



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 11:19 AM UTC

PDB ID : 3NMZ / pdb_00003nmz
Title : Crystal structure of APC complexed with Asef
Authors : Zhang, Z.; Chen, L.; Gao, L.; Lin, K.; Wu, G.
Deposited on : 2010-06-23
Resolution : 3.01 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

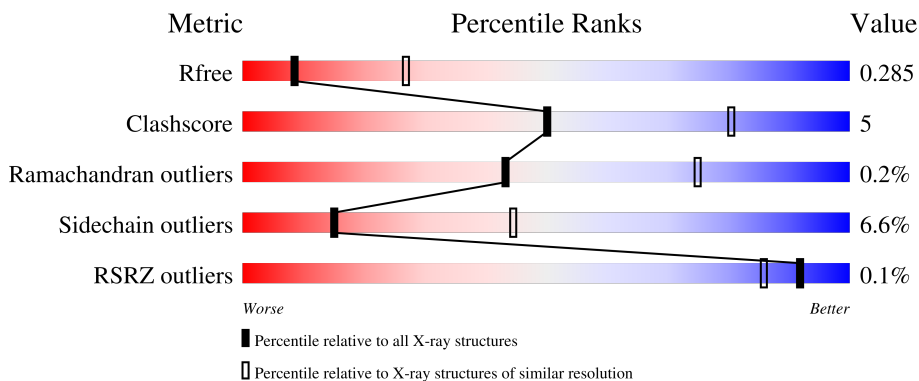
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.01 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))
R_{free}	180053	3131 (3.04-3.00)
Clashscore	190562	3444 (3.04-3.00)
Ramachandran outliers	187476	3319 (3.04-3.00)
Sidechain outliers	187428	3322 (3.04-3.00)
RSRZ outliers	180081	3130 (3.04-3.00)

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 $\leq 5\%$. 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	458	 76% 12% • 11%
1	B	458	 71% 15% • 13%
2	C	116	 60% 12% • 27%
2	D	116	 58% 12% • 28%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 7673 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 APC variant protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	406	3130	1929	576	595	30	0	0	0
1	B	400	3088	1901	570	587	30	0	0	0

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	282	MET	-	expression tag	UNP Q4LE70
A	283	GLY	-	expression tag	UNP Q4LE70
A	284	SER	-	expression tag	UNP Q4LE70
A	285	SER	-	expression tag	UNP Q4LE70
A	286	HIS	-	expression tag	UNP Q4LE70
A	287	HIS	-	expression tag	UNP Q4LE70
A	288	HIS	-	expression tag	UNP Q4LE70
A	289	HIS	-	expression tag	UNP Q4LE70
A	290	HIS	-	expression tag	UNP Q4LE70
A	291	HIS	-	expression tag	UNP Q4LE70
A	292	SER	-	expression tag	UNP Q4LE70
A	293	SER	-	expression tag	UNP Q4LE70
A	294	GLY	-	expression tag	UNP Q4LE70
A	295	LEU	-	expression tag	UNP Q4LE70
A	296	VAL	-	expression tag	UNP Q4LE70
A	297	PRO	-	expression tag	UNP Q4LE70
A	298	ARG	-	expression tag	UNP Q4LE70
A	299	GLY	-	expression tag	UNP Q4LE70
A	300	SER	-	expression tag	UNP Q4LE70
A	301	HIS	-	expression tag	UNP Q4LE70
A	302	MET	-	expression tag	UNP Q4LE70
B	282	MET	-	expression tag	UNP Q4LE70
B	283	GLY	-	expression tag	UNP Q4LE70
B	284	SER	-	expression tag	UNP Q4LE70
B	285	SER	-	expression tag	UNP Q4LE70

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Chain	Residue	Modelled	Actual	Comment	Reference
B	286	HIS	-	expression tag	UNP Q4LE70
B	287	HIS	-	expression tag	UNP Q4LE70
B	288	HIS	-	expression tag	UNP Q4LE70
B	289	HIS	-	expression tag	UNP Q4LE70
B	290	HIS	-	expression tag	UNP Q4LE70
B	291	HIS	-	expression tag	UNP Q4LE70
B	292	SER	-	expression tag	UNP Q4LE70
B	293	SER	-	expression tag	UNP Q4LE70
B	294	GLY	-	expression tag	UNP Q4LE70
B	295	LEU	-	expression tag	UNP Q4LE70
B	296	VAL	-	expression tag	UNP Q4LE70
B	297	PRO	-	expression tag	UNP Q4LE70
B	298	ARG	-	expression tag	UNP Q4LE70
B	299	GLY	-	expression tag	UNP Q4LE70
B	300	SER	-	expression tag	UNP Q4LE70
B	301	HIS	-	expression tag	UNP Q4LE70
B	302	MET	-	expression tag	UNP Q4LE70

