

wwPDB X-ray Structure Validation Summary Report (i)

Oct 19, 2023 – 03:12 AM EDT

PDB ID : 2HAK

Title: Catalytic and ubiqutin-associated domains of MARK1/PAR-1

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Mandelkow, E.

Deposited on : 2006-06-13

Resolution : 2.60 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 (i) 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 (1)) were used in the production of this report:

MolProbity : 4.02b-467

Xtriage (Phenix) : 1.13 EDS : 2.36

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

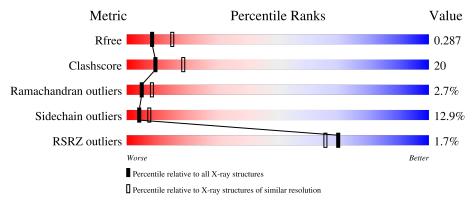
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\mathring{A})}) \end{array}$
R_{free}	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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 <=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	328	62%	27%	5% • 6%
1	В	328	41%	10%	15%
1	С	328	59%	28%	5% • 5%
1	D	328	57%	31%	5% • 6%
1	Е	328	66%	25%	6% •

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Mol	Chain	Length	Quality of	f chain	
1	T.	200	.% •		
1	Г	328	57%	32%	7% •
			3%		
1	G	328	42%	37%	10% • 9%
			5%		
1	H	328	52%	29%	• 16%



2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 19579 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 Serine/threonine-protein kinase MARK1.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	A	309	Total	С	N	О	S	0	0	0
1	A	309	2490	1599	426	453	12	U	0	
1	В	279	Total	С	N	О	S	0	0	0
1	Б	219	2231	1434	380	405	12	U	U	
1	С	310	Total	С	N	О	S	0	0	0
1		310	2512	1612	432	456	12	U	U	U
1	D	309	Total	С	N	Ο	S	0	0	0
1	D	309	2503	1607	432	452	12	U		0
1	Е	318	Total	С	N	O	S	0	0	0
1	ш	310	2538	1627	437	461	13	U		
1	F	318	Total	С	N	O	S	0	0	0
1	I.	310	2562	1641	439	469	13	U	U	
1	G	297	Total	С	Ν	O	S	0	0	0
1	G	291	2349	1506	402	429	12	U	0	
1	Н	277	Total	С	N	О	S	0	0	0
1	11	211	2184	1405	367	400	12	U		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	37	GLY	-	cloning artifact	UNP Q9P0L2
В	37	GLY	-	cloning artifact	UNP Q9P0L2
С	37	GLY	-	cloning artifact	UNP Q9P0L2
D	37	GLY	-	cloning artifact	UNP Q9P0L2
Е	37	GLY	-	cloning artifact	UNP Q9P0L2
F	37	GLY	-	cloning artifact	UNP Q9P0L2
G	37	GLY	-	cloning artifact	UNP Q9P0L2
Н	37	GLY	-	cloning artifact	UNP Q9P0L2

• Molecule 2 is water.



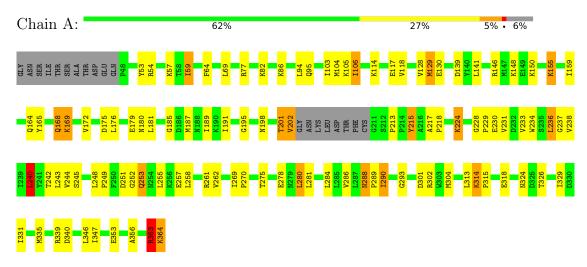
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	27	Total O 27 27	0	0
2	В	17	Total O 17 17	0	0
2	С	47	Total O 47 47	0	0
2	D	24	Total O 24 24	0	0
2	Е	35	Total O 35 35	0	0
2	F	37	Total O 37 37	0	0
2	G	14	Total O 14 14	0	0
2	Н	9	Total O 9 9	0	0



