



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 05:06 am BST

PDB ID : 4I1F
Title : Structure of Parkin-S223P E3 ligase
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Deposited on : 2012-11-20
Resolution : 1.58 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 : 2.11
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) : 2.11

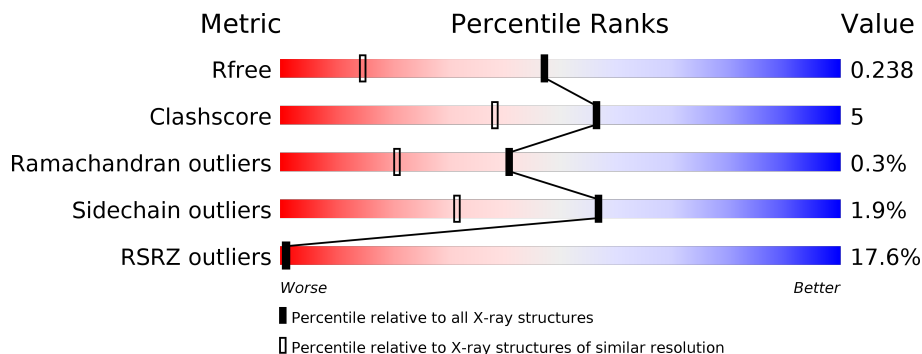
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.58 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	5534 (1.60-1.56)
Clashscore	141614	5861 (1.60-1.56)
Ramachandran outliers	138981	5708 (1.60-1.56)
Sidechain outliers	138945	5703 (1.60-1.56)
RSRZ outliers	127900	5431 (1.60-1.56)

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	325	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	ZN	A	502	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2679 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 E3 ubiquitin-protein ligase parkin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	306	2403	1493	436	435	39	0	1	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	223	PRO	SER	ENGINEERED MUTATION	UNP O60260

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	8	Total	Zn	0	0
			8	8		

- Molecule 3 is BARIUM ION (three-letter code: BA) (formula: Ba).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Ba	0	0
			1	1		

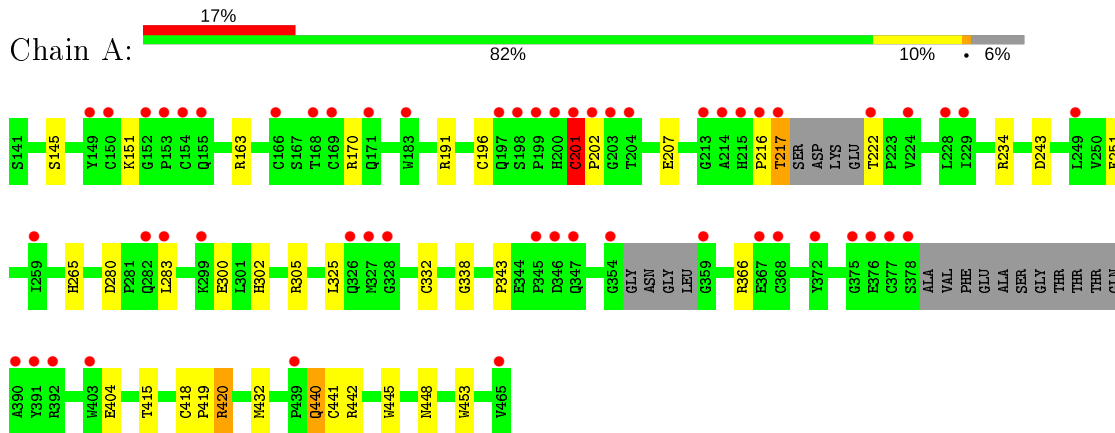
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	267	Total	O	0	0
			267	267		

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 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: E3 ubiquitin-protein ligase parkin



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	86.95Å 133.16Å 65.39Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	72.81 – 1.58 36.40 – 1.58	Depositor EDS
% Data completeness (in resolution range)	99.5 (72.81-1.58) 99.5 (36.40-1.58)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 1.58Å)	Xtrriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.205 , 0.245 0.201 , 0.238	Depositor DCC
R_{free} test set	2649 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	22.3	Xtrriage
Anisotropy	0.059	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 52.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2679	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.51% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical 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

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, BA

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	1.28	9/2468 (0.4%)	1.20	10/3341 (0.3%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	201	CYS	C-O	10.64	1.43	1.23
1	A	453	TRP	CD1-NE1	9.10	1.53	1.38
1	A	145	SER	CB-OG	-6.67	1.33	1.42
1	A	145	SER	CA-CB	6.20	1.62	1.52
1	A	445	TRP	CD2-CE2	5.84	1.48	1.41
1	A	453	TRP	CD2-CE2	5.62	1.48	1.41
1	A	445	TRP	CG-CD1	5.57	1.44	1.36
1	A	418	CYS	CB-SG	-5.06	1.73	1.81
1	A	207	GLU	CD-OE2	-5.02	1.20	1.25

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	163	ARG	NE-CZ-NH2	-6.87	116.86	120.30
1	A	234	ARG	NE-CZ-NH1	-6.83	116.88	120.30
1	A	191	ARG	NE-CZ-NH2	-6.83	116.89	120.30
1	A	420	ARG	NE-CZ-NH1	6.60	123.60	120.30
1	A	404	GLU	OE1-CD-OE2	-5.83	116.30	123.30
1	A	163	ARG	NE-CZ-NH1	5.68	123.14	120.30
1	A	420	ARG	NE-CZ-NH2	-5.46	117.57	120.30
1	A	325	LEU	CB-CG-CD1	-5.22	102.12	111.00
1	A	243	ASP	CB-CG-OD2	-5.21	113.61	118.30
1	A	251	PHE	CB-CG-CD1	-5.07	117.25	120.80

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	2403	0	2272	23	0
2	A	8	0	0	2	0
3	A	1	0	0	1	0
4	A	267	0	0	2	0
All	All	2679	0	2272	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 5.

