



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 21, 2020 – 01:36 PM EDT

PDB ID : 6WME
Title : Human Sun2-KASH3 complex
Deposited on : 2020-04-21
Resolution : 1.53 Å (reported)

This is a Full wwPDB X-ray Structure Validation Report.

This report is produced by the wwPDB biocuration pipeline after annotation of the structure.

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:

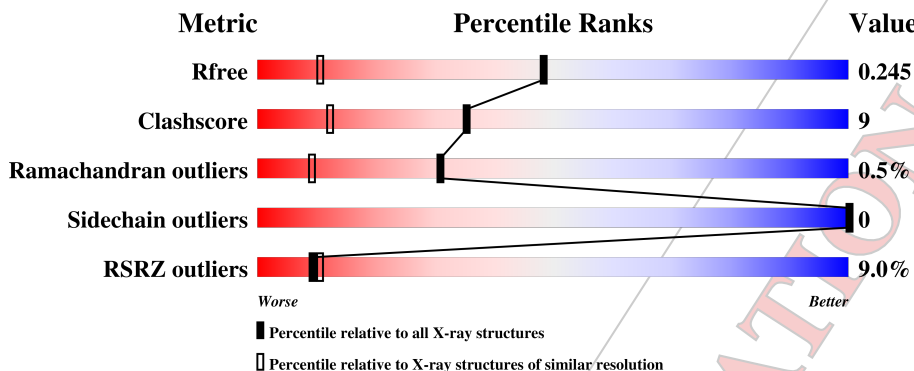
MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.10.1
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.10.1

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 1.53 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}	111664	2055 (1.56-1.52)
Clashscore	122126	2124 (1.56-1.52)
Ramachandran outliers	120053	2083 (1.56-1.52)
Sidechain outliers	120020	2081 (1.56-1.52)
RSRZ outliers	108989	2027 (1.56-1.52)

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	202	<div style="display: flex; align-items: center;"> <div style="width: 8%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 84%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 11%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 1%; height: 10px; background-color: grey;"></div> </div>
2	B	34	<div style="display: flex; align-items: center;"> <div style="width: 9%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 35%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 12%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 43%; height: 10px; background-color: grey;"></div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 1981 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 SUN domain-containing protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	195	1567	999	274	291	3	0	5	0

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	516	GLY	-	expression tag	UNP Q9UH99
A	517	PRO	-	expression tag	UNP Q9UH99
A	518	GLY	-	expression tag	UNP Q9UH99
A	519	GLY	-	expression tag	UNP Q9UH99
A	520	SER	-	expression tag	UNP Q9UH99
A	521	GLY	-	expression tag	UNP Q9UH99
A	534	ASP	GLN	engineered mutation	UNP Q9UH99
A	574	ILE	LEU	engineered mutation	UNP Q9UH99
A	683	GLY	THR	engineered mutation	UNP Q9UH99
A	684	ARG	MET	engineered mutation	UNP Q9UH99
A	685	GLY	ALA	engineered mutation	UNP Q9UH99

- Molecule 2 is a protein called Nesprin-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	16	169	109	31	28	1	0	5	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	942	GLY	-	expression tag	UNP Q6ZMZ3
B	943	PRO	-	expression tag	UNP Q6ZMZ3
B	944	GLY	-	expression tag	UNP Q6ZMZ3
B	945	GLY	-	expression tag	UNP Q6ZMZ3
B	946	SER	-	expression tag	UNP Q6ZMZ3

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Chain	Residue	Modelled	Actual	Comment	Reference
B	947	GLY	-	expression tag	UNP Q6ZMZ3

- Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K).

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

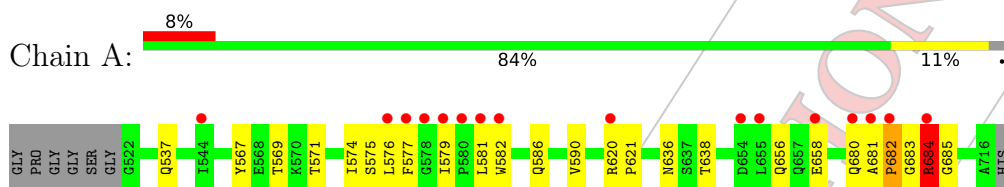
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	226	Total O 226 226	0	0
4	B	18	Total O 18 18	0	0

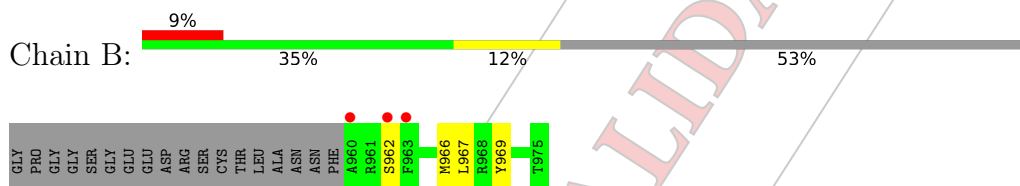
3 Residue-property plots [i](#)

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: SUN domain-containing protein 2



- Molecule 2: Nesprin-3



4 Data and refinement statistics i

Property	Value	Source
Space group	P 63 2 2	Depositor
Cell constants a, b, c, α , β , γ	78.71Å 78.71Å 173.28Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	63.43 – 1.53 63.43 – 1.53	Depositor EDS
% Data completeness (in resolution range)	98.6 (63.43-1.53) 98.6 (63.43-1.53)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.98 (at 1.53Å)	Xtrriage
Refinement program	PHENIX 1.17_3644	Depositor
R, R_{free}	0.209 , 0.245 0.209 , 0.245	Depositor DCC
R_{free} test set	1993 reflections (4.18%)	wwPDB-VP
Wilson B-factor (Å ²)	27.7	Xtrriage
Anisotropy	0.400	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 53.7	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	1981	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.78% 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:
K

