

# Full wwPDB X-ray Structure Validation Report (i)

#### Jan 2, 2024 – 04:40 pm GMT

PDB ID : 5FNQ

Title : Structure of the Keap1 Kelch domain in complex with a small molecule in-

hibitor.

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Deposited on : 2015-11-16

Resolution : 1.91 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 : 1.8.4, 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

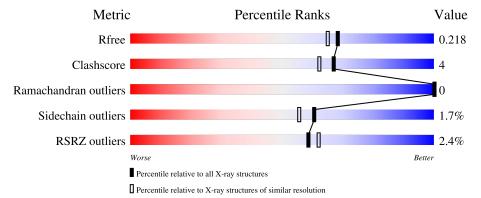
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)

# 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 1.91 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 $(\# \mathrm{Entries})$	Similar resolution $(\#\text{Entries, resolution range}(\mathring{\mathbf{A}}))$
$R_{free}$	130704	7937 (1.94-1.90)
Clashscore	141614	8644 (1.94-1.90)
Ramachandran outliers	138981	8530 (1.94-1.90)
Sidechain outliers	138945	8530 (1.94-1.90)
RSRZ outliers	127900	7793 (1.94-1.90)

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		
			2%		
1	A	304	87%	8%	5%

Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

Validation Pipeline (wwPDB-VP) : 2.36



# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2564 atoms, of which 8 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.

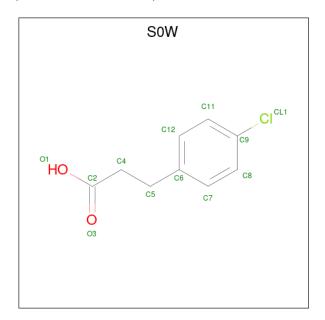
• Molecule 1 is a protein called KELCH-LIKE ECH-ASSOCIATED PROTEIN 1.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Δ	290	Total	С	N	О	S	0	9	0
1	Λ	230	2233	1389	401	426	17	0	2	

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Α	321	GLY	-	expression tag	UNP Q9Z2X8

• Molecule 2 is 3-(4-CHLOROPHENYL)PROPANOIC ACID (three-letter code: S0W) (formula: C<sub>9</sub>H<sub>9</sub>ClO<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
9	Λ	1	Total	С	Cl	Н	О	0	0
2	A	1	20	9	1	8	2	0	U

• Molecule 3 is water.



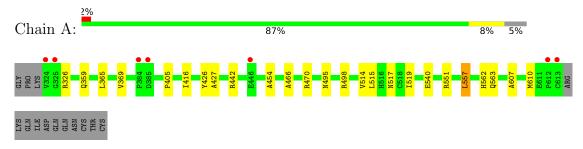
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	311	Total O 311 311	0	0



# 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: KELCH-LIKE ECH-ASSOCIATED PROTEIN 1





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 61	Depositor
Cell constants	103.62Å 103.62Å 56.03Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $120.00^{\circ}$	Depositor
Resolution (Å)	44.87 - 1.91	Depositor
rtesolution (A)	44.87 - 1.91	EDS
% Data completeness	97.7 (44.87-1.91)	Depositor
(in resolution range)	97.6 (44.87-1.91)	EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	5.43 (at 1.91Å)	Xtriage
Refinement program	REFMAC 5.8.0107	Depositor
υ .	0.178 , 0.215	Depositor
$R, R_{free}$	0.180 , $0.218$	DCC
$R_{free}$ test set	1317 reflections $(5.05\%)$	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	18.7	Xtriage
Anisotropy	0.047	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.33 , 40.3	EDS
L-test for twinning <sup>2</sup>	$< L > = 0.51, < L^2> = 0.35$	Xtriage
Estimated twinning fraction	0.035 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	2564	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.25% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>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.



