

Full wwPDB X-ray Structure Validation Report (i)

Dec 10, 2023 – 10:17 am GMT

PDB ID : 8PHB

Title : Crystal structure of apo Camil

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Deposited on : 2023-06-19

Resolution : 1.70 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:

 $\begin{array}{ccc} & Mol Probity & : & 4.02b\text{-}467 \\ & Xtriage \text{ (Phenix)} & : & 1.13 \end{array}$

EDS: 2.36

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)

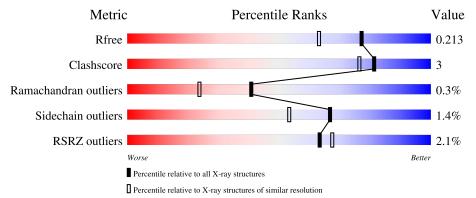
Validation Pipeline (wwPDB-VP) : 2.36

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 1.70 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},{\rm resolution\ range}(\mathring{\rm A})) \end{array}$
R_{free}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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	A	406	86%	7% 7%
1	В	406	86%	5% 8%



2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 6356 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 CRISPR-associated protein, APE2256 family.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	1 A 379	Total	C	N	O	S	0	15	0	
			3027	1936	524	555	12			
1	1 D	В 372	Total	\mathbf{C}	N	O	\mathbf{S}	0	1.4	
	312	2962	1886	511	553	12		14		

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	- initiating methionine		UNP D3RW14
A	2	ALA	_	expression tag	UNP D3RW14
A	382	GLY	_	expression tag	UNP D3RW14
A	383	GLU	_	expression tag	UNP D3RW14
A	384	GLY	_	expression tag	UNP D3RW14
A	385	TRP	_	expression tag	UNP D3RW14
A	386	SER	_	expression tag	UNP D3RW14
A	387	HIS	_	expression tag	UNP D3RW14
A	388	PRO	_	expression tag	UNP D3RW14
A	389	GLN	_	expression tag	UNP D3RW14
A	390	PHE	_	expression tag	UNP D3RW14
A	391	GLU		expression tag expression tag	UNP D3RW14
A	392	LYS		expression tag expression tag	UNP D3RW14
A	393	GLY		expression tag expression tag	UNP D3RW14
A	394	VAL	-	expression tag expression tag	UNP D3RW14
	395	GLU	-		UNP D3RW14
A	396	GLU	_	expression tag	UNP D3RW14
		_	-	expression tag	
A	397	HIS	-	expression tag	UNP D3RW14
A	398	HIS	-	expression tag	UNP D3RW14
A	399	HIS	-	expression tag	UNP D3RW14
A	400	HIS	-	expression tag	UNP D3RW14
A	401	HIS	-	expression tag	UNP D3RW14
A	402	HIS	-	expression tag	UNP D3RW14
A	403	HIS	-	expression tag	UNP D3RW14
A	404	HIS	_	expression tag	UNP D3RW14

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Chain	Residue	Modelled	Actual	Comment	Reference
A	405	HIS	- expression tag		UNP D3RW14
A	406	HIS	-	expression tag	UNP D3RW14
В	1	MET	-	initiating methionine	UNP D3RW14
В	2	ALA	-	expression tag	UNP D3RW14
В	382	GLY	-	expression tag	UNP D3RW14
В	383	GLU	-	expression tag	UNP D3RW14
В	384	GLY	-	expression tag	UNP D3RW14
В	385	TRP	-	expression tag	UNP D3RW14
В	386	SER	-	expression tag	UNP D3RW14
В	387	HIS	-	expression tag	UNP D3RW14
В	388	PRO	-	expression tag	UNP D3RW14
В	389	GLN	-	expression tag	UNP D3RW14
В	390	PHE	-	expression tag	UNP D3RW14
В	391	GLU	-	expression tag	UNP D3RW14
В	392	LYS	-	expression tag	UNP D3RW14
В	393	GLY	-	expression tag	UNP D3RW14
В	394	VAL	-	expression tag	UNP D3RW14
В	395	GLU	-	expression tag	UNP D3RW14
В	396	GLY	-	expression tag	UNP D3RW14
В	397	HIS	-	expression tag	UNP D3RW14
В	398	HIS	-	expression tag	UNP D3RW14
В	399	HIS	-	expression tag	UNP D3RW14
В	400	HIS	-	expression tag	UNP D3RW14
В	401	HIS	_	expression tag	UNP D3RW14
В	402	HIS	-	expression tag	UNP D3RW14
В	403	HIS	-	expression tag	UNP D3RW14
В	404	HIS	-	expression tag	UNP D3RW14
В	405	HIS	-	expression tag	UNP D3RW14
В	406	HIS	-	expression tag	UNP D3RW14

