wwPDB X-ray Structure Validation Summary Report (i)

Dec 14, 2023 – 05:11 am GMT

PDB ID	:	2X7G
Title	:	Structure of human serine-arginine-rich protein-specific kinase 2 (SRPK2) bound to purvalanol B
Authors	:	Pike, A.C.W.; Savitsky, P.; Fedorov, O.; Krojer, T.; Ugochukwu, E.; von Delft, F.; Gileadi, O.; Edwards, A.; Arrowsmith, C.H.; Weigelt, J.; Bountra, C.; Knapp, S.
Deposited on	:	2010-02-26
Resolution	:	2.50 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:

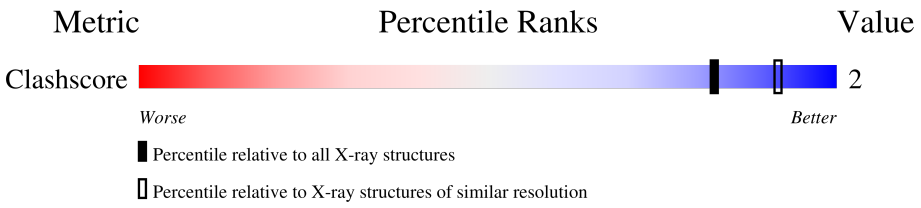
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	FAILED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et 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 2.50 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))
Clashscore	141614	5346 (2.50-2.50)

2 Entry composition (i)

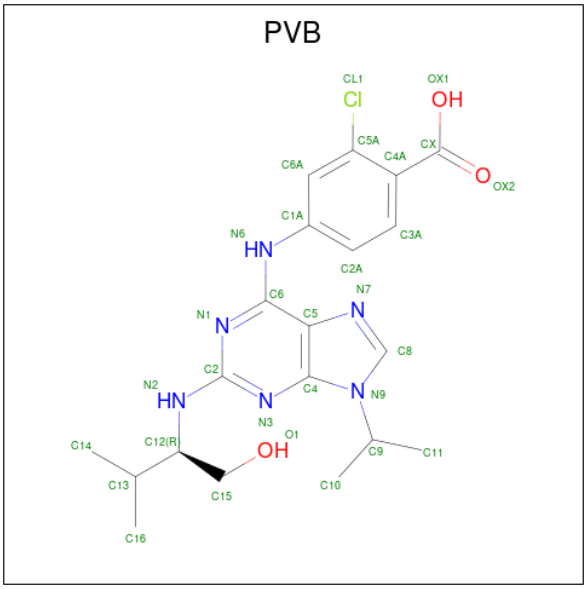
There are 6 unique types of molecules in this entry. The entry contains 2969 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 UNCHARACTERIZED PROTEIN SRPK2.

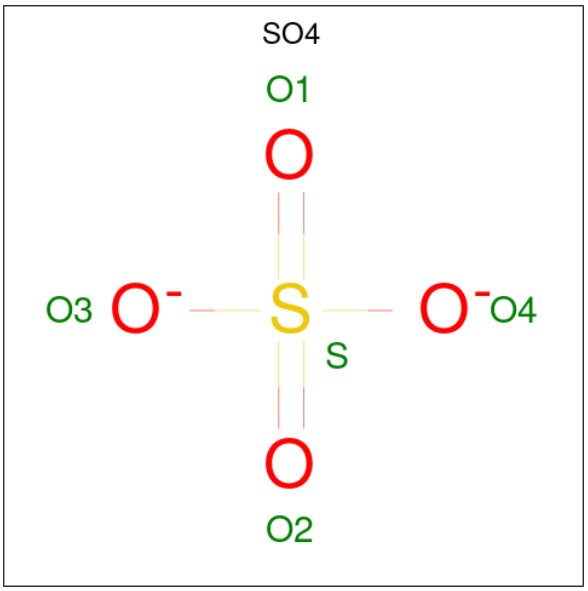
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	344	2765	1777	480	489	19	0	0	0

- Molecule 2 is PURVALANOL B (three-letter code: PVB) (formula: $C_{20}H_{25}ClN_6O_3$).



