test set	1998 reflections $(6.06\%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	23.5	Xtriage
Anisotropy	0.288	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.36 , $42.5$	EDS
L-test for twinning <sup>2</sup>	$ \langle L  \rangle = 0.50, \langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	2375	wwPDB-VP
Average B, all atoms $(Å^2)$	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The analyses of the Patterson function reveals a significant off-origin peak that is 94.79 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.2292e-09. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

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



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: ACT, GOL

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		lengths	Bond angles		
	Unam	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.35	0/1129	0.60	0/1523	
1	В	0.35	0/1138	0.60	0/1537	
All	All	0.35	0/2267	0.60	0/3060	

There are no bond length outliers.

There are no bond angle outliers.

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	А	1096	0	1060	6	0
1	В	1099	0	1055	14	0
2	А	8	0	6	0	0
2	В	4	0	3	2	0
3	А	24	0	32	0	0
3	В	12	0	16	2	0
4	А	65	0	0	2	0
4	В	67	0	0	5	0
All	All	2375	0	2172	18	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 4.



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:THR:HG22	1:B:56:THR:HG22	1.80	0.62
1:B:74:THR:HA	3:B:202:GOL:H2	1.81	0.61
1:B:100:GLU:HG3	2:B:201:ACT:H2	1.83	0.60
1:B:80:ARG:HE	2:B:201:ACT:H1	1.70	0.57
1:A:73:TYR:CE2	1:A:81:HIS:HB2	2.46	0.50
1:B:59:ASN:ND2	4:B:303:HOH:O	2.45	0.49
1:A:54:THR:HG23	4:A:347:HOH:O	2.12	0.47
1:B:54:THR:HG23	4:B:354:HOH:O	2.12	0.47
1:B:35:ARG:NH2	4:B:307:HOH:O	2.49	0.45
1:B:73:TYR:CE2	1:B:81:HIS:HB2	2.52	0.45
1:B:133:LYS:HA	1:B:133:LYS:HD2	1.82	0.45
1:A:9:GLU:OE2	1:B:133:LYS:HE2	2.18	0.43
3:B:202:GOL:H31	4:B:357:HOH:O	2.19	0.43
1:B:56:THR:HG23	4:B:332:HOH:O	2.19	0.43
1:B:86:VAL:CG1	1:B:93[A]:LEU:HG	2.49	0.42
1:A:56:THR:HG23	4:A:321:HOH:O	2.20	0.42
1:A:133:LYS:HE2	1:B:9:GLU:OE2	2.20	0.41
1:B:66:VAL:HG11	1:B:88:TRP:CD1	2.57	0.40

All (18) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

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	Percer	ntiles
1	А	135/133~(102%)	134 (99%)	1 (1%)	0	100	100
1	В	137/133~(103%)	136~(99%)	1 (1%)	0	100	100
All	All	272/266~(102%)	270~(99%)	2(1%)	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	sed Rotameric Outliers		Percentiles		
1	А	119/119~(100%)	118~(99%)	1 (1%)	81 72		
1	В	119/119 (100%)	118 (99%)	1 (1%)	81 72		
All	All	238/238~(100%)	236~(99%)	2(1%)	78 72		

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

Mol	Chain	Res	Type
1	А	9	GLU
1	В	9	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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)

9 ligands are 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	Turne	Chain	Res	Link	B	ond leng	$\operatorname{gths}$	В	ond ang	gles
10101	Type	Unam	nes		Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2
3	GOL	А	206	-	$5,\!5,\!5$	0.86	0	$5,\!5,\!5$	1.09	0
3	GOL	В	203	-	$5,\!5,\!5$	0.95	0	$5,\!5,\!5$	1.06	0
2	ACT	В	201	-	$3,\!3,\!3$	1.04	0	$3,\!3,\!3$	1.62	1 (33%)
3	GOL	А	203	-	$5,\!5,\!5$	0.91	0	$5,\!5,\!5$	0.92	0
3	GOL	А	204	-	$5,\!5,\!5$	0.98	0	$5,\!5,\!5$	0.95	0
3	GOL	В	202	-	$5,\!5,\!5$	1.03	0	$5,\!5,\!5$	1.02	0
2	ACT	А	202	-	$3,\!3,\!3$	1.57	1 (33%)	$3,\!3,\!3$	1.25	0
3	GOL	А	205	-	$5,\!5,\!5$	0.89	0	$5,\!5,\!5$	0.86	0
2	ACT	А	201	-	3,3,3	1.09	0	$3,\!3,\!3$	1.60	0

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
3	GOL	А	206	-	-	2/4/4/4	-
3	GOL	В	203	-	-	4/4/4/4	-
3	GOL	А	203	-	-	0/4/4/4	-
3	GOL	А	204	-	-	2/4/4/4	-
3	GOL	В	202	-	-	3/4/4/4	-
3	GOL	А	205	-	-	3/4/4/4	_

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	А	202	ACT	CH3-C	2.38	1.59	1.49

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	В	201	ACT	O-C-CH3	-2.02	114.45	122.33

There are no chirality outliers.

All (14) torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
3	А	204	GOL	O1-C1-C2-C3
3	В	202	GOL	C1-C2-C3-O3
3	В	203	GOL	C1-C2-C3-O3
3	В	202	GOL	O2-C2-C3-O3
3	А	205	GOL	O1-C1-C2-C3
3	А	205	GOL	C1-C2-C3-O3
3	А	206	GOL	O1-C1-C2-C3
3	В	203	GOL	O1-C1-C2-C3
3	В	203	GOL	O2-C2-C3-O3
3	А	204	GOL	O1-C1-C2-O2
3	А	206	GOL	O1-C1-C2-O2
3	В	203	GOL	O1-C1-C2-O2
3	В	202	GOL	O1-C1-C2-C3
3	А	205	GOL	O2-C2-C3-O3

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	В	201	ACT	2	0
3	В	202	GOL	2	0

### 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,  $95^{th}$  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	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	А	133/133~(100%)	-0.11	1 (0%) 86 88	18, 29, 45, 57	0
1	В	133/133~(100%)	-0.19	2 (1%) 73 77	18, 29, 43, 56	0
All	All	266/266~(100%)	-0.15	3 (1%) 80 83	18, 29, 44, 57	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	27	PHE	3.2
1	В	27	PHE	3.0
1	В	60	TYR	2.7

### 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 monosaccharides in this entry.

### 6.4 Ligands (i)

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. The B-factors column lists the minimum, median,  $95^{th}$  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	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q<0.9
3	GOL	А	205	6/6	0.46	0.33	$76,\!81,\!84,\!86$	0
3	GOL	А	204	6/6	0.68	0.23	39,45,51,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	ACT	В	201	4/4	0.71	0.23	72,73,74,78	0
2	ACT	А	201	4/4	0.75	0.14	$55,\!55,\!58,\!62$	0
3	GOL	А	203	6/6	0.75	0.18	$51,\!57,\!68,\!69$	0
3	GOL	В	202	6/6	0.76	0.19	46,52,60,65	0
2	ACT	А	202	4/4	0.83	0.11	48,52,57,64	0
3	GOL	А	206	6/6	0.90	0.29	45,65,69,69	0
3	GOL	В	203	6/6	0.91	0.20	57,59,63,64	0

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## 6.5 Other polymers (i)

There are no such residues in this entry.