• Molecule 2 is water.

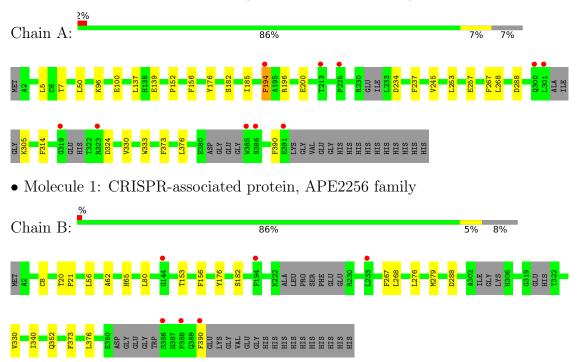
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	166	Total O 166 166	0	0
2	В	201	Total O 201 201	0	0



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: CRISPR-associated protein, APE2256 family





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	65.24Å 90.43Å 65.62Å	Depositor
a, b, c, α , β , γ	90.00° 99.56° 90.00°	Depositor
Resolution (Å)	64.71 - 1.70	Depositor
resolution (A)	64.70 - 1.70	EDS
% Data completeness	99.0 (64.71-1.70)	Depositor
(in resolution range)	99.2 (64.70-1.70)	EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.39 (at 1.70Å)	Xtriage
Refinement program	PHENIX (1.19.2_4158: ???)	Depositor
R, R_{free}	0.186 , 0.215	Depositor
it, it free	0.184 , 0.213	DCC
R_{free} test set	8138 reflections (9.94%)	wwPDB-VP
Wilson B-factor (Å ²)	28.9	Xtriage
Anisotropy	0.493	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.33, 37.3	EDS
L-test for twinning ²	$< L > = 0.48, < L^2> = 0.31$	Xtriage
Estimated twinning fraction	0.076 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6356	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.67% 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)

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	0.38	0/3090	0.59	0/4206	
1	В	0.40	0/3022	0.61	0/4109	
All	All	0.39	0/6112	0.60	0/8315	

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)

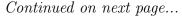
In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3027	0	2927	22	0
1	В	2962	0	2865	12	0
2	A	166	0	0	2	0
2	В	201	0	0	1	0
All	All	6356	0	5792	31	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 (31) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1 Atom-2		$\begin{array}{c} \text{Interatomic} \\ \text{distance (Å)} \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:A:200:GLU:HG3	1:A:333:TRP:HE1	1.49	0.75





