



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 27, 2017 – 04:56 AM EDT

PDB ID : 1G3N
Title : STRUCTURE OF A P18(INK4C)-CDK6-K-CYCLIN TERNARY COMPLEX
Authors : Jeffrey, P.D.; Tong, L.; Pavletich, N.P.
Deposited on : unknown
Resolution : 2.90 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030345

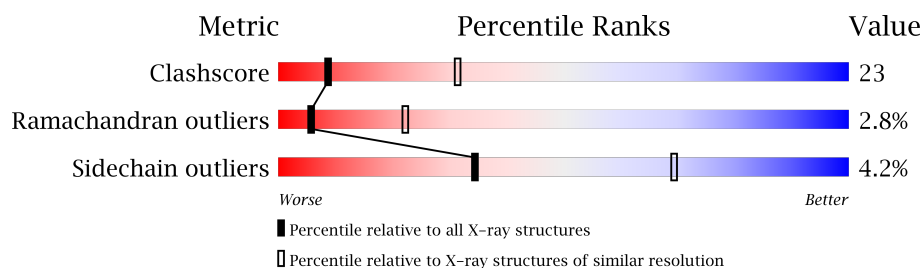
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	112137	1807 (2.90-2.90)
Ramachandran outliers	110173	1768 (2.90-2.90)
Sidechain outliers	110143	1770 (2.90-2.90)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	326	
1	E	326	
2	B	168	
2	F	168	
3	C	257	
3	G	257	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10644 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 CYCLIN-DEPENDENT KINASE 6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	293	Total	C	N	O	S	0	0	0
			2341	1499	405	428	9			
1	E	293	Total	C	N	O	S	0	0	0
			2341	1499	405	428	9			

- Molecule 2 is a protein called CYCLIN-DEPENDENT KINASE 6 INHIBITOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	155	Total	C	N	O	S	0	0	0
			1181	726	227	225	3			
2	F	155	Total	C	N	O	S	0	0	0
			1181	726	227	225	3			

- Molecule 3 is a protein called V-CYCLIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	233	Total	C	N	O	S	0	0	0
			1800	1156	297	339	8			
3	G	233	Total	C	N	O	S	0	0	0
			1800	1156	297	339	8			

There are 4 discrepancies between the modelled and reference sequences:

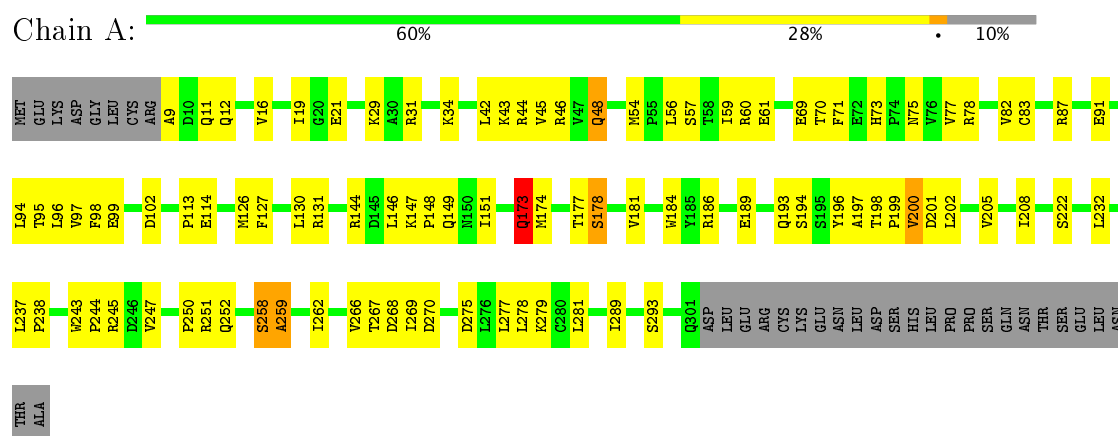
Chain	Residue	Modelled	Actual	Comment	Reference
C	163	VAL	LEU	CONFLICT	UNP O40946
C	188	LEU	LYS	CONFLICT	UNP O40946
G	163	VAL	LEU	CONFLICT	UNP O40946
G	188	LEU	LYS	CONFLICT	UNP O40946

3 Residue-property plots

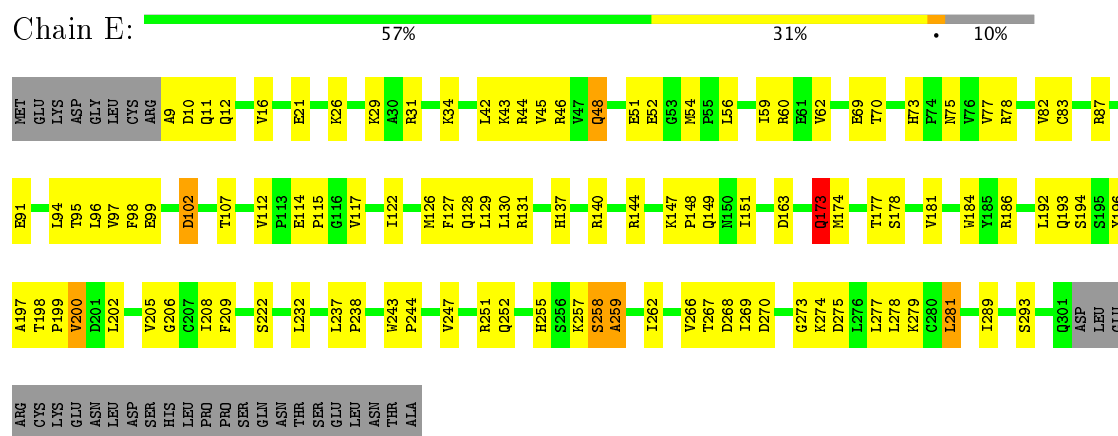
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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.