All (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:201:CYS:O	3:A:509:BA:BA	1.61	1.06
1:A:196:CYS:HG	2:A:502:ZN:ZN	0.80	0.93
1:A:432:MET:HE1	1:A:448:ASN:HB2	1.66	0.77
1:A:415:THR:OG1	4:A:776:HOH:O	2.08	0.72
1:A:196:CYS:SG	1:A:201:CYS:HB3	2.31	0.70
1:A:432:MET:CE	1:A:448:ASN:HB2	2.23	0.69
1:A:420:ARG:HD2	1:A:441:CYS:SG	2.34	0.68
1:A:265:HIS:HD2	4:A:629:HOH:O	1.78	0.67
1:A:217:THR:O	1:A:217:THR:OG1	2.11	0.67
1:A:196:CYS:SG	2:A:502:ZN:ZN	1.82	0.64
1:A:302:HIS:CD2	1:A:305:ARG:HE	2.18	0.62
1:A:440:GLN:H	1:A:440:GLN:CD	2.03	0.60
1:A:201:CYS:SG	1:A:202:PRO:HD2	2.47	0.55
1:A:216:PRO:O	1:A:217:THR:C	2.48	0.52
1:A:222:THR:O	1:A:222:THR:HG23	2.12	0.50
1:A:343:PRO:HG2	1:A:366:ARG:NH1	2.30	0.47
1:A:196:CYS:SG	1:A:201:CYS:CB	3.04	0.45
1:A:442:ARG:HD2	1:A:442:ARG:HA	1.79	0.45
1:A:300:GLU:OE2	1:A:302:HIS:HB2	2.18	0.44
1:A:332:CYS:O	1:A:338:GLY:HA2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:280:ASP:HB3	1:A:283:LEU:HB2	2.02	0.42
1:A:432:MET:HE3	1:A:448:ASN:H	1.85	0.41
1:A:302:HIS:CD2	1:A:305:ARG:NE	2.88	0.41

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	299/325 (92%)	286 (96%)	12 (4%)	1 (0%)	41 21

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	151	LYS

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	268/281 (95%)	263 (98%)	5 (2%)	57 31

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	170	ARG
1	A	201	CYS
1	A	217	THR
1	A	419	PRO
1	A	440	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	178	GLN
1	A	265	HIS
1	A	302	HIS

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](#)

Of 9 ligands modelled in this entry, 9 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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

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	306/325 (94%)	0.98	54 (17%) 1 1	13, 24, 49, 61	15 (4%)

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	201	CYS	7.8
1	A	168	THR	5.5
1	A	392	ARG	5.4
1	A	199	PRO	5.1
1	A	155	GLN	5.0
1	A	378	SER	4.9
1	A	154	CYS	4.8
1	A	391	TYR	4.7
1	A	377	CYS	4.6
1	A	169	CYS	4.3
1	A	200	HIS	4.2
1	A	390	ALA	4.2
1	A	354	GLY	4.2
1	A	347	GLN	4.0
1	A	153	PRO	4.0
1	A	202	PRO	4.0
1	A	214	ALA	3.7
1	A	216	PRO	3.7
1	A	299	LYS	3.6
1	A	152	GLY	3.3
1	A	215	HIS	3.2
1	A	203	GLY	3.2
1	A	228	LEU	3.1
1	A	359	GLY	3.1
1	A	217	THR	3.1
1	A	346	ASP	3.0
1	A	198	SER	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	283	LEU	2.9
1	A	150	CYS	2.9
1	A	183	TRP	2.8
1	A	328	GLY	2.8
1	A	282	GLN	2.8
1	A	224	VAL	2.7
1	A	213	GLY	2.7
1	A	368	CYS	2.5
1	A	403	TRP	2.5
1	A	171	GLN	2.4
1	A	345	PRO	2.3
1	A	222	THR	2.3
1	A	326	GLN	2.2
1	A	439	PRO	2.2
1	A	229	ILE	2.2
1	A	465	VAL	2.2
1	A	367	GLU	2.2
1	A	249	LEU	2.2
1	A	204	THR	2.1
1	A	372	TYR	2.1
1	A	149	TYR	2.1
1	A	197	GLN	2.1
1	A	259	ILE	2.1
1	A	327	MET	2.0
1	A	375	GLY	2.0
1	A	166	CYS	2.0
1	A	376	GLU	2.0

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 carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	ZN	A	501	1/1	0.89	0.08	23,23,23,23	1
3	BA	A	509	1/1	0.92	0.06	38,38,38,38	1
2	ZN	A	502	1/1	0.94	0.07	33,33,33,33	0
2	ZN	A	505	1/1	0.97	0.06	26,26,26,26	0
2	ZN	A	507	1/1	0.97	0.08	28,28,28,28	0
2	ZN	A	506	1/1	0.99	0.04	38,38,38,38	0
2	ZN	A	504	1/1	1.00	0.10	17,17,17,17	0
2	ZN	A	503	1/1	1.00	0.10	17,17,17,17	0
2	ZN	A	508	1/1	1.00	0.09	15,15,15,15	0

6.5 Other polymers

There are no such residues in this entry.