- Molecule 2 is a protein called Rho guanine nucleotide exchange factor 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	84	Total	C	N	O	S	0	0	0
			661	414	116	128	3			
2	C	85	Total	C	N	O	S	0	0	0
			667	417	117	130	3			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	161	MET	-	expression tag	UNP Q9NR80
D	162	GLY	-	expression tag	UNP Q9NR80
D	163	HIS	-	expression tag	UNP Q9NR80
D	164	HIS	-	expression tag	UNP Q9NR80
D	165	HIS	-	expression tag	UNP Q9NR80
D	166	HIS	-	expression tag	UNP Q9NR80
D	167	HIS	-	expression tag	UNP Q9NR80
D	168	HIS	-	expression tag	UNP Q9NR80
D	169	MET	-	expression tag	UNP Q9NR80
C	161	MET	-	expression tag	UNP Q9NR80
C	162	GLY	-	expression tag	UNP Q9NR80
C	163	HIS	-	expression tag	UNP Q9NR80
C	164	HIS	-	expression tag	UNP Q9NR80

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Chain	Residue	Modelled	Actual	Comment	Reference
C	165	HIS	-	expression tag	UNP Q9NR80
C	166	HIS	-	expression tag	UNP Q9NR80
C	167	HIS	-	expression tag	UNP Q9NR80
C	168	HIS	-	expression tag	UNP Q9NR80
C	169	MET	-	expression tag	UNP Q9NR80


- Molecule 3 is water.

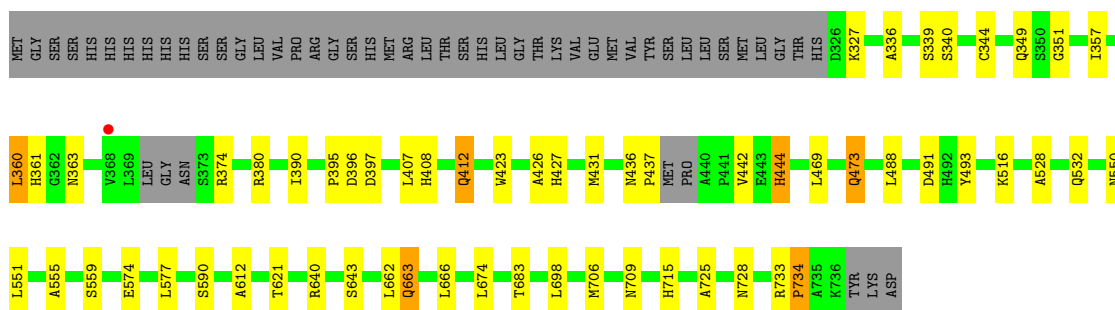
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	50	Total O 50 50	0	0
3	B	56	Total O 56 56	0	0
3	D	11	Total O 11 11	0	0
3	C	10	Total O 10 10	0	0

3 Residue-property plots

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.

