



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 02:57 PM UTC

PDB ID : 5BPT / pdb_00005bpt
Title : Atomic-resolution structures of the APC/C subunits Apc4 and the Apc5 N-terminal domain
Authors : Cronin, N.; Yang, J.; Zhang, Z.; Barford, D.
Deposited on : 2015-05-28
Resolution : 3.20 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 ⓘ 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
Mogul : 2022.3.0, CSD as543be (2022)
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

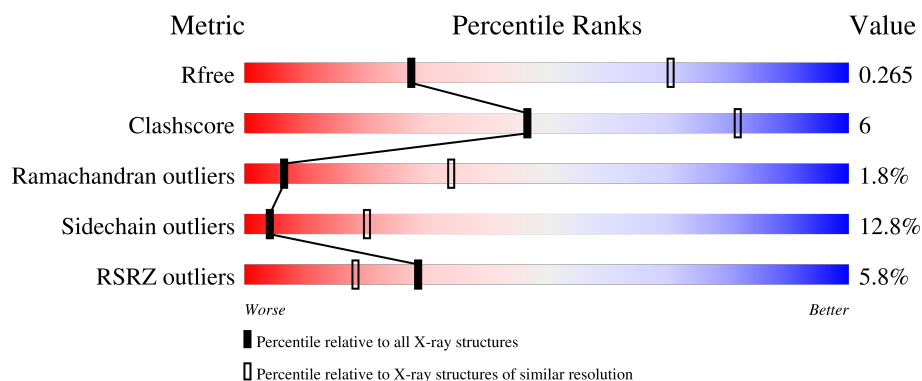
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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	741	5% 62% 19% • 17%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4786 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 MGC81278 protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	614	Total	C	N	O	S	Se	0	0	0
			4786	3045	805	908	13	15			

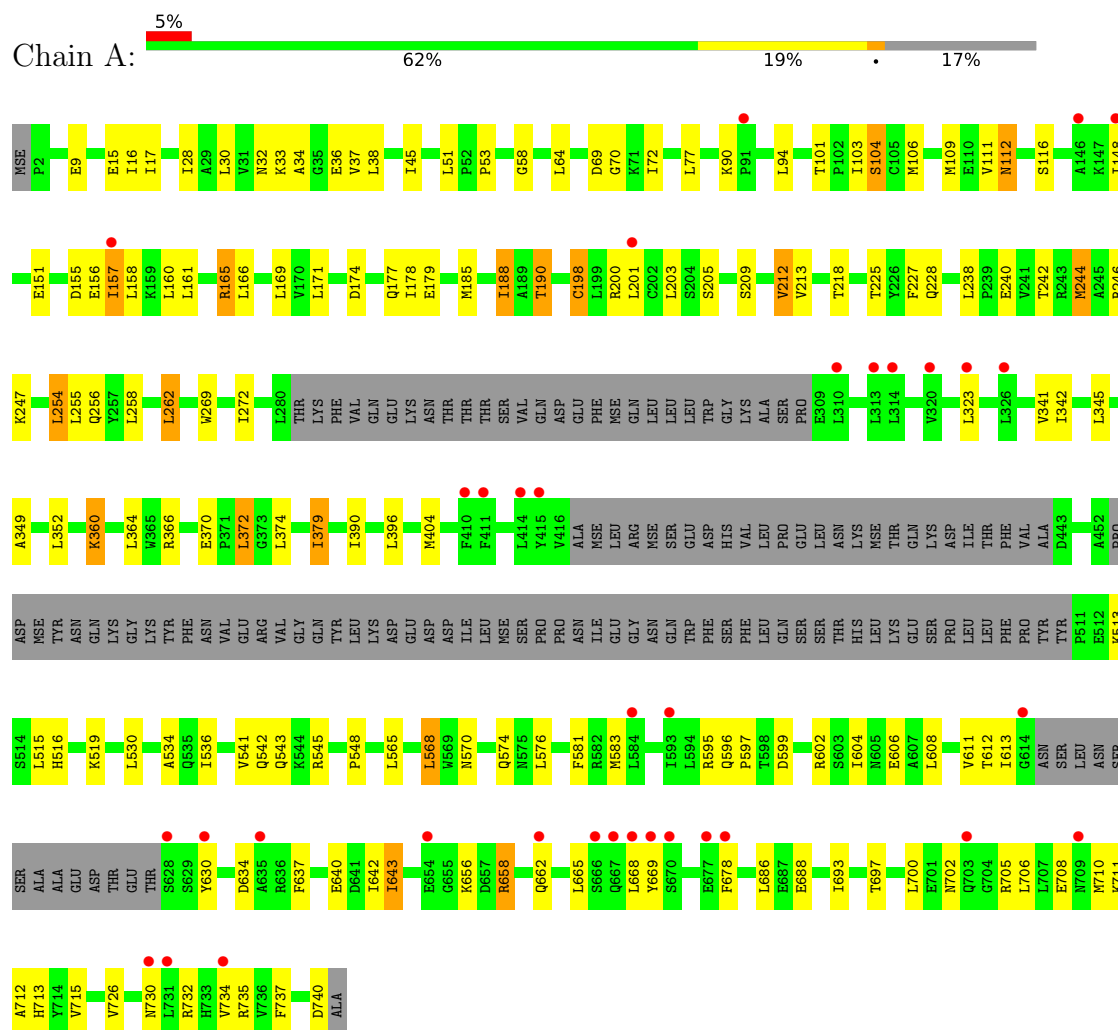
There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	initiating methionine	UNP Q6NU36
A	312	THR	ALA	conflict	UNP Q6NU36
A	738	GLU	-	expression tag	UNP Q6NU36
A	739	MSE	-	expression tag	UNP Q6NU36
A	740	ASP	-	expression tag	UNP Q6NU36
A	741	ALA	-	expression tag	UNP Q6NU36

