



wwPDB EM Map/Model Validation Report ⓘ

Jun 29, 2016 – 03:09 PM EDT

PDB ID : 5FWK
EMDB ID: : 3337
Title : Atomic cryoEM structure of Hsp90-Cdc37-Cdk4 complex
Authors : Verba, K.A.; Wang, R.Y.R.; Arakawa, A.; Liu, Y.; Yokoyama, S.; Agard, D.A.
Deposited on : 2016-02-17
Resolution : 3.90 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027790

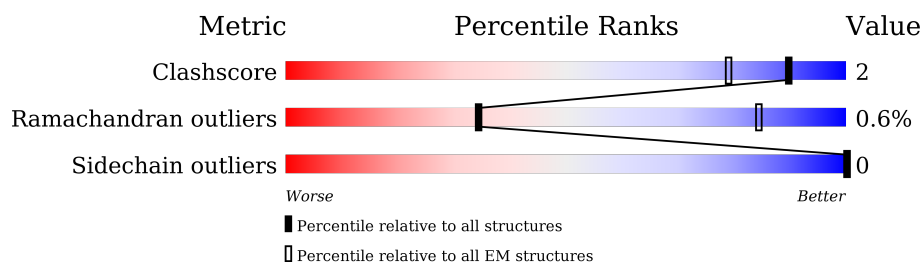
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 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)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	727	
1	B	727	
2	E	378	
3	K	310	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 26225 atoms, of which 13113 are hydrogens and 0 are deuteriums.

In the tables below, 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 HEAT SHOCK PROTEIN HSP 90 BETA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	639	Total	C	H	N	O	S	0	1
			10400	3280	5226	871	1000	23		
1	B	631	Total	C	H	N	O	S	0	1
			10243	3235	5139	857	989	23		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	EXPRESSION TAG	UNP P08238
A	-1	GLY	-	EXPRESSION TAG	UNP P08238
A	0	PHE	-	EXPRESSION TAG	UNP P08238
B	-2	GLY	-	EXPRESSION TAG	UNP P08238
B	-1	GLY	-	EXPRESSION TAG	UNP P08238
B	0	PHE	-	EXPRESSION TAG	UNP P08238

- Molecule 2 is a protein called HSP90 CO-CHAPERONE CDC37.

Mol	Chain	Residues	Atoms							AltConf	Trace
2	E	132	Total	C	H	N	O	P	S	0	1
			2174	672	1070	204	220	1	7		

- Molecule 3 is a protein called CYCLIN-DEPENDENT KINASE 4.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	K	210	Total	C	H	N	O	S	0	1
			3344	1077	1678	285	295	9		

There are 7 discrepancies between the modelled and reference sequences:

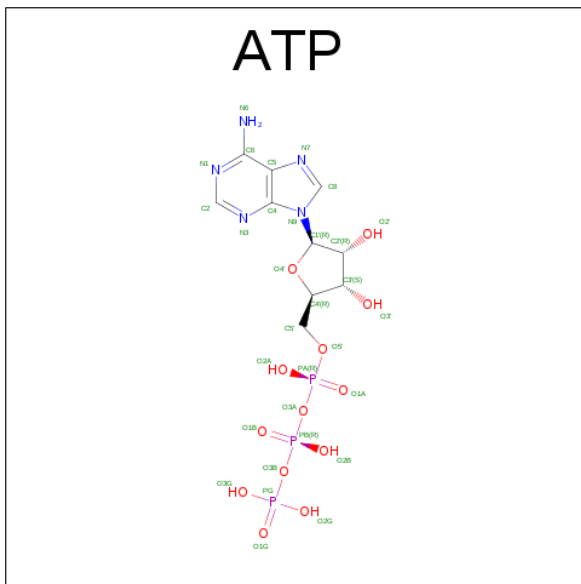
Chain	Residue	Modelled	Actual	Comment	Reference
K	-6	GLY	-	EXPRESSION TAG	UNP P11802
K	-5	ALA	-	EXPRESSION TAG	UNP P11802
K	-4	MET	-	EXPRESSION TAG	UNP P11802

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Chain	Residue	Modelled	Actual	Comment	Reference
K	-3	ASP	-	EXPRESSION TAG	UNP P11802
K	-2	PRO	-	EXPRESSION TAG	UNP P11802
K	-1	GLU	-	EXPRESSION TAG	UNP P11802
K	0	PHE	-	EXPRESSION TAG	UNP P11802