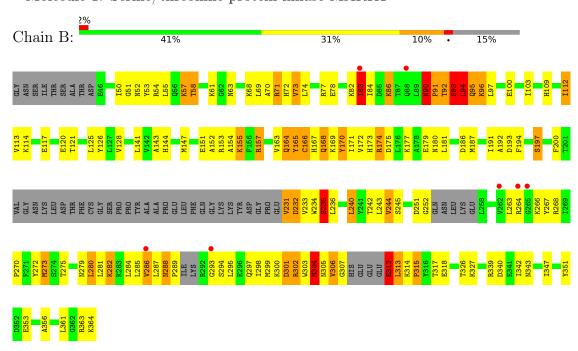
3 Residue-property plots (i)

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: Serine/threonine-protein kinase MARK1

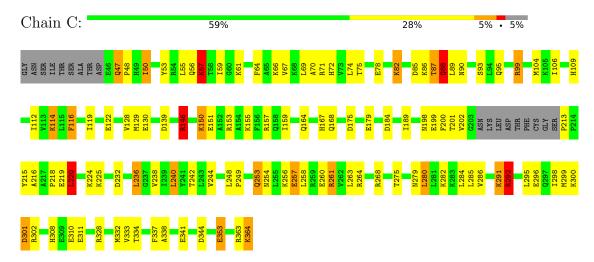


• Molecule 1: Serine/threonine-protein kinase MARK1

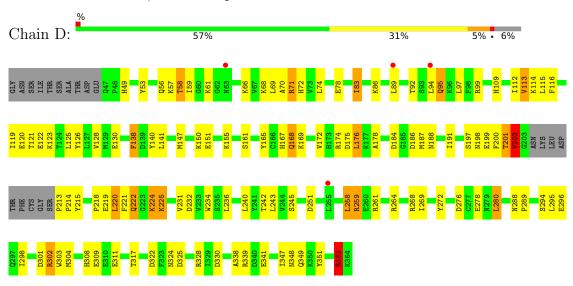


• Molecule 1: Serine/threonine-protein kinase MARK1

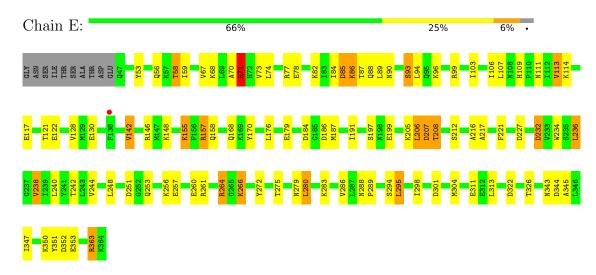




• Molecule 1: Serine/threonine-protein kinase MARK1

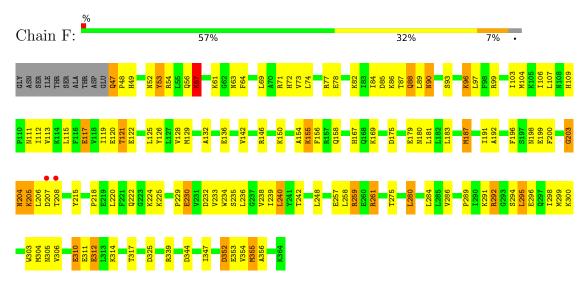


• Molecule 1: Serine/threonine-protein kinase MARK1

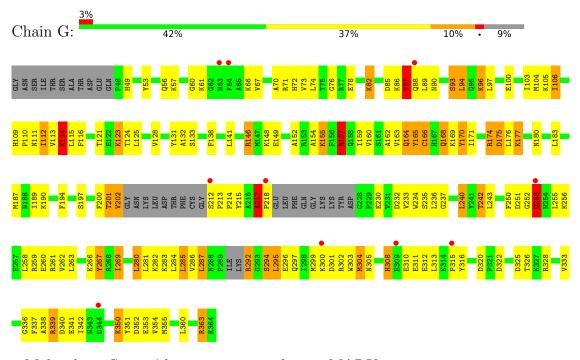


• Molecule 1: Serine/threonine-protein kinase MARK1

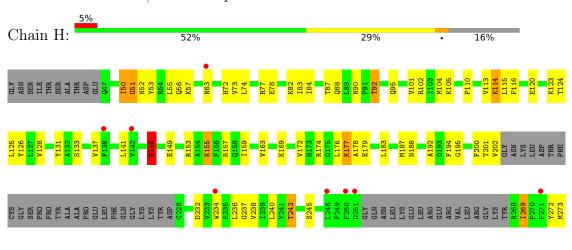




• Molecule 1: Serine/threonine-protein kinase MARK1



• Molecule 1: Serine/threonine-protein kinase MARK1









4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	110.68Å 116.47Å 285.75Å	Danagitan
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 - 2.60	Depositor
Resolution (A)	49.68 - 2.60	EDS
% Data completeness	99.3 (10.00-2.60)	Depositor
(in resolution range)	99.3 (49.68-2.60)	EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.28 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
D.D.	0.212 , 0.290	Depositor
R, R_{free}	0.213 , 0.287	DCC
R_{free} test set	2844 reflections (2.52%)	wwPDB-VP
Wilson B-factor (Å ²)	50.7	Xtriage
Anisotropy	0.181	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.35 , 49.9	EDS
L-test for twinning ²	$< L > = 0.47, < L^2> = 0.30$	Xtriage
Estimated twinning fraction	0.023 for k,h,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	19579	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 9.04% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

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		Во	ond lengths	Bond angles		
WIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z >5	
1	A	1.30	9/2539~(0.4%)	1.17	11/3421 (0.3%)	
1	В	1.31	$6/2269 \; (0.3\%)$	1.27	17/3055 (0.6%)	
1	С	1.41	$11/2561 \ (0.4\%)$	1.25	10/3448 (0.3%)	
1	D	1.33	$11/2552 \ (0.4\%)$	1.16	10/3436 (0.3%)	
1	Е	1.33	8/2589 (0.3%)	1.22	10/3496 (0.3%)	
1	F	1.36	$12/2613 \; (0.5\%)$	1.20	14/3524 (0.4%)	
1	G	1.11	2/2394~(0.1%)	1.06	2/3232 (0.1%)	
1	Н	1.08	0/2225	1.01	4/3007 (0.1%)	
All	All	1.29	59/19742 (0.3%)	1.17	78/26619 (0.3%)	

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a maintenain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	В	0	1
1	Е	0	1
1	F	0	1
1	G	0	3
All	All	0	7

The worst 5 of 59 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\operatorname{\mathring{A}})$	$\operatorname{Ideal}(\operatorname{\AA})$
1	С	353	GLU	CG-CD	11.27	1.68	1.51
1	С	353	GLU	CB-CG	9.91	1.71	1.52
1	В	312	GLU	CG-CD	9.07	1.65	1.51
1	В	363	ARG	CG-CD	-8.25	1.31	1.51
1	A	224	LYS	CE-NZ	7.63	1.68	1.49

The worst 5 of 78 bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$Ideal(^{o})$
1	В	77	ARG	NE-CZ-NH1	9.57	125.08	120.30
1	A	363	ARG	NE-CZ-NH2	-9.11	115.74	120.30
1	A	77	ARG	NE-CZ-NH1	8.97	124.78	120.30
1	В	153	ARG	NE-CZ-NH2	-8.35	116.12	120.30
1	A	77	ARG	NE-CZ-NH2	-8.05	116.27	120.30

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	363	ARG	Peptide
1	В	90	ASN	Peptide
1	Е	363	ARG	Peptide
1	F	203	GLY	Peptide
1	G	114	LYS	Peptide

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	2490	0	2520	77	0
1	В	2231	0	2248	142	1
1	С	2512	0	2551	79	1
1	D	2503	0	2547	77	0
1	Е	2538	0	2541	74	0
1	F	2562	0	2579	89	0
1	G	2349	0	2332	171	0
1	Н	2184	0	2166	64	0
2	A	27	0	0	2	0
2	В	17	0	0	2	0
2	С	47	0	0	8	0
2	D	24	0	0	2	0
2	Е	35	0	0	3	0
2	F	37	0	0	3	0
2	G	14	0	0	11	0
2	Н	9	0	0	2	0
All	All	19579	0	19484	761	1



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 20.