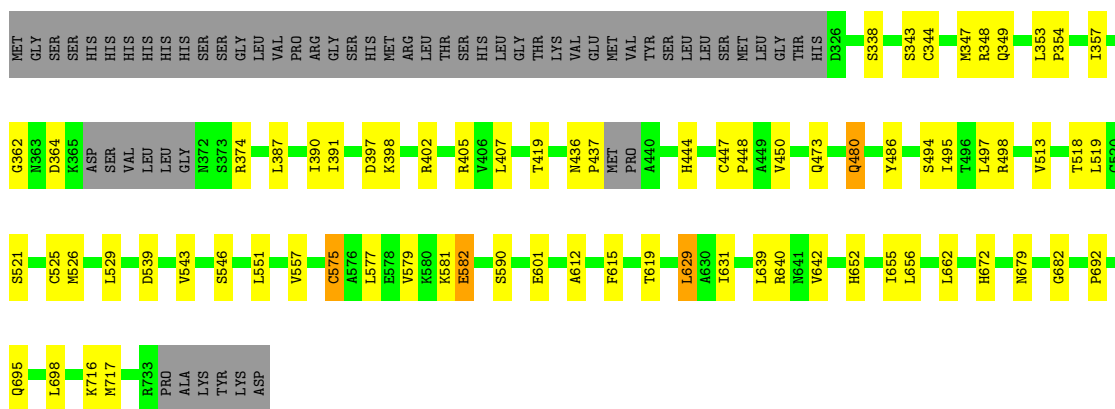
- Molecule 1: APC variant protein

Chain A:  76% 12% 11%



- Molecule 1: APC variant protein

Chain B:  71% 15% 13%



- Molecule 2: Rho guanine nucleotide exchange factor 4

Chain D:  58% 12% 28%



ASP
GLY
GLY
ALA
GLU

- Molecule 2: Rho guanine nucleotide exchange factor 4

Chain C:  60% 12% 27%

MET	GLY	HIS	HIS	HIS	HIS	HIS	MET	SER	S171	H174	Y175	S176	Q184	L185	A186	I187	H205	G214	E222	R235	S246	F247	V248	R251	V252	N253	Q254	D255	GLU	PRO	ALA	ASP	ASP	ASP	ALA	PRO	LEU	ALA	GLY	ASN	SER	GLY	ALA	GLU	ASP	GLY	ALA	GLU
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4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	163.18Å 163.18Å 242.59Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 3.01 50.00 – 3.01	Depositor EDS
% Data completeness (in resolution range)	90.2 (50.00-3.01) 90.7 (50.00-3.01)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	9.62 (at 3.01Å)	Xtrriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.249 , 0.284 0.248 , 0.285	Depositor DCC
R_{free} test set	2202 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	76.2	Xtrriage
Anisotropy	0.004	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 77.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.23$	Xtrriage
Estimated twinning fraction	0.298 for h,-h-k,-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7673	wwPDB-VP
Average B, all atoms (Å ²)	82.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.27% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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.

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	0.37	0/3170	0.84	0/4273
1	B	0.37	0/3127	0.83	1/4214 (0.0%)
2	C	0.42	0/686	0.78	1/933 (0.1%)
2	D	0.39	0/680	0.74	0/925
All	All	0.37	0/7663	0.82	2/10345 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	176	SER	N-CA-C	6.36	117.90	110.97
1	B	343	SER	N-CA-C	-5.13	107.05	113.72

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	3130	0	3160	30	0
1	B	3088	0	3112	34	0
2	C	667	0	600	8	0
2	D	661	0	595	8	0
3	A	50	0	0	1	0
3	B	56	0	0	2	0
3	C	10	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	11	0	0	0	0
All	All	7673	0	7467	79	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 5.

The worst 5 of 79 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:473:GLN:HE21	1:A:473:GLN:H	1.20	0.84
2:D:199:ALA:HB1	2:D:248:VAL:HG13	1.61	0.83
1:B:629:LEU:H	1:B:629:LEU:HD23	1.45	0.80
2:C:251:ARG:HD3	2:C:253:ASN:H	1.48	0.78
1:B:692:PRO:HA	1:B:695:GLN:HG2	1.68	0.75

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	400/458 (87%)	385 (96%)	14 (4%)	1 (0%)	36	68
1	B	394/458 (86%)	379 (96%)	14 (4%)	1 (0%)	36	68
2	C	83/116 (72%)	73 (88%)	10 (12%)	0	100	100
2	D	82/116 (71%)	77 (94%)	5 (6%)	0	100	100
All	All	959/1148 (84%)	914 (95%)	43 (4%)	2 (0%)	43	75

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	362	GLY

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Mol	Chain	Res	Type
1	A	734	PRO

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	345/391 (88%)	328 (95%)	17 (5%)	22	55
1	B	340/391 (87%)	314 (92%)	26 (8%)	12	39
2	C	68/89 (76%)	64 (94%)	4 (6%)	18	49
2	D	67/89 (75%)	60 (90%)	7 (10%)	7	26
All	All	820/960 (85%)	766 (93%)	54 (7%)	15	44

5 of 54 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	480	GLN
1	B	582	GLU
2	D	251	ARG
1	B	486	TYR
1	B	513	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	541	GLN
1	B	686	ASN
2	C	205	HIS
1	B	663	GLN
1	B	712	HIS

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 oligosaccharides 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, 95th 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>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	406/458 (88%)	-0.90	1 (0%) 91 83	56, 79, 108, 162	1 (0%)
1	B	400/458 (87%)	-0.83	0 100 100	55, 80, 128, 160	2 (0%)
2	C	85/116 (73%)	-0.94	0 100 100	62, 81, 112, 124	0
2	D	84/116 (72%)	-0.78	0 100 100	62, 82, 112, 125	0
All	All	975/1148 (84%)	-0.86	1 (0%) 92 86	55, 80, 118, 162	3 (0%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	368	VAL	2.9

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 oligosaccharides 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.