

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

#### Sep 12, 2023 – 06:37 AM EDT

PDB ID : 4NBO

Title: Human steroid receptor RNA activator protein carboxy-terminal domain

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Deposited on : 2013-10-23

Resolution : 2.81 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 Xtriage (Phenix) : 1.13

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)

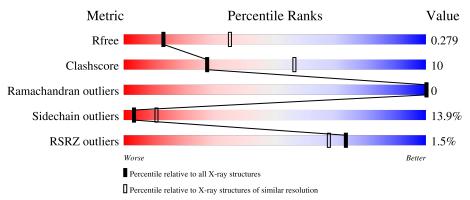
Validation Pipeline (wwPDB-VP) : 2.35.1

## 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 2.81 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	$(\# { m Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
$R_{free}$	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (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 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 chai	in		
1	A	111	61%	24%	6%	8%
1	В	111	67%	23%		8%



## 2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1640 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 Steroid receptor RNA activator 1.

$\mathbf{Mol}$	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace				
1	Λ	102	Total	С	N	О	S	0	0	0	ĺ
1	Α	102	820	511	155	148	6	0	U	U	
1	D	102	Total	С	N	О	S	0	0	0	ĺ
1	Ъ	102	820	511	155	148	6	0	U	U	

There are 2 discrepancies between the modelled and reference sequences:

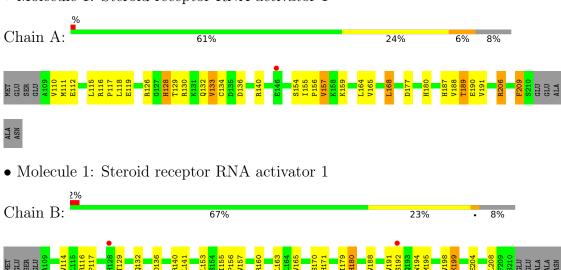
Chain	Residue	Modelled	Actual	Comment	Reference
A	105	MET	-	initiating methionine	UNP Q9HD15
В	105	MET	-	initiating methionine	UNP Q9HD15



# 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: Steroid receptor RNA activator 1





## 4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 43 21 2	Depositor	
Cell constants	85.90Å 85.90Å 100.41Å	Donositor	
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	39.49 - 2.81	Depositor	
Resolution (A)	39.49 - 2.81	EDS	
% Data completeness	99.5 (39.49-2.81)	Depositor	
(in resolution range)	97.5 (39.49-2.81)	EDS	
$R_{merge}$	(Not available)	Depositor	
$R_{sym}$	0.06	Depositor	
$< I/\sigma(I) > 1$	10.22 (at 2.81Å)	Xtriage	
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor	
D D	0.245 , 0.278	Depositor	
$R, R_{free}$	0.241 , $0.279$	DCC	
$R_{free}$ test set	482 reflections (4.99%)	wwPDB-VP	
Wilson B-factor (Å <sup>2</sup> )	56.0	Xtriage	
Anisotropy	0.053	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.35 , 37.3	EDS	
L-test for twinning <sup>2</sup>	$< L > = 0.49, < L^2> = 0.33$	Xtriage	
Estimated twinning fraction	No twinning to report.	Xtriage	
$F_o, F_c$ correlation	0.92	EDS	
Total number of atoms	1640	wwPDB-VP	
Average B, all atoms $(\mathring{A}^2)$	56.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.64% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical 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.



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

## 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			lengths	Bond angles		
MIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.23	0/832	0.46	1/1119 (0.1%)	
1	В	0.24	0/832	0.40	0/1119	
All	All	0.23	0/1664	0.43	1/2238 (0.0%)	

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}({}^{o})$
1	A	209	PHE	C-N-CA	6.70	138.46	121.70