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: MGC81278 protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	90.47Å 90.47Å 115.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.71 – 3.20 48.71 – 3.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.71-3.20) 100.0 (48.71-3.20)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.48 (at 3.19Å)	Xtriage
Refinement program	BUSTER-TNT 2.10.1, BUSTER 2.11.4	Depositor
R, R_{free}	0.223 , 0.265 (Not available) , 0.265	Depositor DCC
R_{free} test set	1016 reflections (6.59%)	wwPDB-VP
Wilson B-factor (Å ²)	90.0	Xtriage
Anisotropy	0.199	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 77.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.048 for h,-k,-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4786	wwPDB-VP
Average B, all atoms (Å ²)	107.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.94% 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	0.73	0/4856	1.29	5/6556 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	254	LEU	N-CA-C	-5.93	102.88	110.53
1	A	174	ASP	CA-CB-CG	5.55	118.15	112.60
1	A	256	GLN	N-CA-C	-5.50	105.36	111.36
1	A	678	PHE	N-CA-C	-5.17	107.00	113.72
1	A	112	ASN	CA-CB-CG	5.01	117.61	112.60

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	4786	0	4755	54	0
All	All	4786	0	4755	54	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 6.

All (54) 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:225:THR:HG22	1:A:548:PRO:HA	1.77	0.66
1:A:104:SER:HB3	1:A:198:CYS:O	2.00	0.61
1:A:106:MSE:HE2	1:A:169:LEU:HD11	1.85	0.59
1:A:576:LEU:HD12	1:A:595:ARG:HB2	1.85	0.59
1:A:16:ILE:H	1:A:732:ARG:HD2	1.69	0.58
1:A:45:ILE:HD13	1:A:734:VAL:HG13	1.85	0.58
1:A:111:VAL:HG23	1:A:165:ARG:HD2	1.86	0.58
1:A:15:GLU:HA	1:A:732:ARG:HG3	1.86	0.57
1:A:637:PHE:HA	1:A:643:ILE:HG22	1.87	0.56
1:A:658:ARG:HH21	1:A:737:PHE:HB2	1.71	0.55
1:A:583:MSE:HE1	1:A:686:LEU:HB3	1.89	0.54
