



# Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 04:33 pm BST

PDB ID : 3KIV  
Title : RECOMBINANT KRINGLE IV-10/M66 VARIANT OF HUMAN APOLIPOPROTEIN(A)  
Authors : Mochalkin, I.; Tulinsky, A.; Scanu, A.  
Deposited on : 1998-09-08  
Resolution : 1.80 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](mailto: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 ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) 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**  
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) : 2.11

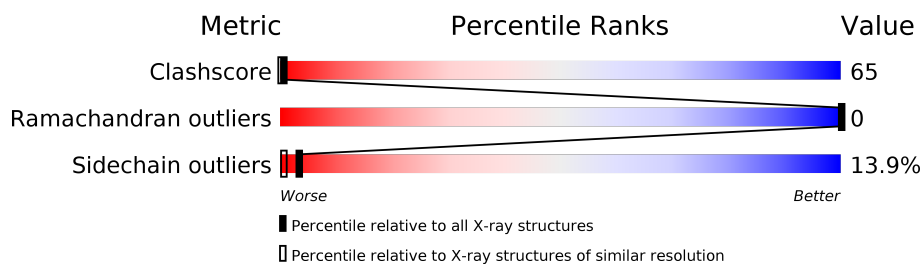
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.80 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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  $\leq 5\%$ .

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	79	

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 763 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.

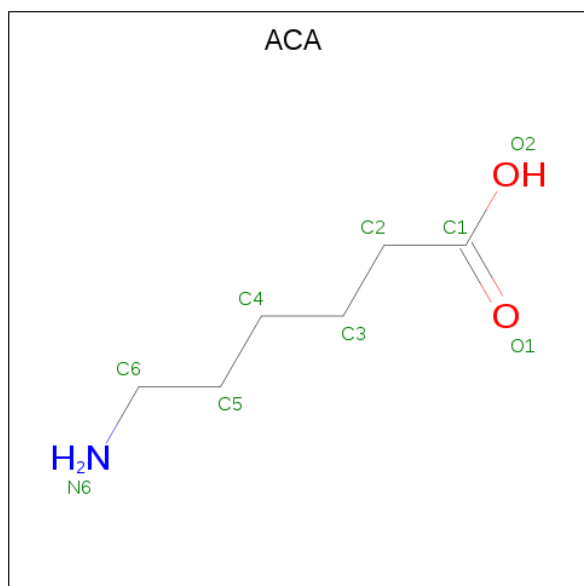
- Molecule 1 is a protein called APOLIPOPROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	79	Total	C	N	O	S	0	1	0
			646	391	122	125	8			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	66	THR	MET	VARIANT	UNP P08519

- Molecule 2 is 6-AMINOHEXANOIC ACID (three-letter code: ACA) (formula:  $C_6H_{13}NO_2$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			9	6	1	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	108	Total 108	O 108	0	0



Note EDS was not executed.

- Molecule 1: APOLIPOPROTEIN

Q0	Y2		N5	G6	Q7	S8	Y9	R10	G11	T12		T16	V17	T18	G19	R20		M28	T29	P30	H31	R32	H33	Q34	R35		N40	Y41	P42	N43	D44	G45	L46	T47	M48	N49	Y50	C51	R52		D55	A56	D57		T65	T66	D67	P68	S69	I70	R71	W72	E73	Y74		T78	R79	G80
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## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	24.30 Å 45.67 Å 63.36 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	9.00 – 1.80	Depositor
% Data completeness (in resolution range)	92.0 (9.00-1.80)	Depositor
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	PROFFT	Depositor
R, $R_{free}$	0.182 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	763	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	15.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ACA