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	820	0	839	15	0
1	В	820	0	839	18	0
All	All	1640	0	1678	33	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 (33) 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)
1:B:191:VAL:O	1:B:195:MET:HB2	1.99	0.62
1:B:188:VAL:O	1:B:192:SER:OG	2.18	0.61
1:B:114:VAL:HG13	1:B:165:VAL:HG21	1.83	0.61
1:B:160:ARG:HG3	1:B:179:ILE:HG23	1.86	0.57
1:B:180:HIS:HB2	1:B:195:MET:CE	2.34	0.57
1:A:116:ARG:HB2	1:A:117:PRO:HD3	1.86	0.57
1:A:154:SER:OG	1:A:157:VAL:HG13	2.09	0.53
1:A:177:ASP:OD2	1:A:206:ARG:NH2	2.41	0.53
1:A:164:LEU:O	1:A:168:LEU:HD23	2.10	0.52
1:A:111:MET:HG3	1:A:115:LEU:HD12	1.91	0.52
1:B:116:ARG:HB2	1:B:117:PRO:HD3	1.93	0.51
1:B:191:VAL:O	1:B:195:MET:CB	2.59	0.51
1:A:129:THR:OG1	1:A:134:CYS:SG	2.70	0.50
1:B:180:HIS:NE2	1:B:199:LYS:HG3	2.27	0.49
1:A:155:ILE:N	1:A:156:PRO:CD	2.76	0.48
1:A:187:HIS:O	1:A:191:VAL:HG22	2.15	0.46
1:B:155:ILE:HB	1:B:156:PRO:HD3	1.98	0.46
1:B:191:VAL:HG12	1:B:194:TRP:CH2	2.51	0.45
1:B:180:HIS:CB	1:B:195:MET:CE	2.95	0.45
1:B:114:VAL:HG13	1:B:165:VAL:CG2	2.47	0.44
1:A:155:ILE:N	1:A:155:ILE:HD12	2.32	0.44
1:B:188:VAL:O	1:B:192:SER:CB	2.66	0.44
1:A:110:VAL:HG12	1:A:112:GLU:H	1.83	0.44
1:A:128:HIS:ND1	1:A:128:HIS:N	2.67	0.43
1:A:136:ASP:O	1:A:140:ARG:HG3	2.18	0.43
1:B:155:ILE:N	1:B:156:PRO:CD	2.82	0.43
1:A:130:ARG:HB2	1:A:133:VAL:HG13	2.01	0.43
1:A:188:VAL:HG13	1:A:189:THR:N	2.34	0.42
1:B:191:VAL:HG12	1:B:194:TRP:CZ2	2.53	0.42
1:B:129:THR:HG21	1:B:204:GLU:HB3	2.02	0.42
1:B:136:ASP:O	1:B:140:ARG:HG2	2.21	0.41
1:B:180:HIS:HA	1:B:195:MET:HE2	2.03	0.41
1:A:115:LEU:O	1:A:119:GLU:HG2	2.21	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	Perce	ntiles
1	A	100/111 (90%)	100 (100%)	0	0	100	100
1	В	100/111 (90%)	95 (95%)	5 (5%)	0	100	100
All	All	$200/222 \ (90\%)$	195 (98%)	5 (2%)	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	90/97 (93%)	76 (84%)	14 (16%)	2 8
1	В	90/97~(93%)	79 (88%)	11 (12%)	5 15
All	All	180/194 (93%)	155 (86%)	25 (14%)	3 11

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	118	LEU
1	A	126	ARG
1	A	128	HIS
1	A	132	GLN
1	A	133	VAL
1	A	157	VAL
1	A	159	LYS
1	A	165	VAL
1	A	168	LEU
1	A	180	HIS
1	A	189	THR
1	A	190	GLU
1	A	206	ARG
1	A	209	PHE

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Continued	trom	nremone	naae
Continuaca	110116	predudas	puqc

Mol	Chain	Res	Type
1	В	132	GLN
1	В	141	LEU
1	В	153	LEU
1	В	157	VAL
1	В	163	LEU
1	В	170	SER
1	В	171	HIS
1	В	180	HIS
1	В	198	VAL
1	В	199	LYS
1	В	208	LEU

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)

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,  $95^{th}$  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	<RSRZ $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q < 0.9
1	A	102/111 (91%)	-0.05	1 (0%) 82 77	36, 54, 77, 89	0
1	В	102/111 (91%)	-0.13	2 (1%) 65 56	38, 54, 74, 88	0
All	All	204/222 (91%)	-0.09	3 (1%) 73 68	36, 54, 77, 89	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	192	SER	2.8
1	В	128	HIS	2.6
1	A	146	GLU	2.3

### 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)

There are no ligands in this entry.

## 6.5 Other polymers (i)

There are no such residues in this entry.