1:A:36:GLU:HB3	1:A:53:PRO:HD3	1.91	0.52
1:A:212:VAL:HG13	1:A:227:PHE:HB2	1.92	0.52
1:A:254:LEU:O	1:A:255:LEU:HB3	2.10	0.52
1:A:341:VAL:HA	1:A:345:LEU:HB2	1.93	0.51
1:A:613:ILE:HD11	1:A:700:LEU:HD21	1.92	0.51
1:A:360:LYS:HB2	1:A:379:ILE:HD11	1.92	0.50
1:A:597:PRO:HD3	1:A:604:ILE:HB	1.94	0.50
1:A:166:LEU:HB2	1:A:242:THR:HG23	1.94	0.50
1:A:581:PHE:HE2	1:A:583:MSE:HE3	1.78	0.49
1:A:200:ARG:HB2	1:A:213:VAL:HB	1.95	0.49
1:A:656:LYS:HG3	1:A:711:LYS:HA	1.95	0.48
1:A:244:MSE:HE2	1:A:374:LEU:HB2	1.95	0.47
1:A:366:ARG:HA	1:A:370:GLU:HB2	1.97	0.47
1:A:612:THR:HB	1:A:697:THR:HG22	1.97	0.47
1:A:634:ASP:HB2	1:A:713:HIS:O	2.14	0.47
1:A:516:HIS:HA	1:A:519:LYS:HE2	1.96	0.46
1:A:32:ASN:C	1:A:34:ALA:H	2.25	0.45
1:A:396:LEU:HD22	1:A:515:LEU:HD22	1.99	0.45
1:A:205:SER:H	1:A:570:ASN:HD21	1.63	0.45
1:A:244:MSE:HE2	1:A:374:LEU:HD13	1.99	0.45
1:A:148:ILE:HG23	1:A:156:GLU:HB2	1.99	0.44
1:A:710:MSE:HE1	1:A:726:VAL:HB	1.99	0.44
1:A:37:VAL:HG21	1:A:64:LEU:HD21	1.99	0.44
1:A:269:TRP:HA	1:A:272:ILE:HD12	1.99	0.44
1:A:581:PHE:CE2	1:A:583:MSE:HE3	2.53	0.43
1:A:349:ALA:HB3	1:A:390:ILE:HD12	2.00	0.43
1:A:255:LEU:H	1:A:258:LEU:HD13	1.84	0.43
1:A:599:ASP:HB3	1:A:602:ARG:HD3	2.01	0.43
1:A:101:THR:HG21	1:A:177:GLN:HB3	2.00	0.43
1:A:366:ARG:O	1:A:370:GLU:HB3	2.19	0.42
1:A:188:ILE:O	1:A:534:ALA:HA	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244:MSE:HE3	1:A:372:LEU:HB3	2.02	0.42
1:A:370:GLU:C	1:A:372:LEU:H	2.27	0.42
1:A:161:LEU:HG	1:A:185:MSE:HE1	2.02	0.41
1:A:200:ARG:HB3	1:A:568:LEU:HD12	2.02	0.41
1:A:179:GLU:HG2	1:A:190:THR:HG23	2.03	0.41
1:A:642:ILE:HG22	1:A:662:GLN:HA	2.03	0.41
1:A:9:GLU:HG3	1:A:735:ARG:HG3	2.01	0.41
1:A:157:ILE:HD12	1:A:158:LEU:HG	2.03	0.41
1:A:228:GLN:HB3	1:A:545:ARG:HB2	2.03	0.41
1:A:94:LEU:HD22	1:A:156:GLU:HB3	2.02	0.40
1:A:262:LEU:HD11	1:A:515:LEU:HD21	2.04	0.40
1:A:58:GLY:HA3	1:A:77:LEU:HD13	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	604/741 (82%)	558 (92%)	35 (6%)	11 (2%)	6	34