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	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	1.17	0/672	1.97	31/915 (3.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	52	ARG	CD-NE-CZ	14.53	143.94	123.60
1	A	35	ARG	NE-CZ-NH1	8.59	124.60	120.30
1	A	52	ARG	NE-CZ-NH1	7.87	124.23	120.30
1	A	41	TYR	CB-CG-CD2	-7.69	116.39	121.00
1	A	52	ARG	NE-CZ-NH2	7.33	123.97	120.30
1	A	52	ARG	NH1-CZ-NH2	-7.01	111.69	119.40
1	A	32[A]	ARG	CA-CB-CG	6.84	128.45	113.40
1	A	32[B]	ARG	CA-CB-CG	6.84	128.45	113.40
1	A	44	ASP	CB-CG-OD2	6.54	124.18	118.30
1	A	32[A]	ARG	NE-CZ-NH2	6.52	123.56	120.30
1	A	32[B]	ARG	NE-CZ-NH2	6.52	123.56	120.30
1	A	20	ARG	CA-CB-CG	6.15	126.92	113.40
1	A	20	ARG	NE-CZ-NH2	-6.07	117.27	120.30
1	A	66	THR	OG1-CB-CG2	5.72	123.15	110.00
1	A	41	TYR	CB-CG-CD1	5.69	124.42	121.00
1	A	10	ARG	NE-CZ-NH2	-5.65	117.47	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	35	ARG	O-C-N	5.63	131.71	122.70
1	A	32[A]	ARG	CG-CD-NE	5.59	123.54	111.80
1	A	32[B]	ARG	CG-CD-NE	5.59	123.54	111.80
1	A	74	TYR	CB-CG-CD2	-5.59	117.65	121.00
1	A	71	ARG	NE-CZ-NH1	-5.56	117.52	120.30
1	A	32[A]	ARG	NH1-CZ-NH2	-5.54	113.31	119.40
1	A	32[B]	ARG	NH1-CZ-NH2	-5.54	113.31	119.40
1	A	57	ASP	CB-CA-C	5.38	121.15	110.40
1	A	66	THR	CA-CB-OG1	-5.33	97.80	109.00
1	A	51	CYS	O-C-N	5.28	131.14	122.70
1	A	35	ARG	NE-CZ-NH2	-5.25	117.67	120.30
1	A	48	MET	CG-SD-CE	5.20	108.51	100.20
1	A	32[A]	ARG	NE-CZ-NH1	5.17	122.88	120.30
1	A	32[B]	ARG	NE-CZ-NH1	5.17	122.88	120.30
1	A	44	ASP	CB-CG-OD1	-5.11	113.70	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	20	ARG	Sidechain

## 5.2 Too-close contacts ⓘ

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	646	0	575	81	0
2	A	9	0	12	3	0
3	A	108	0	0	12	0
All	All	763	0	587	81	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 65.

