



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 19, 2020 – 09:10 AM BST

PDB ID : 6MF6
Title : Crystal structure of budding yeast Cdc5 polo-box domain in complex with the Dbf4 polo-interacting region.
Authors : Guarne, A.; Almawi, A.W.
Deposited on : 2018-09-09
Resolution : 3.40 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.14.6
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)	:	2.14.6

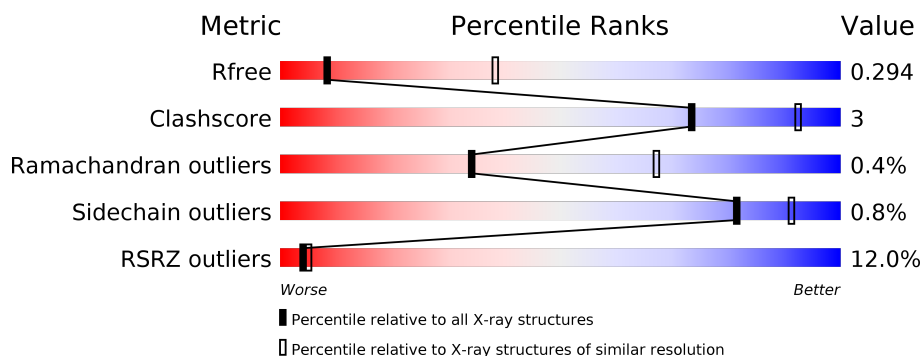
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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}	130704	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)
RSRZ outliers	127900	2173 (3.50-3.30)

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 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	290	<div> <div>11%</div> <div>76%</div> <div>8%</div> <div>16%</div> </div>
1	B	290	<div> <div>9%</div> <div>76%</div> <div>7%</div> <div>18%</div> </div>
2	C	21	<div> <div>10%</div> <div>29%</div> <div>10%</div> <div>62%</div> </div>
2	D	21	<div> <div>43%</div> <div>5%</div> <div>52%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7178 atoms, of which 3477 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 Cell cycle serine/threonine-protein kinase CDC5/MSD2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	244	Total	C	H	N	O	S	0	0	0
			3495	1164	1685	295	345	6			
1	B	239	Total	C	H	N	O	S	0	0	0
			3459	1145	1684	289	335	6			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	416	GLY	-	expression tag	UNP P32562
A	417	ALA	-	expression tag	UNP P32562
B	416	GLY	-	expression tag	UNP P32562
B	417	ALA	-	expression tag	UNP P32562

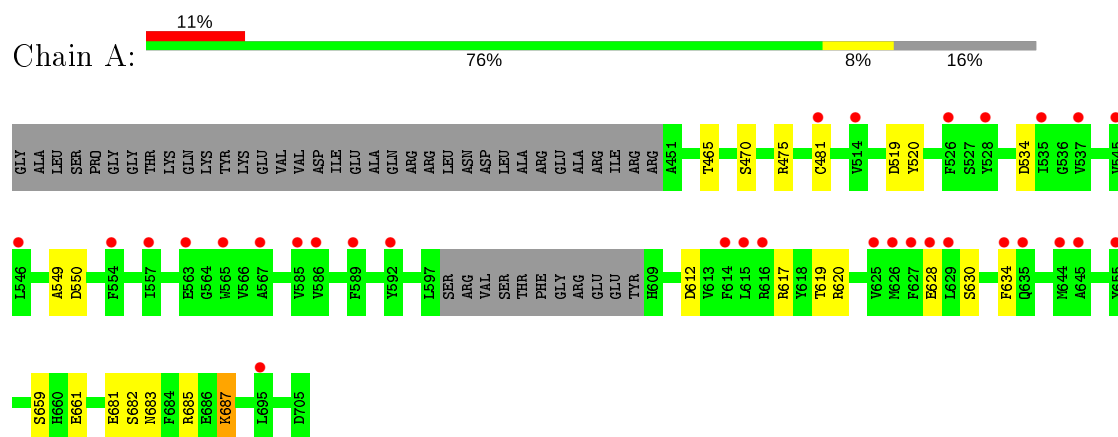
- Molecule 2 is a protein called DDK kinase regulatory subunit DBF4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	10	Total	C	H	N	O	0	0	0
			128	39	61	14	14			
2	C	8	Total	C	H	N	O	0	0	0
			96	29	47	11	9			