- Molecule 4 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
4	A	1	Total	C	N	O	P	0
			31	10	5	13	3	
4	B	1	Total	C	N	O	P	0
			31	10	5	13	3	


- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

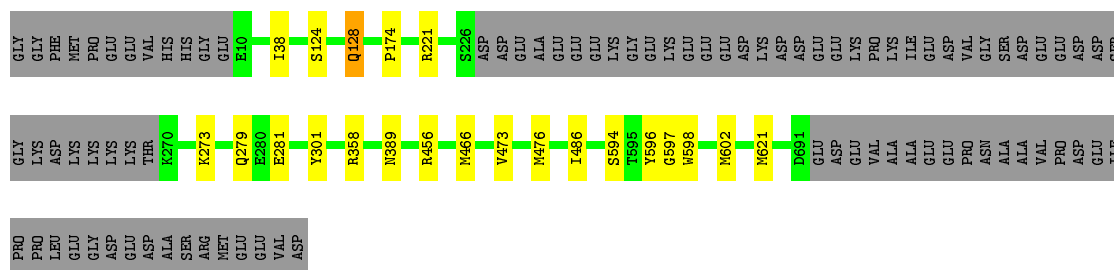
Mol	Chain	Residues	Atoms		AltConf
5	B	1	Total	Mg	0
			1	1	
5	A	1	Total	Mg	0
			1	1	

3 Residue-property plots [i](#)


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

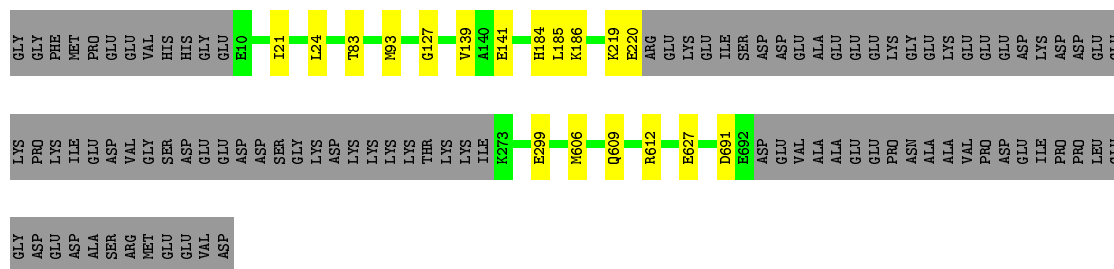
• Molecule 1: HEAT SHOCK PROTEIN HSP 90 BETA

Chain A:  85% 12%



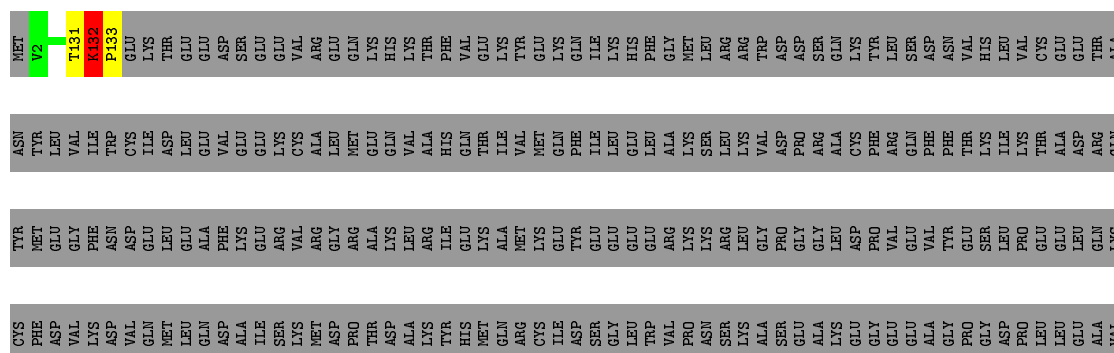
• Molecule 1: HEAT SHOCK PROTEIN HSP 90 BETA

Chain B:  84% 13%



• Molecule 2: HSP90 CO-CHAPERONE CDC37

Chain E:  34% 65%



PRO
LYS
THR
GLY
ASP
GLU
LYS
ASP
VAL
SER
VAL

● Molecule 3: CYCLIN-DEPENDENT KINASE 4



GLY
ALA
MET
PRO
GLU
PHE
MET
ALA
THR
SER
ARG
TYR
GLU
PRO
VAL
ALA
GLU
ILE
GLY
VAL
GLY
ALA
TTR
GLY
THR
VAL
TYR
LYS
ALA
ARG
ASP
PRO
HIS
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THR
ASP
ARG
GLU
187
P113
K142
P143
L161
I164
P183
L187
Q188
S189
T190
E206
R210
P233
V242
S243
L244

