

wwPDB X-ray Structure Validation Summary Report (i)

Nov 1, 2023 – 05:26 AM EDT

PDB ID : 3NSQ

Title: Crystal structure of tetrameric RXRalpha-LBD complexed with antagonist

danthron

Authors: Zhang, H.; Hu, T.; Li, L.; Zhou, R.; Chen, L.; Hu, L.; Jiang, H.; Shen, X.

Deposited on : 2010-07-02

Resolution : 2.60 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
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 EDS : 2.36

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

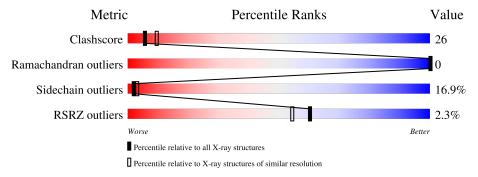
Validation Pipeline (wwPDB-VP) : 2.36

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 2.60 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	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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	Qua	lity of chain		
1	A	240	44%	30%	5%	20%
1	В	240	45%	27%	10% •	17%

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	CHZ	В	1	-	-	-	X



2 Entry composition (i)

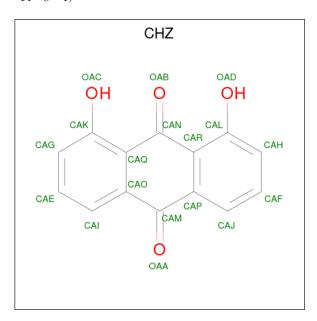
There are 3 unique types of molecules in this entry. The entry contains 3201 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Retinoid X receptor, alpha.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	A	193	Total 1526	C 983		O 270	S 9	0	0	0
1	В	199	Total 1573	C 1012	N 273	O 278	S 10	0	0	0

• Molecule 2 is 1,8-dihydroxyanthracene-9,10-dione (three-letter code: CHZ) (formula: $C_{14}H_8O_4$).



Mol	Chain	Residues	Ato	oms		ZeroOcc	AltConf
2	В	1	Total	C 14	O 4	0	0

• Molecule 3 is water.

]	Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
	3	A	46	Total O 46 46	0	0

Continued on next page...



Continued from previous page...

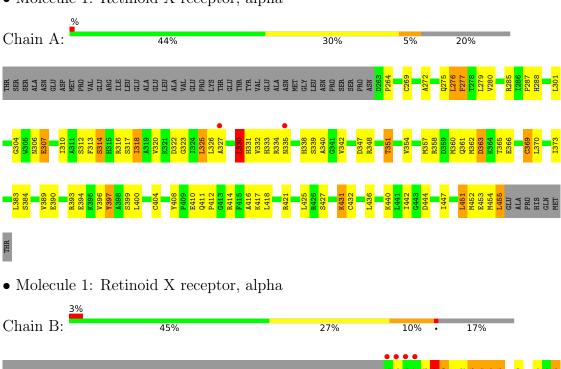
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	38	Total O 38 38	0	0

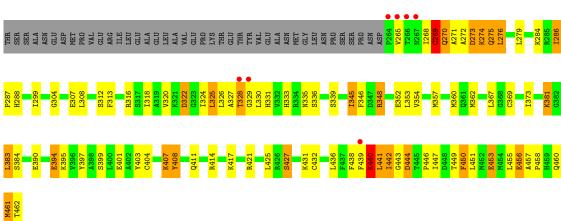


3 Residue-property plots (i)

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: Retinoid X receptor, alpha







4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants	115.03Å 99.92Å 47.20Å	Donogitor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	14.88 - 2.60	Depositor
rtesolution (A)	14.88 - 2.60	EDS
% Data completeness	95.4 (14.88-2.60)	Depositor
(in resolution range)	95.5 (14.88-2.60)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	4.39 (at 2.61Å)	Xtriage
Refinement program	CNS, REFMAC 5.2.0019	Depositor
P. P.	0.265 , 0.318	Depositor
R, R_{free}	0.252 , (Not available)	DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	43.6	Xtriage
Anisotropy	0.087	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.37, 60.8	EDS
L-test for twinning ²	$ < L > = 0.48, < L^2> = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	3201	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.99% of the height of the origin peak. No significant pseudotranslation is detected.