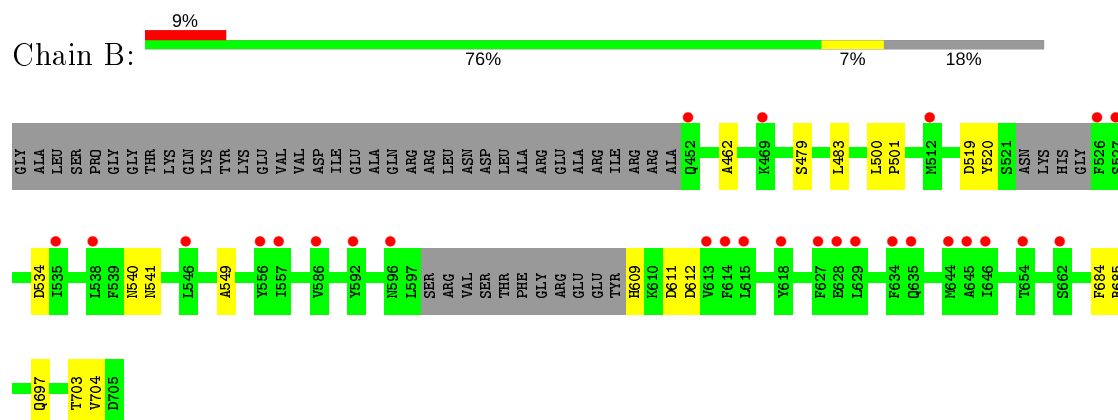
3 Residue-property plots [i](#)

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.

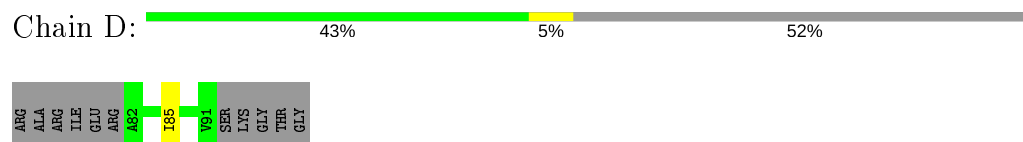
- Molecule 1: Cell cycle serine/threonine-protein kinase CDC5/MSD2



- Molecule 1: Cell cycle serine/threonine-protein kinase CDC5/MSD2



- Molecule 2: DDK kinase regulatory subunit DBF4



- Molecule 2: DDK kinase regulatory subunit DBF4



ARG	ALA	ARG	ILE	GLU	ARG	ALA	R83	S84	T85	E86	G87	G90	VAL	SER	LYS	GLY	THR	GLY

4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	135.05Å 135.05Å 75.16Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	44.21 – 3.40 67.53 – 3.40	Depositor EDS
% Data completeness (in resolution range)	99.6 (44.21-3.40) 91.9 (67.53-3.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.91 (at 3.41Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.243 , 0.283 0.252 , 0.294	Depositor DCC
R_{free} test set	561 reflections (5.14%)	wwPDB-VP
Wilson B-factor (Å ²)	129.7	Xtriage
Anisotropy	0.313	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 166.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.106 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	7178	wwPDB-VP
Average B, all atoms (Å ²)	193.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.70% 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	0.27	0/1854	0.40	0/2531
1	B	0.26	0/1818	0.39	0/2481
2	C	0.35	0/48	0.52	0/63
2	D	0.32	0/66	0.63	0/87
All	All	0.27	0/3786	0.40	0/5162

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	1810	1685	1615	14	0
1	B	1775	1684	1605	9	0
2	C	49	47	42	2	0
2	D	67	61	59	1	0
All	All	3701	3477	3321	23	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.

The worst 5 of 23 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:683:ASN:O	1:A:687:LYS:NZ	2.35	0.60
1:B:534:ASP:OD1	1:B:549:ALA:N	2.35	0.59
1:B:612:ASP:HB2	2:D:85:ILE:HG22	1.84	0.59
1:A:682:SER:O	1:A:687:LYS:NZ	2.29	0.57
1:B:540:ASN:OD1	1:B:541:ASN:N	2.38	0.56

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	240/290 (83%)	223 (93%)	16 (7%)	1 (0%)	34	67
1	B	233/290 (80%)	217 (93%)	15 (6%)	1 (0%)	34	67
2	C	6/21 (29%)	5 (83%)	1 (17%)	0	100	100
2	D	8/21 (38%)	7 (88%)	1 (12%)	0	100	100
All	All	487/622 (78%)	452 (93%)	33 (7%)	2 (0%)	34	67

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	470	SER
1	B	462	ALA

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	172/257 (67%)	170 (99%)	2 (1%)	71	85
1	B	173/257 (67%)	172 (99%)	1 (1%)	86	94
2	C	3/15 (20%)	3 (100%)	0	100	100
2	D	5/15 (33%)	5 (100%)	0	100	100
All	All	353/544 (65%)	350 (99%)	3 (1%)	81	91

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	620	ARG
1	A	687	LYS
1	B	697	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	642	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	244/290 (84%)	0.55	31 (12%) 3 4	138, 194, 264, 293	0
1	B	239/290 (82%)	0.61	27 (11%) 5 6	137, 191, 266, 295	0
2	C	8/21 (38%)	1.37	2 (25%) 0 0	182, 228, 263, 284	0
2	D	10/21 (47%)	-0.30	0 100 100	193, 225, 254, 254	0
All	All	501/622 (80%)	0.58	60 (11%) 4 5	137, 194, 265, 295	0

The worst 5 of 60 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	645	ALA	7.1
1	B	526	PHE	6.6
1	A	627	PHE	6.3
1	A	535	ILE	5.7
1	B	645	ALA	5.6

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.