The worst 5 of 761 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} \text{Interatomic} \\ \text{distance (Å)} \end{array}$	Clash overlap (Å)
1:A:224:LYS:CE	1:A:224:LYS:NZ	1.68	1.55
1:D:347:ILE:CD1	1:D:347:ILE:CG1	1.78	1.54
1:G:164:GLN:NE2	1:G:315:PRO:HB3	1.37	1.37
1:B:125:LEU:HD12	1:B:126:TYR:N	1.56	1.21
1:A:290:ILE:HD12	1:A:290:ILE:O	1.51	1.11

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
1:B:327:LYS:NZ	1:C:364:LYS:O[4_455]	2.11	0.09

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	Perce	ntiles
1	A	305/328~(93%)	290 (95%)	12 (4%)	3 (1%)	15	32
1	В	269/328~(82%)	230 (86%)	20 (7%)	19 (7%)	1	1
1	С	306/328 (93%)	290 (95%)	12 (4%)	4 (1%)	12	24
1	D	305/328~(93%)	279 (92%)	22 (7%)	4 (1%)	12	24
1	E	316/328 (96%)	294 (93%)	18 (6%)	4 (1%)	12	24
1	F	316/328 (96%)	293 (93%)	17 (5%)	6 (2%)	8	15
1	G	289/328 (88%)	241 (83%)	33 (11%)	15 (5%)	2	2
1	Н	271/328 (83%)	237 (88%)	25 (9%)	9 (3%)	4	6
All	All	2377/2624 (91%)	2154 (91%)	159 (7%)	64 (3%)	5	8



5 of 64 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	В	90	ASN
1	В	93	SER
1	В	94	LEU
1	В	301	ASP
1	В	306	VAL

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	$269/290 \ (93\%)$	237 (88%)	32 (12%)	5 9
1	В	240/290 (83%)	203 (85%)	37 (15%)	2 4
1	С	272/290 (94%)	238 (88%)	34 (12%)	4 8
1	D	271/290 (93%)	231 (85%)	40 (15%)	3 5
1	E	271/290 (93%)	244 (90%)	27 (10%)	7 14
1	F	277/290 (96%)	247 (89%)	30 (11%)	6 12
1	G	249/290 (86%)	208 (84%)	41 (16%)	2 3
1	Н	232/290 (80%)	205 (88%)	27 (12%)	5 10
All	All	2081/2320 (90%)	1813 (87%)	268 (13%)	4 7

5 of 268 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	295	LEU
1	G	350	LYS
1	Н	269	ILE
1	С	302	ARG
1	С	291	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:



Mol	Chain	Res	Type
1	F	90	ASN
1	G	164	GLN
1	F	253	GLN
1	G	56	GLN
1	G	198	ASN

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 monosaccharides 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, 95^{th} 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>	$\# \mathrm{RSRZ}{>}2$	$\mathbf{OWAB}(\mathbf{\mathring{A}}^2)$	Q < 0.9
1	A	309/328 (94%)	-0.15	0 100 100	25, 42, 77, 89	0
1	В	279/328 (85%)	0.03	7 (2%) 57 51	25, 52, 81, 93	0
1	С	310/328 (94%)	-0.22	0 100 100	20, 36, 62, 73	0
1	D	309/328 (94%)	-0.12	4 (1%) 77 73	26, 43, 72, 84	0
1	E	318/328 (96%)	-0.22	1 (0%) 94 93	23, 40, 59, 72	0
1	F	318/328 (96%)	-0.18	2 (0%) 89 88	20, 39, 64, 75	0
1	G	297/328~(90%)	0.14	10 (3%) 45 38	38, 62, 95, 101	0
1	Н	277/328 (84%)	0.14	16 (5%) 23 17	34, 60, 87, 94	0
All	All	2417/2624 (92%)	-0.08	40 (1%) 70 66	20, 46, 81, 101	0

The worst 5 of 40 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Н	286	VAL	6.0
1	Н	250	PHE	5.2
1	Н	284	LEU	4.5
1	Н	285	LEU	4.3
1	G	63	ASN	4.3

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.