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



¹Intensities 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: CHZ

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		nd lengths	Bond angles		
MIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	1.75	7/1558 (0.4%)	1.02	$4/2106 \ (0.2\%)$	
1	В	1.76	11/1607 (0.7%)	0.99	$2/2172 \ (0.1\%)$	
All	All	1.75	$18/3165 \ (0.6\%)$	1.01	6/4278 (0.1%)	

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(\text{\AA})$
1	В	269	CYS	CB-SG	-7.70	1.69	1.82
1	A	369	CYS	CB-SG	-7.45	1.69	1.82
1	В	453	GLU	CG-CD	-7.38	1.40	1.51
1	В	401	GLU	CD-OE2	-6.91	1.18	1.25
1	В	432	CYS	CB-SG	-6.74	1.70	1.82

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}(^{o})$
1	A	276	LEU	CB-CA-C	-8.61	93.83	110.20
1	A	455	LEU	CA-CB-CG	-7.49	98.08	115.30
1	A	277	PHE	N-CA-C	-6.13	94.44	111.00
1	A	330	LEU	CA-CB-CG	5.98	129.06	115.30
1	В	348	ARG	NE-CZ-NH2	-5.94	117.33	120.30

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)	$\mathbf{H}(\mathbf{added})$	Clashes	Symm-Clashes
1	A	1526	0	1567	62	1
1	В	1573	0	1613	100	2
2	В	18	0	6	1	0
3	A	46	0	0	1	0
3	В	38	0	0	4	0
All	All	3201	0	3186	161	2

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 26.

The worst 5 of 161 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:B:440:LYS:C	1:B:441:LEU:HD12	1.42	1.37
1:B:440:LYS:C	1:B:441:LEU:CD1	1.96	1.32
1:B:440:LYS:O	1:B:441:LEU:CD1	1.84	1.24
1:B:440:LYS:O	1:B:441:LEU:HD13	1.10	1.22
1:B:451:LEU:O	1:B:455:LEU:HD13	1.45	1.17

All (2) 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	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:A:269:CYS:SG	1:B:270:GLN:CG[2_655]	1.40	0.80
1:B:335:ASN:ND2	1:B:384:SER:OG[1_556]	1.71	0.49

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	Perce	entiles
1	A	191/240 (80%)	185 (97%)	6 (3%)	0	100	100
1	В	197/240 (82%)	188 (95%)	9 (5%)	0	100	100
All	All	388/480 (81%)	373 (96%)	15 (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	166/207 (80%)	143 (86%)	23 (14%)	3 6		
1	В	171/207 (83%)	137 (80%)	34 (20%)	1 2		
All	All	337/414 (81%)	280 (83%)	57 (17%)	2 3		

5 of 57 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	275	GLN
1	В	456	GLU
1	В	320	VAL
1	В	450	PHE
1	В	436	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	В	411	GLN
1	В	288	HIS
1	A	411	GLN
1	A	338	HIS
1	В	270	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	Гуре Chain	Chain	Ros	Link	Bond		$ ag{ths}$	Bond angles		
		Type		rtes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2	
	2	CHZ	В	1	-	20,20,20	1.86	4 (20%)	30,30,30	0.69	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	\mathbf{Type}	Chain	Res	Link	Chirals	Torsions	Rings
2	CHZ	В	1	-	-	-	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(ext{ iny A})$
2	В	1	CHZ	CAP-CAM	-4.36	1.39	1.48
2	В	1	CHZ	CAO-CAM	-4.26	1.39	1.48
2	В	1	CHZ	CAQ-CAN	-3.45	1.39	1.47
2	В	1	CHZ	CAR-CAN	-3.45	1.39	1.47



There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	В	1	CHZ	1	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	$\langle { m RSRZ} \rangle$	$\#\mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q<0.9
1	A	193/240 (80%)	-0.21	2 (1%) 82 80	21, 38, 59, 64	0
1	В	199/240 (82%)	0.03	7 (3%) 44 36	20, 37, 64, 71	0
All	All	392/480 (81%)	-0.09	9 (2%) 60 54	20, 38, 60, 71	0

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	329	GLY	5.8
1	В	264	PRO	5.2
1	В	266	THR	4.6
1	В	328	THR	4.4
1	В	265	VAL	3.5

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.



Mo	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
2	CHZ	В	1	18/18	0.53	0.51	72,72,73,73	18

6.5 Other polymers (i)

There are no such residues in this entry.

