



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 31, 2021 – 11:43 PM EDT

PDB ID : 1WMK
Title : Human death-associated kinase DRP-1, mutant S308D d40
Authors : Kursula, P.; Shani, G.; Kimchi, A.; Wilmanns, M.
Deposited on : 2004-07-11
Resolution : 3.60 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 ⓘ 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	:	2.23.2
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)	:	2.23.2

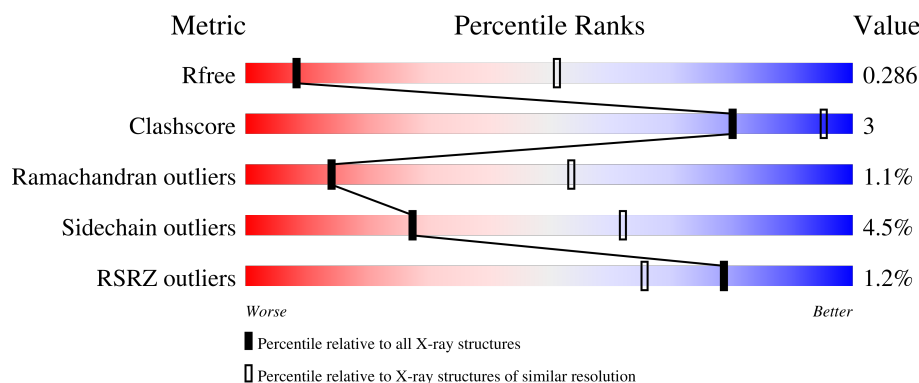
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.60 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1257 (3.70-3.50)
Clashscore	141614	1353 (3.70-3.50)
Ramachandran outliers	138981	1307 (3.70-3.50)
Sidechain outliers	138945	1307 (3.70-3.50)
RSRZ outliers	127900	1161 (3.70-3.50)

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	321	
1	B	321	
1	C	321	
1	D	321	
1	E	321	

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Mol	Chain	Length	Quality of chain
1	F	321	<div><div><div>%</div><div><div></div><div>81%</div><div>12%</div><div>• 6%</div></div></div></div>
1	G	321	<div><div><div>2%</div><div><div></div><div>85%</div><div>10%</div><div>• •</div></div></div></div>
1	H	321	<div><div><div>%</div><div><div></div><div>82%</div><div>11%</div><div>• 5%</div></div></div></div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 19951 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 Death-associated protein kinase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	303	Total	C	N	O	S	0	0	0
			2467	1578	421	464	4			
1	E	313	Total	C	N	O	S	0	0	0
			2517	1608	431	474	4			
1	C	303	Total	C	N	O	S	0	0	0
			2467	1578	421	464	4			
1	B	314	Total	C	N	O	S	0	0	0
			2522	1611	432	475	4			
1	F	303	Total	C	N	O	S	0	0	0
			2467	1578	421	464	4			
1	D	314	Total	C	N	O	S	0	0	0
			2522	1611	432	475	4			
1	H	304	Total	C	N	O	S	0	0	0
			2472	1581	422	465	4			
1	G	313	Total	C	N	O	S	0	0	0
			2517	1608	431	474	4			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	cloning artifact	UNP Q9UIK4
A	308	ASP	SER	engineered mutation	UNP Q9UIK4
B	0	GLY	-	cloning artifact	UNP Q9UIK4
B	308	ASP	SER	engineered mutation	UNP Q9UIK4
C	0	GLY	-	cloning artifact	UNP Q9UIK4
C	308	ASP	SER	engineered mutation	UNP Q9UIK4
D	0	GLY	-	cloning artifact	UNP Q9UIK4
D	308	ASP	SER	engineered mutation	UNP Q9UIK4
E	0	GLY	-	cloning artifact	UNP Q9UIK4
E	308	ASP	SER	engineered mutation	UNP Q9UIK4
F	0	GLY	-	cloning artifact	UNP Q9UIK4
F	308	ASP	SER	engineered mutation	UNP Q9UIK4
G	0	GLY	-	cloning artifact	UNP Q9UIK4