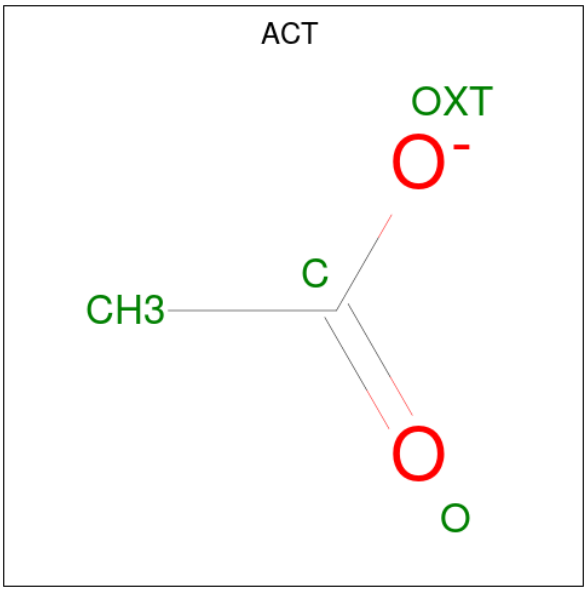
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Cl	N	O		
2	A	1	30	20	1	6	3	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



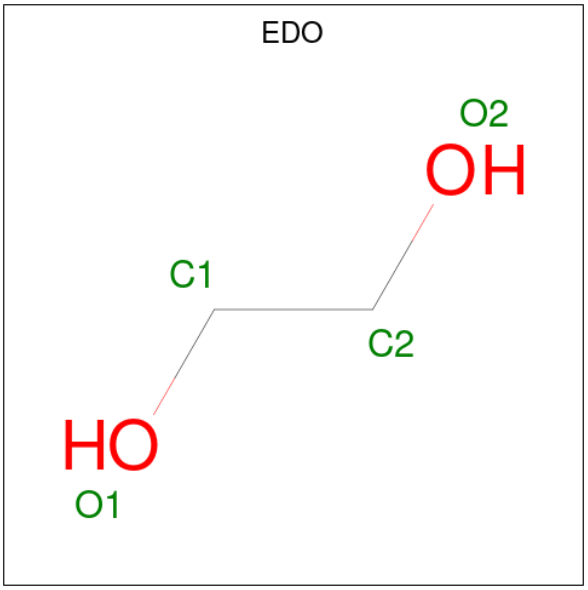
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	O	S			
3	A	1	5	4	1		0	0
3	A	1	5	4	1		0	0
3	A	1	5	4	1		0	0
3	A	1	5	4	1		0	0
3	A	1	5	4	1		0	0
3	A	1	5	4	1		0	0
3	A	1	5	4	1		0	0

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
4	A	1	4	2	2	0	0

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
5	A	1	4	2	2	0	0
5	A	1	4	2	2	0	0
5	A	1	4	2	2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
5	A	1	4	2	2	0	0
			Total	C	O		
5	A	1	4	2	2	0	0
			Total	C	O		
5	A	1	4	2	2	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	111	111	111	0	0

SEQUENCE-PLOTS INFOmissingINFO

3 Data and refinement statistics (i)

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	110.31Å 110.31Å 90.59Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	45.00 – 2.50	Depositor
% Data completeness (in resolution range)	99.5 (45.00-2.50)	Depositor
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.88 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.183 , 0.249	Depositor
Wilson B-factor (Å^2)	37.1	Xtriage
Anisotropy	0.097	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.031 for -h,-k,l	Xtriage
Total number of atoms	2969	wwPDB-VP
Average B, all atoms (Å^2)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.70% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical 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.

4 Model quality (i)

4.1 Standard geometry (i)

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

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	0.61	0/2838	0.68	0/3844

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

4.2 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	2765	0	2716	12	0
2	A	30	0	24	1	0
3	A	35	0	0	1	0
4	A	4	0	3	1	0
5	A	24	0	36	0	0
6	A	111	0	0	0	0
All	All	2969	0	2779	14	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.

