

Full wwPDB X-ray Structure Validation Report (i)

Nov 14, 2023 – 03:21 AM JST

PDB ID	:	8WF4
Title	:	The Crystal Structure of RSK1 from Biortus.
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Deposited on		
Resolution	:	2.65 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 (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:

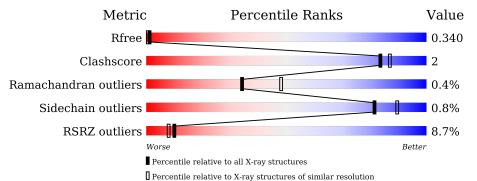
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 2.65 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R _{free}	130704	1332 (2.68-2.64)
Clashscore	141614	1374(2.68-2.64)
Ramachandran outliers	138981	1349 (2.68-2.64)
Sidechain outliers	138945	1349 (2.68-2.64)
RSRZ outliers	127900	1318 (2.68-2.64)

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	А	325	85%	·	11%
1	В	325	81%	8%	11%



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2 Entry composition (i)

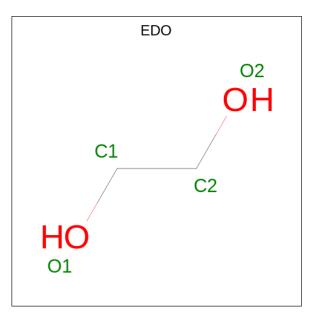
There are 3 unique types of molecules in this entry. The entry contains 4647 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Ribosomal protein S6 kinase alpha-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Λ	288	Total	С	Ν	0	\mathbf{S}	0	0	0
			2274	1439	390	433	12			
1	В	290	Total	С	Ν	0	S	0	0	0
	1 В		2285	1445	392	436	12	0	0	0

• Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
2	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
2	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
2	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0



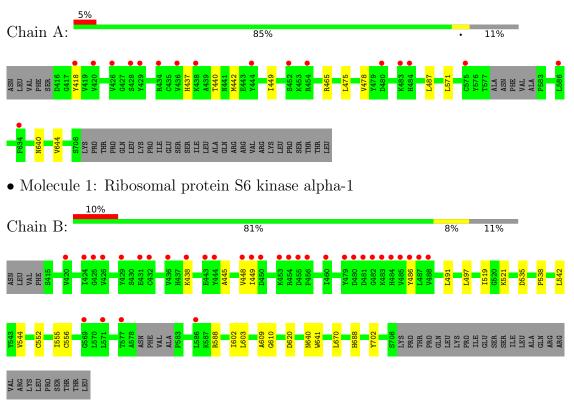
• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	33	Total O 33 33	0	0
3	В	39	Total O 39 39	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: Ribosomal protein S6 kinase alpha-1



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	39.68Å 143.63Å 60.23Å	Depositor
a, b, c, α , β , γ	90.00° 95.83° 90.00°	Depositor
Resolution (Å)	46.05 - 2.65	Depositor
Resolution (A)	46.01 - 2.65	EDS
% Data completeness	99.8 (46.05-2.65)	Depositor
(in resolution range)	99.9 (46.01 - 2.65)	EDS
R _{merge}	0.14	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.23 (at 2.65 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.8.0352	Depositor
D D.	0.239 , 0.309	Depositor
R, R_{free}	0.262 , 0.340	DCC
R_{free} test set	948 reflections (4.88%)	wwPDB-VP
Wilson B-factor $(Å^2)$	54.8	Xtriage
Anisotropy	0.520	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.32 , 48.0	EDS
L-test for twinning ²	$ \langle L \rangle = 0.50, \langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4647	wwPDB-VP
Average B, all atoms $(Å^2)$	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.92% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

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: EDO

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 Cha	Chain		lengths	Bond angles		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.25	0/2320	0.43	0/3136	
1	В	0.25	0/2331	0.43	0/3151	
All	All	0.25	0/4651	0.43	0/6287	

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	А	2274	0	2268	7	0
1	В	2285	0	2278	15	0
2	А	8	0	12	0	0
2	В	8	0	12	0	0
3	А	33	0	0	0	0
3	В	39	0	0	0	0
All	All	4647	0	4570	22	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.

All (22) close contacts within the same asymmetric unit are listed below, sorted by their clash



