

Full wwPDB X-ray Structure Validation Report (i)

Oct 10, 2021 – 03:47 PM EDT

PDB ID	:	3D95
Title	:	Crystal Structure of the R132K:Y134F:R111L:L121E:T54V Mutant of Apo-
		Cellular Retinoic Acid Binding Protein Type II at 1.20 Angstroms Resolution
Authors	:	Vaezeslami, S.; Geiger, J.H.
Deposited on		
Resolution	:	1.20 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 following versions of software and data (see references (1)) were used in the production of this report:

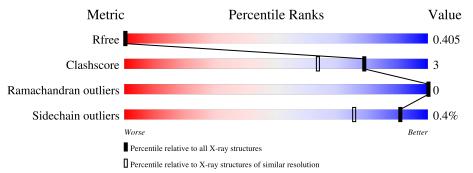
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

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 1.20 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R _{free}	130704	1223 (1.22-1.18)
Clashscore	141614	1286 (1.22-1.18)
Ramachandran outliers	138981	1240 (1.22-1.18)
Sidechain outliers	138945	1239 (1.22-1.18)

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%

Mol	Chain	Length	Quality of chain				
1	А	137	94%	6%			
1	В	137	96%	•			



2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 2589 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	Λ	137	Total	С	Ν	0	S	0	6	0
	I A	197	1078	681	174	218	5	0	0	0
1	В	137	Total	С	Ν	0	S	0	0	0
	D	107	1096	696	176	217	$\overline{7}$	0	9	U

• Molecule 1 is a protein called Cellular retinoic acid-binding protein 2.

Chain	Residue	Modelled	Actual	Comment	Reference
A	54	VAL	THR	engineered mutation	UNP P29373
А	111	LEU	ARG	engineered mutation	UNP P29373
А	121	GLU	LEU	engineered mutation	UNP P29373
A	132	LYS	ARG	engineered mutation	UNP P29373
А	134	PHE	TYR	engineered mutation	UNP P29373
В	54	VAL	THR	engineered mutation	UNP P29373
В	111	LEU	ARG	engineered mutation	UNP P29373
В	121	GLU	LEU	engineered mutation	UNP P29373
В	132	LYS	ARG	engineered mutation	UNP P29373
В	134	PHE	TYR	engineered mutation	UNP P29373

There are 10 discrepancies between the modelled and reference sequences:

• Molecule 2 is water.

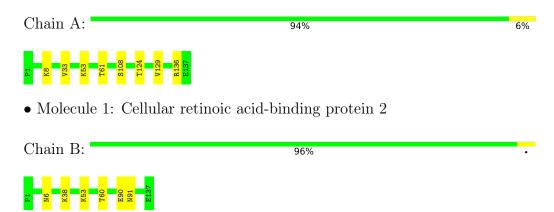
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	211	Total O 229 229	0	18
2	В	182	Total O 186 186	2	6



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.

 \bullet Molecule 1: Cellular retinoic acid-binding protein 2





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants	34.59Å 36.90 Å 57.81 Å	Depositor
a, b, c, α , β , γ	73.28° 75.91° 87.76°	Depositor
Resolution (Å)	40.00 - 1.20	Depositor
Resolution (A)	16.48 - 1.20	EDS
% Data completeness	90.0 (40.00-1.20)	Depositor
(in resolution range)	90.1 (16.48-1.20)	EDS
R _{merge}	0.07	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$4.69 (at 1.20 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
D D.	0.138 , 0.176	Depositor
R, R_{free}	0.403 , 0.405	DCC
R_{free} test set	7560 reflections (10.04%)	wwPDB-VP
Wilson B-factor $(Å^2)$	16.6	Xtriage
Anisotropy	0.282	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.43 , 57.7	EDS
L-test for twinning ²	$ \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	0.95	EDS
Total number of atoms	2589	wwPDB-VP
Average B, all atoms $(Å^2)$	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 10.24% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities 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	Boi	nd lengths	Bond angles		
		RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.85	1/1118~(0.1%)	0.91	2/1512~(0.1%)	
1	В	0.83	0/1149	0.81	0/1553	
All	All	0.84	1/2267~(0.0%)	0.86	2/3065~(0.1%)	

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	А	8	LYS	CB-CG	-5.24	1.38	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	136	ARG	NE-CZ-NH2	-10.24	115.18	120.30
1	А	136	ARG	NE-CZ-NH1	7.05	123.83	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)	H(added)	Clashes	Symm-Clashes
1	А	1078	0	1046	8	0
1	В	1096	0	1082	4	0
2	А	229	0	0	6	0
2	В	186	0	0	1	0
All	All	2589	0	2128	12	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 3.

All (12) 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:A:124[A]:THR:HG21	2:A:229:HOH:O	1.81	0.79
1:A:124[A]:THR:HG23	2:A:144:HOH:O	1.86	0.74
1:B:90:GLU:HG3	1:B:91[B]:ASN:HD22	1.60	0.64
1:A:61:THR:HG23	2:A:183:HOH:O	2.00	0.60
1:A:61:THR:HG22	2:A:160:HOH:O	1.99	0.60
1:A:108:SER:HG	1:A:124[A]:THR:HG1	1.48	0.59
1:A:33:VAL:HG12	2:A:246[A]:HOH:O	2.01	0.59
1:A:53:LYS:NZ	2:A:278:HOH:O	2.44	0.49
1:B:6:ASN:HB3	2:B:225:HOH:O	2.12	0.48
1:B:53:LYS:HD2	1:B:60:THR:HG21	1.98	0.46
1:B:90:GLU:HG3	1:B:91[B]:ASN:ND2	2.30	0.41
1:A:124[A]:THR:HG22	1:A:129:VAL:HG22	2.02	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	Percer	ntiles
1	А	140/137~(102%)	138~(99%)	2(1%)	0	100	100
1	В	144/137~(105%)	142 (99%)	2(1%)	0	100	100
All	All	284/274~(104%)	280 (99%)	4 (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	Rotameric	Outliers	Percentiles	
1	А	121/123~(98%)	121 (100%)	0	100 100	
1	В	125/123~(102%)	124 (99%)	1 (1%)	81 55	
All	All	246/246~(100%)	245 (100%)	1 (0%)	91 76	

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	38	LYS

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. There are no such side chains 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)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