P245
R255
P256
H296
LYS
ASP
GLU
ASN
PRO
GLU

4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	Not provided	Depositor
Microscope	OTHER	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	44	Depositor
Minimum defocus (nm)	1400	Depositor
Maximum defocus (nm)	3800	Depositor
Magnification	22500	Depositor
Image detector	GATAN K2 SUMMIT (4K X 4K)	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ATP, SEP

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	$\# Z > 2$	RMSZ	$\# Z > 2$
1	A	0.95	1/5258 (0.0%)	0.56	0/7064
1	B	0.95	0/5188	0.55	0/6974
2	E	1.04	1/1109 (0.1%)	0.49	0/1478
3	K	0.78	0/1712	0.60	0/2332
All	All	0.94	2/13267 (0.0%)	0.56	0/17848

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	132	LYS	C-N	-5.80	1.23	1.34
1	A	301	TYR	CB-CG	-5.65	1.43	1.51

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	5174	5226	5224	12	0
1	B	5104	5139	5137	27	0
2	E	1104	1070	1069	4	0
3	K	1666	1678	1677	10	0
4	A	31	0	12	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	31	0	12	2	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
All	All	13112	13113	13131	57	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 2.

The worst 5 of 57 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:B:606:MET:CE	1:B:612:ARG:CZ	2.17	1.21
1:B:609:GLN:HB2	1:B:612:ARG:CG	1.78	1.12
1:B:609:GLN:HB2	1:B:612:ARG:HG3	1.31	1.10
1:B:609:GLN:CB	1:B:612:ARG:HG2	1.99	0.93
1:B:606:MET:HE3	1:B:612:ARG:CZ	2.00	0.90

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 PDB entries followed by that with respect to all EM entries.

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	635/727 (87%)	612 (96%)	20 (3%)	3 (0%)	34	76
1	B	627/727 (86%)	607 (97%)	18 (3%)	2 (0%)	46	82
2	E	129/378 (34%)	123 (95%)	5 (4%)	1 (1%)	24	68
3	K	208/310 (67%)	183 (88%)	21 (10%)	4 (2%)	10	53
All	All	1599/2142 (75%)	1525 (95%)	64 (4%)	10 (1%)	34	73

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	132	LYS
3	K	256	PRO
1	A	174	PRO
1	A	281	GLU
1	B	691	ASP

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 PDB entries followed by that with respect to all EM entries.

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	577/653 (88%)	577 (100%)	0	100	100
1	B	569/653 (87%)	569 (100%)	0	100	100
2	E	119/340 (35%)	119 (100%)	0	100	100
3	K	183/262 (70%)	183 (100%)	0	100	100
All	All	1448/1908 (76%)	1448 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SEP	E	13	2	7,9,10	1.55	1 (14%)	8,12,14	1.43	1 (12%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SEP	E	13	2	-	0/5/8/10	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	13	SEP	P-O1P	3.15	1.60	1.50

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	13	SEP	OG-CB-CA	3.29	111.12	108.26

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	ATP	A	725	5	26,33,33	1.15	3 (11%)	26,52,52	1.73	3 (11%)
4	ATP	B	725	5	26,33,33	1.04	1 (3%)	26,52,52	1.72	3 (11%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	ATP	A	725	5	-	0/18/38/38	0/3/3/3
4	ATP	B	725	5	-	0/18/38/38	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	725	ATP	C2'-C1'	-2.03	1.50	1.53
4	A	725	ATP	O4'-C1'	2.36	1.44	1.41
4	B	725	ATP	C5-C4	3.10	1.47	1.40
4	A	725	ATP	C5-C4	3.13	1.47	1.40

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	725	ATP	N3-C2-N1	-6.87	123.48	128.87
4	B	725	ATP	N3-C2-N1	-6.75	123.57	128.87
4	A	725	ATP	O3G-PG-O2G	2.04	114.94	107.44
4	B	725	ATP	O3G-PG-O2G	2.06	115.01	107.44
4	A	725	ATP	O2G-PG-O1G	2.24	117.95	110.63

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	725	ATP	3	0
4	B	725	ATP	2	0

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.