Note EDS was not executed.

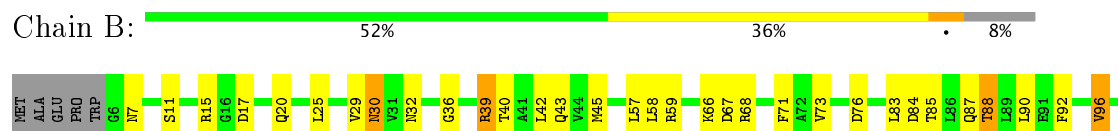
• Molecule 1: CYCLIN-DEPENDENT KINASE 6



• Molecule 1: CYCLIN-DEPENDENT KINASE 6



• Molecule 2: CYCLIN-DEPENDENT KINASE 6 INHIBITOR

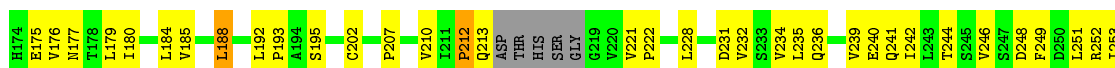
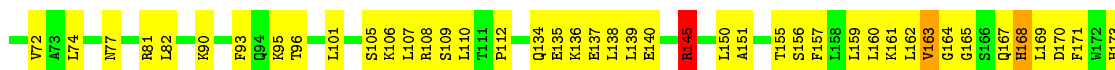
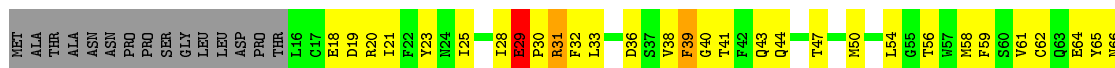




• Molecule 2: CYCLIN-DEPENDENT KINASE 6 INHIBITOR



• Molecule 3: V-CYCLIN



• Molecule 3: V-CYCLIN



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, α , β , γ	77.78 Å 146.95 Å 164.82 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.90	Depositor
% Data completeness (in resolution range)	(Not available) (15.00-2.90)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.224 , 0.262	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	10644	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.67	2/2393 (0.1%)	0.88	1/3243 (0.0%)
1	E	0.67	3/2393 (0.1%)	0.85	1/3243 (0.0%)
2	B	0.61	0/1195	0.83	0/1615
2	F	0.58	0/1195	0.82	0/1615
3	C	0.58	0/1830	0.81	2/2489 (0.1%)
3	G	0.55	0/1830	0.78	0/2489
All	All	0.62	5/10836 (0.0%)	0.83	4/14694 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	147	LYS	CD-CE	6.88	1.68	1.51
1	A	147	LYS	CD-CE	6.12	1.66	1.51
1	A	147	LYS	CE-NZ	6.05	1.64	1.49
1	E	147	LYS	CE-NZ	5.39	1.62	1.49
1	E	147	LYS	CG-CD	5.05	1.69	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	147	LYS	CD-CE-NZ	8.08	130.28	111.70
1	E	147	LYS	CD-CE-NZ	7.17	128.18	111.70
3	C	145	ARG	NE-CZ-NH1	5.60	123.10	120.30
3	C	36	ASP	N-CA-CB	-5.59	100.54	110.60

There are no chirality outliers.

There are no planarity outliers.

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	2341	0	2358	97	0
1	E	2341	0	2358	114	0
2	B	1181	0	1174	60	0
2	F	1181	0	1174	68	0
3	C	1800	0	1848	87	0
3	G	1800	0	1848	96	0
All	All	10644	0	10760	486	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 23.

The worst 5 of 486 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:E:48:GLN:H	1:E:48:GLN:NE2	1.67	0.91
1:A:173:GLN:H	1:A:173:GLN:NE2	1.68	0.91
3:C:171:PHE:O	3:C:175:GLU:HG2	1.71	0.89
3:G:56:THR:HG23	3:G:185:VAL:HG11	1.56	0.88
2:B:42:LEU:HG	2:B:73:VAL:HG21	1.57	0.86

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	291/326 (89%)	259 (89%)	27 (9%)	5 (2%)	11	36
1	E	291/326 (89%)	258 (89%)	28 (10%)	5 (2%)	11	36
2	B	153/168 (91%)	134 (88%)	17 (11%)	2 (1%)	14	43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	F	153/168 (91%)	136 (89%)	16 (10%)	1 (1%)	25	60
3	C	229/257 (89%)	198 (86%)	19 (8%)	12 (5%)	2	8
3	G	229/257 (89%)	189 (82%)	27 (12%)	13 (6%)	2	6
All	All	1346/1502 (90%)	1174 (87%)	134 (10%)	38 (3%)	6	22

5 of 38 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	258	SER
1	A	259	ALA
3	C	39	PHE
3	C	65	TYR
3	C	212	PRO

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	258/289 (89%)	249 (96%)	9 (4%)	41	75
1	E	258/289 (89%)	250 (97%)	8 (3%)	45	79
2	B	122/130 (94%)	115 (94%)	7 (6%)	24	56
2	F	122/130 (94%)	114 (93%)	8 (7%)	19	49
3	C	205/225 (91%)	196 (96%)	9 (4%)	33	67
3	G	205/225 (91%)	197 (96%)	8 (4%)	37	72
All	All	1170/1288 (91%)	1121 (96%)	49 (4%)	34	69

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	160	LEU
1	E	94	LEU
3	G	137	GLU
3	C	240	GLU

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Mol	Chain	Res	Type
1	E	102	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	223	GLN
1	E	73	HIS
3	G	94	GLN
3	C	236	GLN
1	E	12	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 carbohydrates 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 ⓘ

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.