<sup>&</sup>lt;sup>1</sup>Intensities 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: S0W

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	$\mathbf{lengths}$	Bond angles		
MIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.58	0/2294	0.73	0/3123	

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	A	2233	0	2125	17	0
2	A	12	8	0	0	0
3	A	311	0	0	5	0
All	All	2556	8	2125	17	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 4.

All (17) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	$egin{array}{c} { m Clash} \\ { m overlap} \ ({ m \AA}) \end{array}$
1:A:466:ALA:HB1	1:A:514:VAL:HG23	1.61	0.82

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Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	${ m distance}({ m \AA})$	overlap (Å)
1:A:454:ALA:H	1:A:495:ASN:HD21	1.42	0.66
1:A:514:VAL:HG22	1:A:519:ILE:HD13	1.82	0.62
1:A:517:ASN:ND2	1:A:540:GLU:HG2	2.21	0.56
1:A:470:ARG:NH2	3:A:2169:HOH:O	2.29	0.55
1:A:551:ARG:HG3	3:A:2299:HOH:O	2.06	0.54
1:A:359:GLN:NE2	3:A:2034:HOH:O	2.43	0.49
1:A:359:GLN:HE22	1:A:405:PRO:HD3	1.76	0.49
1:A:557:LEU:H	1:A:557:LEU:HD23	1.81	0.46
1:A:369:VAL:HG23	1:A:607:ALA:HB1	1.99	0.44
1:A:365:LEU:H	1:A:365:LEU:HD23	1.83	0.44
1:A:517:ASN:HD21	1:A:540:GLU:HG2	1.83	0.42
1:A:562:HIS:CE1	1:A:563:GLN:HG3	2.55	0.42
1:A:470:ARG:HD3	3:A:2165:HOH:O	2.20	0.41
1:A:416:ILE:HD11	1:A:427:ALA:HB1	2.02	0.41
1:A:498:ARG:NH2	3:A:2210:HOH:O	2.53	0.41
1:A:426:TYR:CZ	1:A:442:ARG:HD3	2.56	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	290/304 (95%)	281 (97%)	9 (3%)	0	100 100

There are no Ramachandran outliers to report.

#### 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.

M	[ol	Chain	Analysed	Rotameric	Outliers	Percentiles	
	1	A	239/250 (96%)	235 (98%)	4 (2%)	60 55	

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

Mol	Chain	Res	Type
1	A	326	ARG
1	A	515	LEU
1	A	557	LEU
1	A	610	MET

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

Mol	Chain	$\operatorname{Res}$	Type
1	A	359	GLN
1	A	495	ASN
1	A	517	ASN
1	A	575	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 monosaccharides in this entry.

## 5.6 Ligand geometry (i)

1 ligand is 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 angl				Bond lengths Bond angles			les
	WIOI	туре	Chain	nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	Counts   RMSZ   $\# Z $	# Z  > 2		
	2	S0W	A	1614	-	12,12,12	0.64	0	15,15,15	0.59	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	S0W	A	1614	-	-	2/5/5/5	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	A	1614	S0W	O1-C2-C4-C5
2	A	1614	S0W	O3-C2-C4-C5

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	<rsrz></rsrz>	$\# \mathrm{RSRZ}{>}2$		$OWAB(A^2)$	Q < 0.9
1	A	290/304 (95%)	-0.17	7 (2%) 5	59 62	11, 23, 48, 75	0

All (7) RSRZ outliers are listed below:

Mol	Chain	$\operatorname{Res}$	Type	RSRZ
1	A	324	VAL	10.5
1	A	613	CYS	5.2
1	A	325	GLY	3.4
1	A	384	PRO	3.0
1	A	385	ASP	2.6
1	A	446	GLU	2.3
1	A	612	PRO	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 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	$ m B ext{-}factors(\AA^2)$	Q<0.9
2	S0W	A	1614	12/12	0.97	0.10	15,18,23,28	20



# 6.5 Other polymers (i)

There are no such residues in this entry.