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	0.35	0/1612	0.63	2/2198 (0.1%)
2	B	0.32	0/174	0.47	0/234
All	All	0.34	0/1786	0.62	2/2432 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
2	B	0	1
All	All	0	2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	684[A]	ARG	C-N-CA	-5.48	110.79	122.30
1	A	684[B]	ARG	C-N-CA	-5.48	110.79	122.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	682[A]	PRO	Peptide
2	B	962[B]	SER	Peptide

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	1567	0	1509	29	0
2	B	169	0	168	2	0
3	A	1	0	0	0	0
4	A	226	0	0	7	1
4	B	18	0	0	0	0
All	All	1981	0	1677	30	1

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 9.

All (30) 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:620:ARG:NH2	4:A:901:HOH:O	2.00	0.93
1:A:685:GLY:O	4:A:901:HOH:O	1.88	0.89
1:A:620:ARG:NH2	1:A:621:PRO:HD2	2.05	0.71
1:A:537:GLN:NE2	4:A:903:HOH:O	2.14	0.70
1:A:681[A]:ALA:HB3	1:A:682[A]:PRO:HD3	1.73	0.69
1:A:567:TYR:O	4:A:902:HOH:O	2.13	0.66
1:A:620:ARG:HD3	1:A:684[B]:ARG:HA	1.79	0.63
1:A:575:SER:HA	1:A:581:LEU:HD13	1.81	0.61
1:A:586:GLN:HB3	1:A:590[B]:VAL:HG21	1.86	0.58
1:A:620:ARG:HH21	1:A:621:PRO:HD2	1.71	0.56
1:A:569:THR:HG23	1:A:571:THR:H	1.71	0.54
1:A:581:LEU:HB3	1:A:582:TRP:CD1	2.43	0.54
1:A:620:ARG:CD	1:A:684[B]:ARG:HA	2.41	0.50
1:A:682[B]:PRO:HG3	4:A:966:HOH:O	2.11	0.50
1:A:576:LEU:HG	1:A:577:PHE:CE2	2.47	0.50
1:A:680:GLN:HG3	1:A:681[A]:ALA:N	2.27	0.49
1:A:656:GLN:NE2	1:A:658:GLU:O	2.47	0.48
1:A:575:SER:HB2	1:A:579:ILE:O	2.15	0.47
1:A:620:ARG:HD3	1:A:684[B]:ARG:C	2.35	0.46
1:A:683[B]:GLY:O	1:A:685:GLY:N	2.48	0.45
1:A:680:GLN:HG3	1:A:681[B]:ALA:N	2.31	0.45
1:A:620:ARG:NH1	4:A:914:HOH:O	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:681[A]:ALA:CB	1:A:682[A]:PRO:HD3	2.45	0.42
1:A:574:ILE:O	1:A:581:LEU:HB2	2.19	0.41
1:A:569:THR:HG21	4:A:905:HOH:O	2.21	0.41
1:A:571:THR:O	2:B:969:TYR:HA	2.21	0.40
1:A:636:ASN:O	1:A:638:THR:HG23	2.21	0.40
1:A:682[A]:PRO:C	1:A:683[A]:GLY:O	2.59	0.40
2:B:966:MET:CE	2:B:967:LEU:H	2.35	0.40
1:A:620:ARG:HA	1:A:620:ARG:HD2	1.74	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:910:HOH:O	4:A:990:HOH:O[9_765]	2.08	0.12

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	198/202 (98%)	188 (95%)	8 (4%)	2 (1%)	17	3
2	B	18/34 (53%)	13 (72%)	5 (28%)	0	100	100
All	All	216/236 (92%)	201 (93%)	13 (6%)	2 (1%)	31	3

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	684[A]	ARG
1	A	684[B]	ARG

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	166/168 (99%)	166 (100%)	0	100	100
2	B	18/27 (67%)	18 (100%)	0	100	100
All	All	184/195 (94%)	184 (100%)	0	100	100

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

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	680	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is 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.

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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	195/202 (96%)	0.44	16 (8%) 11 13	23, 34, 61, 81	0
2	B	16/34 (47%)	1.18	3 (18%) 1 1	28, 36, 42, 48	0
All	All	211/236 (89%)	0.50	19 (9%) 9 10	23, 35, 60, 81	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	578	GLY	8.4
1	A	684[A]	ARG	7.8
2	B	963[A]	PHE	7.6
1	A	655	LEU	5.4
1	A	577	PHE	5.3
1	A	682[A]	PRO	5.0
2	B	960[A]	ALA	4.7
1	A	680	GLN	4.6
1	A	579	ILE	4.2
1	A	681[A]	ALA	4.1
1	A	582	TRP	3.2
1	A	654	ASP	3.2
2	B	962[A]	SER	3.1
1	A	658	GLU	3.0
1	A	576	LEU	3.0
1	A	580	PRO	3.0
1	A	581	LEU	2.9
1	A	620	ARG	2.9
1	A	544	ILE	2.1

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
3	K	A	801	1/1	0.98	0.16	44,44,44,44	0

6.5 Other polymers [i](#)

There are no such residues in this entry.