



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 17, 2024 – 07:12 PM EST

PDB ID : 3UJG
Title : Crystal structure of SnRK2.6 in complex with HAB1
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Deposited on : 2011-11-07
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 ⓘ 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 ⓘ](#)) 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

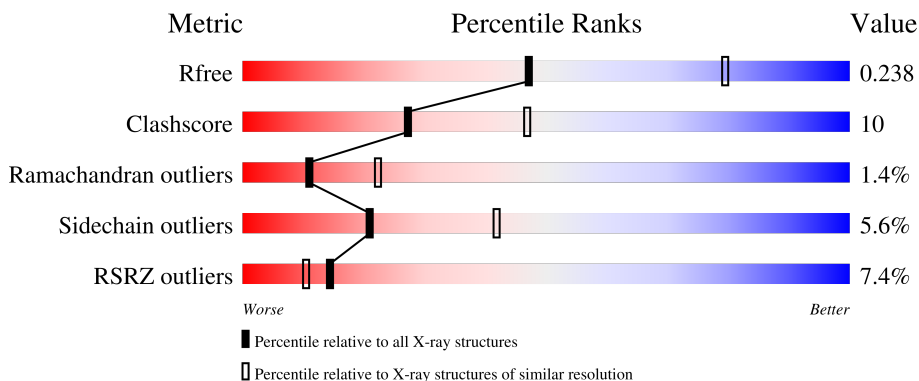
1 Overall quality at a glance

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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
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 $\leq 5\%$. 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	361	 7% 57% 21% • 20%
2	B	350	 5% 73% 15% • 10%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4941 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 SRK2E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	290	2326	1481	406	426	13	0	0	0

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	MET	-	expression tag	UNP Q940H6
A	3	ALA	-	expression tag	UNP Q940H6
A	4	HIS	-	expression tag	UNP Q940H6
A	5	HIS	-	expression tag	UNP Q940H6
A	6	HIS	-	expression tag	UNP Q940H6
A	7	HIS	-	expression tag	UNP Q940H6
A	8	HIS	-	expression tag	UNP Q940H6
A	9	HIS	-	expression tag	UNP Q940H6
A	10	ALA	-	expression tag	UNP Q940H6
A	296	ALA	ASP	engineered mutation	UNP Q940H6
A	297	ALA	GLU	engineered mutation	UNP Q940H6

- Molecule 2 is a protein called Protein phosphatase 2C 16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	315	2452	1545	433	456	18	0	0	0

There are 10 discrepancies between the modelled and reference sequences:

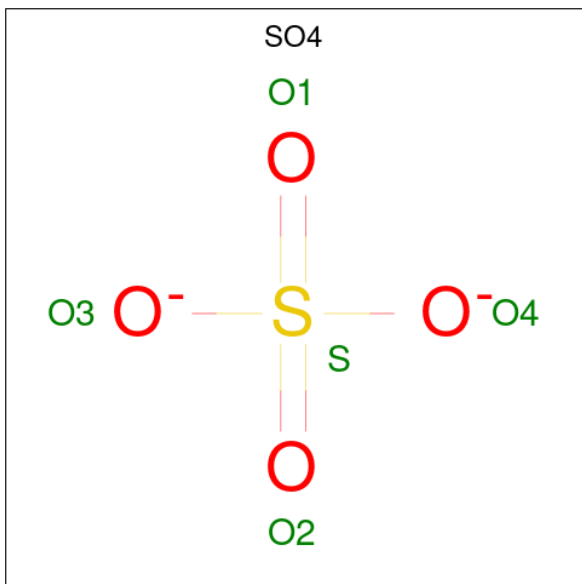
Chain	Residue	Modelled	Actual	Comment	Reference
B	162	GLY	-	expression tag	UNP Q9CAJ0
B	163	SER	-	expression tag	UNP Q9CAJ0
B	164	GLY	-	expression tag	UNP Q9CAJ0
B	165	SER	-	expression tag	UNP Q9CAJ0
B	166	ALA	-	expression tag	UNP Q9CAJ0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	167	GLY	-	expression tag	UNP Q9CAJ0
B	168	SER	-	expression tag	UNP Q9CAJ0
B	169	ALA	-	expression tag	UNP Q9CAJ0
B	170	ALA	-	expression tag	UNP Q9CAJ0
B	171	GLY	-	expression tag	UNP Q9CAJ0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
3	A	1	5	4	1	0	0
3	A	1	5	4	1	0	0
3	B	1	5	4	1	0	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
4	B	2	2	2	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	71	Total O 71 71	0	0
5	B	75	Total O 75 75	0	0