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A 1 1		Interatomic	Clash
Atom-1	Atom-2	${\rm distance}(\mathring{\rm A})$	overlap (Å)
1:A:194:PHE:HB3	1:A:196[B]:ARG:HG3	1.74	0.69
1:A:7[A]:THR:HG21	2:A:535:HOH:O	1.94	0.67
1:A:390:PHE:HB2	1:B:330:VAL:HB	1.77	0.65
1:A:152:PRO:HG2	1:A:176[B]:TYR:CD2	2.34	0.62
1:A:330:VAL:HB	1:B:390:PHE:HB2	1.83	0.61
1:A:196[A]:ARG:NH2	1:A:257:GLU:OE2	2.34	0.61
1:A:194:PHE:HB3	1:A:196[A]:ARG:HD2	1.83	0.59
1:B:352:GLN:NE2	2:B:504:HOH:O	2.37	0.57
1:A:200:GLU:CG	1:A:333:TRP:HE1	2.18	0.55
1:B:268:LEU:HD11	1:B:376:LEU:HD13	1.91	0.53
1:B:279[A]:MET:HE1	1:B:340:ILE:HG21	1.92	0.51
1:B:276:LEU:HA	1:B:279[A]:MET:HE2	1.94	0.49
1:A:390:PHE:CB	1:B:330:VAL:HB	2.42	0.49
1:A:5:LEU:HD21	1:A:139:GLU:HG2	1.95	0.48
1:A:305:LYS:HG3	1:A:314:PHE:CD2	2.49	0.48
1:A:176[A]:TYR:CZ	1:A:185[A]:ILE:HG23	2.49	0.48
1:A:267:PHE:HB3	1:A:373:PHE:HB3	1.96	0.47
1:B:8[B]:CYS:SG	1:B:80:LEU:HB3	2.54	0.47
1:A:237:PHE:HB3	1:A:245:VAL:CG1	2.45	0.46
1:A:7[A]:THR:HG23	2:A:558:HOH:O	2.18	0.44
1:A:137[A]:LEU:HD11	1:A:253:LEU:CD2	2.49	0.43
1:A:176[A]:TYR:CE1	1:A:185[A]:ILE:HG23	2.52	0.43
1:B:20:THR:HA	1:B:21:PRO:C	2.38	0.43
1:A:137[A]:LEU:HD11	1:A:253:LEU:HD21	2.00	0.43
1:B:62:ALA:HB1	1:B:153:THR:HG22	2.02	0.42
1:A:268:LEU:HD11	1:A:376:LEU:HD13	2.02	0.42
1:B:267:PHE:HB3	1:B:373:PHE:HB3	2.01	0.42
1:A:96:LYS:NZ	1:A:100:GLU:OE2	2.50	0.42
1:B:56:LEU:HG	1:B:65:HIS:CD2	2.55	0.42
1:A:50:LEU:HD23	1:A:50:LEU:HA	1.87	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	384/406 (95%)	377 (98%)	6 (2%)	1 (0%)	41	24
1	В	376/406 (93%)	371 (99%)	4 (1%)	1 (0%)	41	24
All	All	760/812 (94%)	748 (98%)	10 (1%)	2 (0%)	41	24

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	В	156	PHE
1	A	156	PHE

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	305/341 (89%)	300 (98%)	5 (2%)	62 48
1	В	304/341 (89%)	300 (99%)	4 (1%)	69 56
All	All	609/682 (89%)	600 (98%)	9 (2%)	67 51

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	182	SER
1	A	194	PHE
1	A	234	ASP
1	A	288	ASP
1	A	324	ASP
1	В	176	TYR
1	В	182[A]	SER
1	В	182[B]	SER
1	В	288	ASP

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 $>$	$\# \mathrm{RSRZ} {>} 2$	2	$\mathbf{OWAB}(\mathrm{\AA}^2)$	Q<0.9
1	A	379/406~(93%)	-0.16	10 (2%) 56	60	21, 35, 59, 81	7 (1%)
1	В	372/406 (91%)	-0.25	6 (1%) 72	76	22, 31, 52, 78	5 (1%)
All	All	751/812 (92%)	-0.20	16 (2%) 63	67	21, 33, 57, 81	12 (1%)

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	233	LEU	3.4
1	A	213	THR	3.2
1	В	386	SER	3.0
1	В	388	PRO	2.9
1	В	194	PHE	2.7
1	A	301	LEU	2.6
1	A	225	PRO	2.6
1	A	391	GLU	2.6
1	A	386	SER	2.5
1	A	194	PHE	2.5
1	A	385	TRP	2.5
1	A	300	GLN	2.3
1	В	390	PHE	2.3
1	A	323	ARG	2.1
1	В	144	GLY	2.1
1	A	319	GLY	2.0

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.