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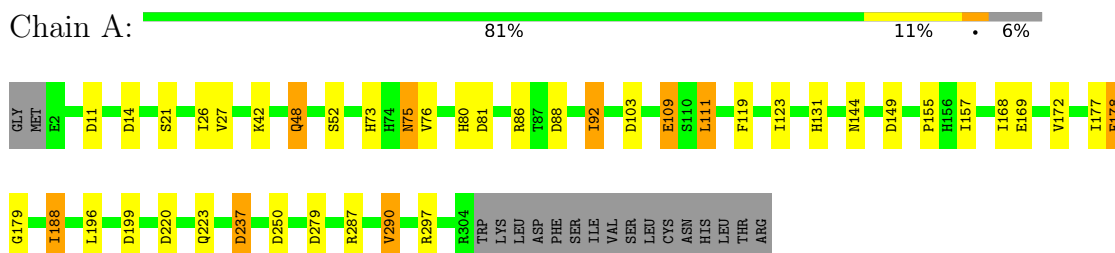
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Chain	Residue	Modelled	Actual	Comment	Reference
G	308	ASP	SER	engineered mutation	UNP Q9UIK4
H	0	GLY	-	cloning artifact	UNP Q9UIK4
H	308	ASP	SER	engineered mutation	UNP Q9UIK4

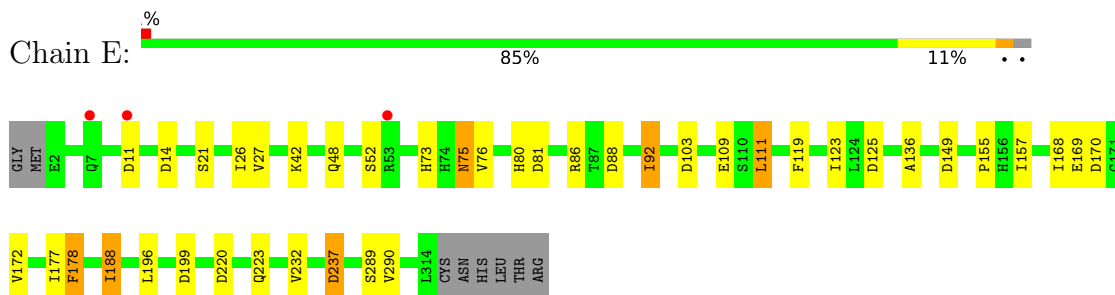
3 Residue-property plots [i](#)

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.

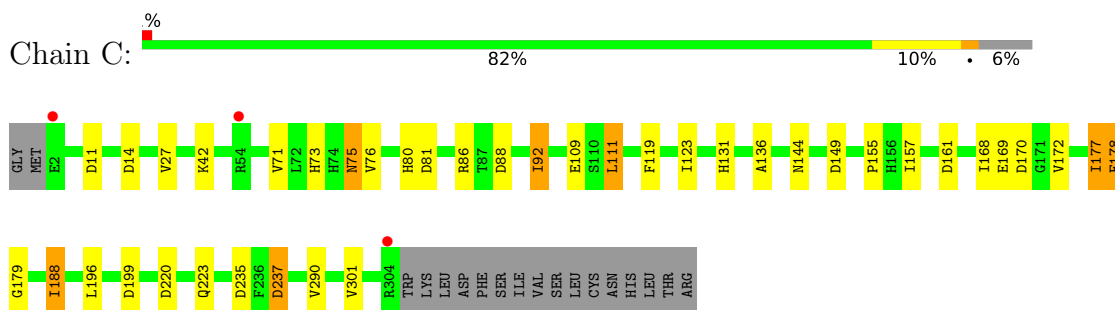
- Molecule 1: Death-associated protein kinase 2