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:440:THR:HG23	1:A:442:MET:HG2	1.86	0.57
1:A:449:ILE:HD13	1:A:487:LEU:HD13	1.91	0.53
1:B:445:ALA:HB2	1:B:491:LEU:HD12	1.91	0.53
1:A:465:ARG:NH1	1:A:571:LEU:HD12	2.27	0.50
1:B:609:ALA:HB2	1:B:641:TRP:CZ2	2.49	0.48
1:B:448:VAL:HG23	1:B:448:VAL:O	2.14	0.47
1:A:475:LEU:HD21	1:A:478:VAL:CG1	2.46	0.45
1:A:640:ASN:O	1:A:644:VAL:HG23	2.17	0.44
1:B:542:LEU:HD13	1:B:556:CYS:SG	2.59	0.43
1:A:449:ILE:HD12	1:A:449:ILE:N	2.34	0.43
1:B:544:VAL:HG12	1:B:552:CYS:HB3	2.01	0.43
1:B:521:LYS:HA	1:B:670:LEU:HD11	2.01	0.42
1:B:610:GLY:HA3	1:B:688:HIS:HA	2.01	0.42
1:B:497:LEU:HD23	1:B:603:LEU:HD11	2.02	0.42
1:B:602:ILE:HD11	1:B:702:TYR:CZ	2.54	0.42
1:B:609:ALA:O	1:B:640:ASN:ND2	2.53	0.41
1:B:449:ILE:HD12	1:B:449:ILE:N	2.35	0.41
1:A:440:THR:HG23	1:A:442:MET:CG	2.49	0.41
1:B:519:ILE:HG23	1:B:555:ILE:HD11	2.02	0.41
1:B:602:ILE:HD11	1:B:702:TYR:OH	2.20	0.41
1:B:538:PRO:HG3	1:B:603:LEU:HD13	2.01	0.41
1:B:448:VAL:HG12	1:B:486:TYR:HD1	1.85	0.40

magnitude.

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	Perce	ntiles
1	А	284/325~(87%)	269~(95%)	14~(5%)	1 (0%)	34	48
1	В	286/325~(88%)	274 (96%)	11 (4%)	1 (0%)	41	56
All	All	570/650~(88%)	543 (95%)	25~(4%)	2~(0%)	34	48



All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	В	535	ASP
1	А	437	HIS

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	А	253/287~(88%)	252~(100%)	1 (0%)	91 95
1	В	254/287~(88%)	251 (99%)	3 (1%)	71 84
All	All	507/574~(88%)	503~(99%)	4 (1%)	81 89

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	418	TYR
1	В	438	LYS
1	В	588	ARG
1	В	620	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	441	ASN
1	А	549	ASN
1	А	706	ASN
1	В	504	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)

4 ligands are 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).

ſ	Mol	Mol Type Chain Res Linl		Link	Bond lengths			Bond angles			
	WIOI	Type	Chain	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2
ſ	2	EDO	А	801	-	3,3,3	0.05	0	2,2,2	0.16	0
	2	EDO	В	801	-	3,3,3	0.07	0	2,2,2	0.19	0
	2	EDO	А	802	-	3,3,3	0.07	0	2,2,2	0.15	0
	2	EDO	В	802	-	3,3,3	0.07	0	2,2,2	0.14	0

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	EDO	А	801	-	-	0/1/1/1	-
2	EDO	В	801	-	-	1/1/1/1	-
2	EDO	А	802	-	-	1/1/1/1	-
2	EDO	В	802	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
2	В	801	EDO	O1-C1-C2-O2
2	А	802	EDO	O1-C1-C2-O2

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 (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	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	А	288/325~(88%)	0.46	17 (5%) 22 19	53, 76, 130, 151	1 (0%)
1	В	290/325~(89%)	0.58	33 (11%) 5 3	54, 76, 130, 143	1 (0%)
All	All	578/650~(88%)	0.52	50 (8%) 10 8	53, 76, 131, 151	2 (0%)

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	418	TYR	5.5
1	В	429	TYR	5.0
1	А	484	HIS	4.7
1	А	436	VAL	4.6
1	В	448	VAL	4.1
1	В	484	HIS	4.0
1	В	485	VAL	4.0
1	В	426	VAL	3.8
1	В	481	ASP	3.8
1	А	434	ARG	3.8
1	В	450	ASP	3.8
1	В	569	GLY	3.7
1	В	479	TYR	3.6
1	В	487	LEU	3.5
1	В	482	GLY	3.5
1	В	454	ARG	3.4
1	В	431	GLU	3.4
1	А	438	LYS	3.3
1	В	449	ILE	3.3
1	А	420	VAL	3.2
1	В	486	TYR	3.2
1	А	428	SER	3.1
1	В	455	ASP	3.1
1	А	429	TYR	3.0

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Mol	Chain	Res	Type	RSRZ
1	А	444	TYR	3.0
1	В	488	VAL	2.8
1	А	483	LYS	2.8
1	А	575	CYS	2.8
1	А	586	LEU	2.7
1	В	424	ILE	2.7
1	В	480	ASP	2.7
1	В	444	TYR	2.7
1	А	480	ASP	2.6
1	А	452	SER	2.6
1	В	432	CYS	2.6
1	В	425	GLY	2.5
1	В	443	GLU	2.5
1	В	453	LYS	2.4
1	В	420	VAL	2.3
1	В	571	LEU	2.2
1	А	634	PHE	2.2
1	В	456	PRO	2.2
1	В	436	VAL	2.2
1	В	460	ILE	2.1
1	В	586	LEU	2.1
1	В	438	LYS	2.1
1	В	577	THR	2.1
1	А	454	ARG	2.0
1	В	483	LYS	2.0
1	А	426	VAL	2.0

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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)

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, 95^{th} 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	EDO	А	802	4/4	0.75	0.21	73,74,74,74	0
2	EDO	В	801	4/4	0.84	0.31	93,95,95,96	0
2	EDO	В	802	4/4	0.91	0.21	64,65,66,67	0
2	EDO	А	801	4/4	0.93	0.14	71,73,73,74	0

6.5 Other polymers (i)

There are no such residues in this entry.