The worst 5 of 14 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:188:ILE:HD11	1:A:588:LEU:HD23	1.81	0.62
1:A:84:ILE:N	1:A:84:ILE:HD12	2.24	0.53
3:A:1706:SO4:O4	4:A:1707:ACT:OXT	2.27	0.52
1:A:574:THR:N	1:A:575:PRO:CD	2.77	0.48
1:A:137:ILE:HD11	1:A:175:MET:HG2	1.98	0.46

There are no symmetry-related clashes.

4.3 Torsion angles (i)

4.3.1 Protein backbone (i)

There are no protein backbone outliers to report in this entry.

4.3.2 Protein sidechains (i)

There are no protein residues with a non-rotameric sidechain to report in this entry.

4.3.3 RNA (i)

There are no RNA molecules in this entry.

4.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

4.5 Carbohydrates (i)

There are no monosaccharides in this entry.

4.6 Ligand geometry (i)

15 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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	SO4	A	1703	-	4,4,4	0.17	0	6,6,6	0.50	0
2	PVB	A	800	-	29,32,32	1.59	3 (10%)	37,46,46	2.08	8 (21%)
3	SO4	A	1704	-	4,4,4	0.50	0	6,6,6	0.60	0
5	EDO	A	1708	-	3,3,3	0.42	0	2,2,2	0.37	0
3	SO4	A	1701	-	4,4,4	0.17	0	6,6,6	0.28	0
3	SO4	A	1705	-	4,4,4	0.26	0	6,6,6	0.35	0
5	EDO	A	1711	-	3,3,3	0.30	0	2,2,2	0.44	0
5	EDO	A	1710	-	3,3,3	0.56	0	2,2,2	0.08	0
3	SO4	A	1702	-	4,4,4	0.13	0	6,6,6	0.28	0
5	EDO	A	1712	-	3,3,3	0.37	0	2,2,2	0.34	0
5	EDO	A	1713	-	3,3,3	0.47	0	2,2,2	0.50	0
3	SO4	A	1706	-	4,4,4	0.15	0	6,6,6	0.12	0
4	ACT	A	1707	-	3,3,3	0.70	0	3,3,3	1.79	2 (66%)
3	SO4	A	1700	-	4,4,4	0.19	0	6,6,6	0.85	0
5	EDO	A	1709	-	3,3,3	0.54	0	2,2,2	0.21	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	PVB	A	800	-	-	7/22/22/22	0/3/3/3
5	EDO	A	1708	-	-	1/1/1/1	-
5	EDO	A	1713	-	-	1/1/1/1	-
5	EDO	A	1710	-	-	1/1/1/1	-
5	EDO	A	1712	-	-	1/1/1/1	-
5	EDO	A	1711	-	-	0/1/1/1	-
5	EDO	A	1709	-	-	0/1/1/1	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	800	PVB	C4A-C5A	6.46	1.48	1.39
2	A	800	PVB	C5-C4	2.52	1.47	1.40
2	A	800	PVB	C5A-CL1	2.19	1.78	1.73

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	800	PVB	N6-C6-N1	7.64	125.83	118.66
2	A	800	PVB	C5-C6-N1	-4.78	116.84	120.81
2	A	800	PVB	C2-N3-C4	4.40	120.28	115.28
2	A	800	PVB	C5A-C4A-CX	-3.51	119.21	123.83
2	A	800	PVB	C2-N1-C6	2.89	123.00	116.39

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	800	PVB	C10-C9-N9-C4
2	A	800	PVB	C10-C9-N9-C8
2	A	800	PVB	C5A-C4A-CX-OX2
5	A	1713	EDO	O1-C1-C2-O2
2	A	800	PVB	C5A-C4A-CX-OX1