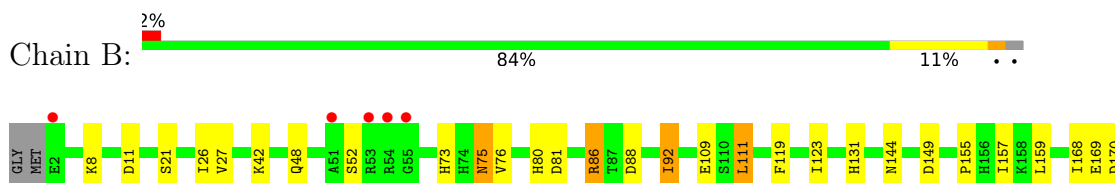
- Molecule 1: Death-associated protein kinase 2



- Molecule 1: Death-associated protein kinase 2

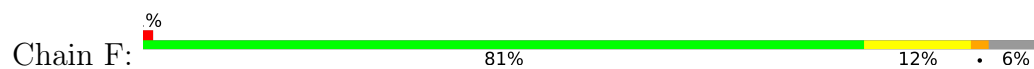


- Molecule 1: Death-associated protein kinase 2

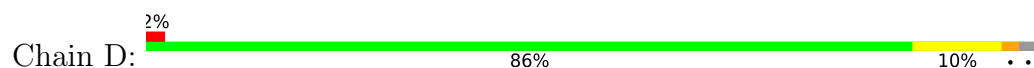




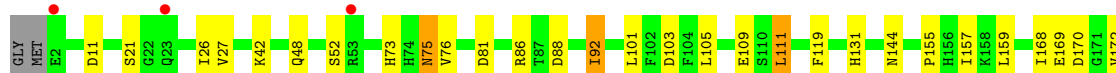
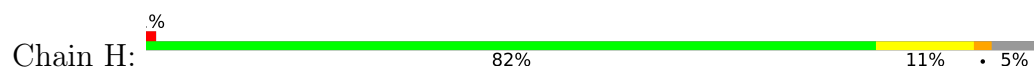
- Molecule 1: Death-associated protein kinase 2



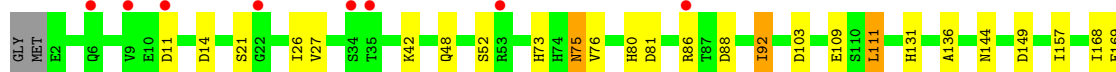
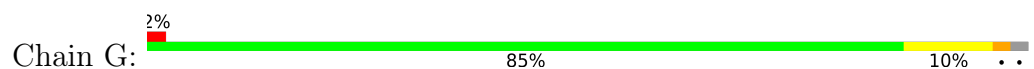
- Molecule 1: Death-associated protein kinase 2



- Molecule 1: Death-associated protein kinase 2



- Molecule 1: Death-associated protein kinase 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	86.19Å 143.29Å 255.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.60 19.99 – 3.60	Depositor EDS
% Data completeness (in resolution range)	100.0 (20.00-3.60) 100.0 (19.99-3.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.17	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.15 (at 3.62Å)	Xtriage
Refinement program	REFMAC 5.2.0000	Depositor
R, R_{free}	0.276 , 0.296 0.266 , 0.286	Depositor DCC
R_{free} test set	1864 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	81.2	Xtriage
Anisotropy	0.558	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.20 , 64.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.33$, $\langle L^2 \rangle = 0.16$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	19951	wwPDB-VP
Average B, all atoms (Å ²)	134.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.90% 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	0.34	0/2514	0.65	11/3391 (0.3%)
1	B	0.34	0/2569	0.66	9/3468 (0.3%)
1	C	0.34	0/2514	0.65	10/3391 (0.3%)
1	D	0.34	0/2569	0.65	11/3468 (0.3%)
1	E	0.33	0/2564	0.65	11/3461 (0.3%)
1	F	0.31	0/2514	0.64	10/3391 (0.3%)
1	G	0.32	0/2564	0.64	11/3461 (0.3%)
1	H	0.34	0/2519	0.65	10/3398 (0.3%)
All	All	0.33	0/20327	0.65	83/27429 (0.3%)

There are no bond length outliers.