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	116	SER
1	A	640	GLU
1	A	712	ALA
1	A	70	GLY
1	A	630	TYR
1	A	705	ARG
1	A	198	CYS
1	A	668	LEU
1	A	33	LYS

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Mol	Chain	Res	Type
1	A	151	GLU
1	A	669	TYR

5.3.2 Protein sidechains ⓘ

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	493/648 (76%)	430 (87%)	63 (13%)	4 20

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	ILE
1	A	28	ILE
1	A	30	LEU
1	A	38	LEU
1	A	51	LEU
1	A	69	ASP
1	A	72	ILE
1	A	90	LYS
1	A	103	ILE
1	A	104	SER
1	A	109	MSE
1	A	112	ASN
1	A	155	ASP
1	A	157	ILE
1	A	160	LEU
1	A	165	ARG
1	A	171	LEU
1	A	178	ILE
1	A	188	ILE
1	A	190	THR
1	A	201	LEU
1	A	203	LEU
1	A	209	SER
1	A	212	VAL

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Mol	Chain	Res	Type
1	A	218	THR
1	A	238	LEU
1	A	240	GLU
1	A	244	MSE
1	A	246	ARG
1	A	247	LYS
1	A	262	LEU
1	A	323	LEU
1	A	342	ILE
1	A	352	LEU
1	A	360	LYS
1	A	364	LEU
1	A	372	LEU
1	A	379	ILE
1	A	404	MSE
1	A	513	LYS
1	A	530	LEU
1	A	536	ILE
1	A	541	VAL
1	A	542	GLN
1	A	543	GLN
1	A	565	LEU
1	A	568	LEU
1	A	574	GLN
1	A	596	GLN
1	A	606	GLU
1	A	608	LEU
1	A	611	VAL
1	A	643	ILE
1	A	658	ARG
1	A	665	LEU
1	A	688	GLU
1	A	693	ILE
1	A	702	ASN
1	A	706	LEU
1	A	708	GLU
1	A	715	VAL
1	A	730	ASN
1	A	740	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	40	HIS
1	A	123	ASN
1	A	338	GLN
1	A	406	ASN
1	A	535	GLN
1	A	570	ASN
1	A	577	HIS
1	A	596	GLN
1	A	650	ASN
1	A	667	GLN

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

6.1 Protein, DNA and RNA chains

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	599/741 (80%)	0.45	35 (5%) 29 18	56, 98, 191, 257	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	670	SER	4.3
1	A	314	LEU	3.6
1	A	148	ILE	3.6
1	A	614	GLY	3.4
1	A	677	GLU	3.3
1	A	628	SER	3.2
1	A	734	VAL	3.1
1	A	410	PHE	3.1
1	A	730	ASN	2.9
1	A	678	PHE	2.9
1	A	310	LEU	2.8
1	A	662	GLN	2.7
1	A	415	TYR	2.7
1	A	709	ASN	2.7
1	A	669	TYR	2.7
1	A	323	LEU	2.7
1	A	584	LEU	2.5
1	A	414	LEU	2.5
1	A	731	LEU	2.3
1	A	654	GLU	2.3
1	A	320	VAL	2.3
1	A	91	PRO	2.2
1	A	593	ILE	2.2
1	A	411	PHE	2.2
1	A	635	ALA	2.2
1	A	703	GLN	2.2
1	A	668	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	313	LEU	2.1
1	A	201	LEU	2.1
1	A	630	TYR	2.1
1	A	326	LEU	2.1
1	A	146	ALA	2.1
1	A	666	SER	2.0
1	A	157	ILE	2.0
1	A	667	GLN	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 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.