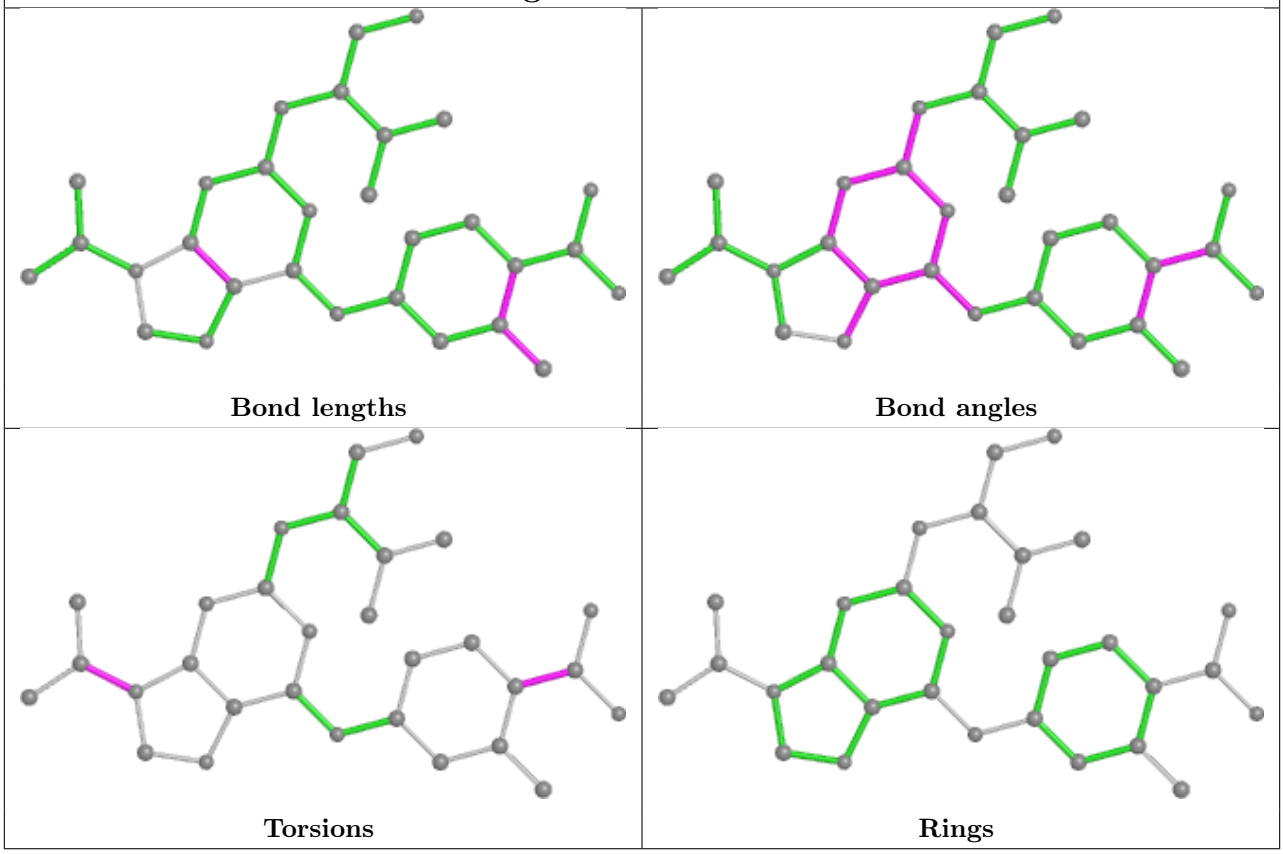
There are no ring outliers.

3 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	800	PVB	1	0
3	A	1706	SO4	1	0
4	A	1707	ACT	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand PVB A 800



4.7 Other polymers (i)

There are no such residues in this entry.

4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

5 Fit of model and data (i)

5.1 Protein, DNA and RNA chains (i)

EDS failed to run properly - this section is therefore empty.

5.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS failed to run properly - this section is therefore empty.

5.3 Carbohydrates (i)

EDS failed to run properly - this section is therefore empty.

5.4 Ligands (i)

EDS failed to run properly - this section is therefore empty.

5.5 Other polymers (i)

EDS failed to run properly - this section is therefore empty.