The worst 5 of 83 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	81	ASP	CB-CG-OD2	6.82	124.44	118.30
1	F	81	ASP	CB-CG-OD2	6.67	124.31	118.30
1	C	81	ASP	CB-CG-OD2	6.59	124.23	118.30
1	B	199	ASP	CB-CG-OD2	6.40	124.06	118.30
1	B	81	ASP	CB-CG-OD2	6.38	124.05	118.30

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	2467	0	2476	18	0
1	B	2522	0	2498	18	0
1	C	2467	0	2476	16	0
1	D	2522	0	2498	11	0
1	E	2517	0	2496	12	0
1	F	2467	0	2476	14	0
1	G	2517	0	2496	12	0
1	H	2472	0	2478	13	0
All	All	19951	0	19894	107	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 107 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:C:235:ASP:OD2	1:D:254:LYS:NZ	2.30	0.64
1:D:75:ASN:ND2	1:D:157:ILE:O	2.31	0.64
1:A:287:ARG:HD3	1:B:8:LYS:HE2	1.81	0.63
1:E:178:PHE:HB2	1:E:188:ILE:HD12	1.83	0.60
1:F:178:PHE:HB2	1:F:188:ILE:HD12	1.84	0.60

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	301/321 (94%)	273 (91%)	25 (8%)	3 (1%)	15 55
1	B	312/321 (97%)	282 (90%)	25 (8%)	5 (2%)	9 46
1	C	301/321 (94%)	274 (91%)	25 (8%)	2 (1%)	22 61
1	D	312/321 (97%)	282 (90%)	26 (8%)	4 (1%)	12 50

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	311/321 (97%)	281 (90%)	27 (9%)	3 (1%)	15	55
1	F	301/321 (94%)	274 (91%)	25 (8%)	2 (1%)	22	61
1	G	311/321 (97%)	281 (90%)	27 (9%)	3 (1%)	15	55
1	H	302/321 (94%)	269 (89%)	29 (10%)	4 (1%)	12	50
All	All	2451/2568 (95%)	2216 (90%)	209 (8%)	26 (1%)	14	53

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	86	ARG
1	A	111	LEU
1	E	86	ARG
1	E	111	LEU
1	C	86	ARG

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	271/289 (94%)	259 (96%)	12 (4%)	28	63
1	B	271/289 (94%)	259 (96%)	12 (4%)	28	63
1	C	271/289 (94%)	259 (96%)	12 (4%)	28	63
1	D	271/289 (94%)	259 (96%)	12 (4%)	28	63
1	E	271/289 (94%)	259 (96%)	12 (4%)	28	63
1	F	271/289 (94%)	259 (96%)	12 (4%)	28	63
1	G	271/289 (94%)	258 (95%)	13 (5%)	25	60
1	H	271/289 (94%)	259 (96%)	12 (4%)	28	63
All	All	2168/2312 (94%)	2071 (96%)	97 (4%)	27	62

5 of 97 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	223	GLN
1	D	290	VAL
1	F	290	VAL
1	D	168	ILE
1	H	111	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	144	ASN
1	D	144	ASN
1	G	74	HIS
1	D	74	HIS
1	D	223	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 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, 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	303/321 (94%)	-0.60	0 100 100	35, 115, 216, 226	0
1	B	314/321 (97%)	-0.52	5 (1%) 72 57	32, 116, 224, 226	0
1	C	303/321 (94%)	-0.52	3 (0%) 82 70	34, 122, 214, 226	0
1	D	314/321 (97%)	-0.50	6 (1%) 66 51	46, 131, 216, 226	0
1	E	313/321 (97%)	-0.41	3 (0%) 82 70	40, 129, 226, 226	0
1	F	303/321 (94%)	-0.36	2 (0%) 87 78	58, 159, 226, 226	0
1	G	313/321 (97%)	-0.41	8 (2%) 56 40	35, 135, 226, 226	0
1	H	304/321 (94%)	-0.56	3 (0%) 82 70	44, 124, 218, 226	0
All	All	2467/2568 (96%)	-0.48	30 (1%) 79 66	32, 129, 225, 226	0

The worst 5 of 30 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	53	ARG	6.0
1	B	54	ARG	5.7
1	G	11	ASP	4.8
1	B	2	GLU	4.5
1	B	53	ARG	4.0

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 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.