All (81) 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:16:THR:CG2	1:A:18:THR:HG22	1.64	1.26
1:A:20:ARG:HG2	1:A:65:THR:HG23	1.20	1.11
1:A:20:ARG:HG2	1:A:65:THR:CG2	1.83	1.08
1:A:65:THR:HG22	1:A:67:ASP:H	1.16	1.04
1:A:20:ARG:NH1	1:A:70:ILE:HG13	1.73	1.04
1:A:20:ARG:CD	1:A:65:THR:HG21	1.91	1.01
1:A:16:THR:HG21	1:A:73:GLU:OE2	1.67	0.93
1:A:35:ARG:HD2	3:A:236:HOH:O	1.72	0.90
1:A:33:HIS:HD2	1:A:35:ARG:H	1.15	0.88
1:A:66:THR:HG21	3:A:285:HOH:O	1.71	0.88
1:A:16:THR:HG22	1:A:18:THR:HG22	1.56	0.88
1:A:5:ASN:HD21	1:A:7:GLN:HB2	1.37	0.87
1:A:20:ARG:HH12	1:A:70:ILE:HG13	1.44	0.82
1:A:16:THR:HG21	1:A:18:THR:HG22	1.60	0.82
1:A:41:TYR:HB3	1:A:44:ASP:OD2	1.80	0.82
1:A:20:ARG:CG	1:A:65:THR:CG2	2.57	0.81
1:A:20:ARG:HD2	1:A:65:THR:HG21	1.63	0.79
1:A:65:THR:HG22	1:A:67:ASP:N	1.97	0.78
1:A:20:ARG:HD3	1:A:67:ASP:CB	2.15	0.77
1:A:16:THR:HG23	1:A:18:THR:HG22	1.65	0.76
1:A:5:ASN:ND2	1:A:7:GLN:HB2	2.00	0.76
1:A:16:THR:HG22	1:A:20:ARG:H	1.50	0.75
1:A:20:ARG:NH1	1:A:70:ILE:CG1	2.53	0.71
1:A:20:ARG:CG	1:A:65:THR:HG23	2.09	0.71
1:A:20:ARG:CD	1:A:65:THR:CG2	2.69	0.69
1:A:20:ARG:HD3	1:A:67:ASP:HB3	1.74	0.69
1:A:33:HIS:CD2	1:A:35:ARG:H	2.05	0.68
1:A:29:THR:HG22	1:A:30:PRO:HA	1.77	0.67
1:A:1:CYS:SG	3:A:201:HOH:O	2.53	0.66
1:A:18:THR:HG21	1:A:20:ARG:NH2	2.10	0.66
1:A:20:ARG:HH11	1:A:70:ILE:HG13	1.56	0.66
1:A:16:THR:CG2	1:A:18:THR:CG2	2.59	0.66
1:A:33:HIS:HD2	1:A:35:ARG:N	1.92	0.65
1:A:16:THR:CG2	1:A:73:GLU:OE2	2.44	0.64
1:A:18:THR:CG2	1:A:20:ARG:HH21	2.11	0.63
1:A:65:THR:HB	1:A:70:ILE:O	2.00	0.62
1:A:20:ARG:HH11	1:A:70:ILE:CG1	2.11	0.61
1:A:20:ARG:HD3	1:A:67:ASP:HB2	1.82	0.60
1:A:49:ASN:H	1:A:49:ASN:HD22	1.48	0.60
1:A:20:ARG:HD3	1:A:65:THR:HG21	1.82	0.58
1:A:18:THR:CG2	1:A:20:ARG:NH2	2.67	0.58
1:A:32[B]:ARG:NH1	3:A:207:HOH:O	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:31:HIS:CE1	1:A:65:THR:O	2.57	0.57
1:A:55:ASP:HB3	3:A:291:HOH:O	2.04	0.57
1:A:18:THR:CG2	1:A:73:GLU:OE1	2.53	0.56
1:A:29:THR:CG2	1:A:30:PRO:HA	2.37	0.55
1:A:5:ASN:HD21	1:A:7:GLN:CB	2.16	0.53
1:A:69:SER:O	1:A:70:ILE:HD13	2.10	0.51
1:A:9:TYR:CZ	1:A:11:GLY:HA3	2.46	0.51
1:A:40:ASN:C	1:A:42:PRO:HD3	2.32	0.51
1:A:41:TYR:N	1:A:42:PRO:HD3	2.25	0.51
1:A:18:THR:HB	1:A:73:GLU:OE1	2.10	0.50
1:A:18:THR:HB	3:A:262:HOH:O	2.10	0.50
1:A:69:SER:C	1:A:70:ILE:HD13	2.32	0.50
1:A:1:CYS:HB3	1:A:78:THR:HG23	1.94	0.49
1:A:18:THR:CB	3:A:262:HOH:O	2.60	0.49
1:A:16:THR:HG21	1:A:20:ARG:HB2	1.93	0.49
1:A:32[B]:ARG:CZ	3:A:256:HOH:O	2.60	0.49
1:A:41:TYR:HB2	1:A:46:LEU:HD22	1.95	0.49
1:A:16:THR:HG23	1:A:73:GLU:OE1	2.13	0.48
1:A:73:GLU:HA	3:A:238:HOH:O	2.13	0.48
1:A:35:ARG:HG3	1:A:35:ARG:HH11	1.78	0.47
1:A:55:ASP:CB	3:A:291:HOH:O	2.62	0.47
1:A:31:HIS:CE1	1:A:70:ILE:O	2.68	0.47
1:A:16:THR:HG22	1:A:18:THR:CG2	2.37	0.46
1:A:12:THR:HG22	1:A:50:TYR:CE2	2.51	0.46
1:A:72:TRP:CE2	2:A:100:ACA:H62	2.50	0.46
1:A:12:THR:HG22	1:A:50:TYR:CZ	2.52	0.45
1:A:72:TRP:CD1	2:A:100:ACA:H41	2.52	0.45
1:A:16:THR:CG2	1:A:73:GLU:CD	2.85	0.45
1:A:2:TYR:CE1	1:A:79:ARG:HG2	2.52	0.45
1:A:10:ARG:HA	1:A:52:ARG:CZ	2.46	0.44
1:A:51:CYS:C	1:A:52:ARG:HG2	2.38	0.44
1:A:28:MET:HB3	1:A:32[B]:ARG:HG3	2.01	0.43
1:A:18:THR:HG21	1:A:20:ARG:CZ	2.48	0.43
1:A:35:ARG:CZ	2:A:100:ACA:O2	2.67	0.42
1:A:20:ARG:HG3	3:A:268:HOH:O	2.20	0.41
1:A:49:ASN:N	1:A:49:ASN:HD22	2.15	0.41
1:A:16:THR:HG21	1:A:20:ARG:CB	2.50	0.41
1:A:65:THR:CG2	1:A:67:ASP:H	2.08	0.41
1:A:7:GLN:NE2	3:A:297:HOH:O	2.54	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	78/79 (99%)	75 (96%)	3 (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	73/72 (101%)	63 (86%)	10 (14%)	3	1

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

Mol	Chain	Res	Type
1	A	0	GLN
1	A	5	ASN
1	A	7	GLN
1	A	8	SER
1	A	16	THR
1	A	29	THR
1	A	34	GLN
1	A	46	LEU
1	A	49	ASN
1	A	66	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	0	GLN
1	A	3	HIS
1	A	5	ASN
1	A	31	HIS
1	A	33	HIS
1	A	49	ASN

### 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 carbohydrates 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		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	ACA	A	100	-	5,8,8	0.80	0	4,8,8	1.01	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
2	ACA	A	100	-	-	1/4/6/6	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	100	ACA	C2-C3-C4-C5

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	100	ACA	3	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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.