4 Data and refinement statistics i

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, α , β , γ	154.84Å 154.84Å 70.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.78 – 2.60 29.78 – 2.58	Depositor EDS
% Data completeness (in resolution range)	100.0 (29.78-2.60) 99.4 (29.78-2.58)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.34 (at 2.57Å)	Xtrriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.207 , 0.238 0.205 , 0.238	Depositor DCC
R_{free} test set	1878 reflections (7.11%)	wwPDB-VP
Wilson B-factor (Å ²)	50.1	Xtrriage
Anisotropy	0.516	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 46.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.016 for -k,-h,-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4941	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.14% 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

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, MG

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	0.55	0/2373	0.66	2/3204 (0.1%)
2	B	0.60	0/2497	0.66	0/3366
All	All	0.58	0/4870	0.66	2/6570 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	256	ARG	NE-CZ-NH1	6.06	123.33	120.30
1	A	256	ARG	NE-CZ-NH2	-5.35	117.62	120.30

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	2326	0	2323	61	0
2	B	2452	0	2446	38	0
3	A	10	0	0	1	0
3	B	5	0	0	0	0
4	B	2	0	0	0	0
5	A	71	0	0	4	0
5	B	75	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	4941	0	4769	97	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 10.

The worst 5 of 97 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)
2:B:470:ILE:HD12	2:B:475:GLN:HE21	1.31	0.93
2:B:211:HIS:H	2:B:237:HIS:HD2	1.31	0.76
1:A:205:VAL:O	1:A:209:VAL:HG23	1.88	0.72
1:A:146:THR:CG2	1:A:156:LEU:HD13	2.25	0.67
2:B:250:VAL:HG13	2:B:301:ILE:HD13	1.77	0.66

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	280/361 (78%)	254 (91%)	21 (8%)	5 (2%)	8	16
2	B	307/350 (88%)	293 (95%)	11 (4%)	3 (1%)	15	32
All	All	587/711 (83%)	547 (93%)	32 (6%)	8 (1%)	11	22

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	216	PRO
1	A	59	ASP
1	A	109	ALA
2	B	273	LEU

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Mol	Chain	Res	Type
1	A	53	GLU

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	256/319 (80%)	242 (94%)	14 (6%)	21	43
2	B	264/288 (92%)	249 (94%)	15 (6%)	20	41
All	All	520/607 (86%)	491 (94%)	29 (6%)	21	42

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	213	LEU
2	B	422	ARG
2	B	272	GLU
2	B	355	LYS
2	B	218	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	259	HIS
2	B	475	GLN
1	A	235	ASN
1	A	274	HIS
1	A	287	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](#)

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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	$\# Z > 2$
3	SO4	B	513	-	4,4,4	0.20	0	6,6,6	0.31	0
3	SO4	A	364	-	4,4,4	0.16	0	6,6,6	0.53	0
3	SO4	A	363	-	4,4,4	0.23	0	6,6,6	0.45	0

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	363	SO4	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

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	290/361 (80%)	0.33	27 (9%) 8 6	34, 60, 101, 105	0
2	B	315/350 (90%)	0.09	18 (5%) 23 18	30, 45, 82, 107	0
All	All	605/711 (85%)	0.20	45 (7%) 14 10	30, 50, 96, 107	0

The worst 5 of 45 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	44	ASN	5.5
2	B	310	VAL	5.3
1	A	166	SER	5.1
1	A	55	GLY	5.0
1	A	168	VAL	4.8

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, 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(\AA^2)	Q<0.9
4	MG	B	100	1/1	0.58	0.33	69,69,69,69	0
4	MG	B	512	1/1	0.91	0.31	45,45,45,45	0
3	SO4	A	364	5/5	0.98	0.11	37,39,41,42	0
3	SO4	B	513	5/5	0.98	0.10	56,57,57,58	0
3	SO4	A	363	5/5	0.99	0.09	41,41,43,44	0

6.5 Other polymers [i](#)

There are no such residues in this entry.