



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 18, 2021 – 09:52 am BST

PDB ID : 6TG8  
Title : Crystal structure of the Kelch domain in complex with 11 amino acid peptide (model of the ETGE loop)  
Authors : Kekez, I.; Matic, S.; Tomic, S.; Matkovic-Calogovic, D.  
Deposited on : 2019-11-15  
Resolution : 2.75 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](mailto: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.

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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 : 2.23.2  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0267  
CCP4 : 7.1.010 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.23.2

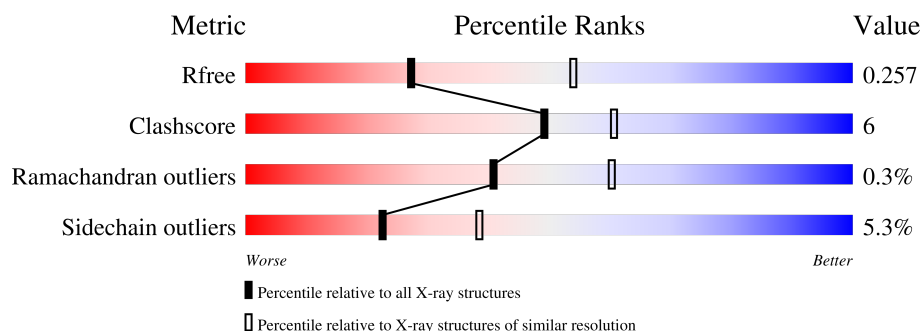
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.75 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	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)

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  $\geq 3$ , 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  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	AAA	288	
2	PPP	11	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2334 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 Kelch-like ECH-associated protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	288	Total	C	N	O	S	0	3	0
			2239	1394	406	424	15			

- Molecule 2 is a protein called VAL-ILE-ASN-PRO-GLU-THR-GLY-GLU-GLN-ILE-GLN.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	PPP	11	Total	C	N	O	0	0	0
			85	52	14	19			

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	AAA	1	Total	Na	0	0
			1	1		

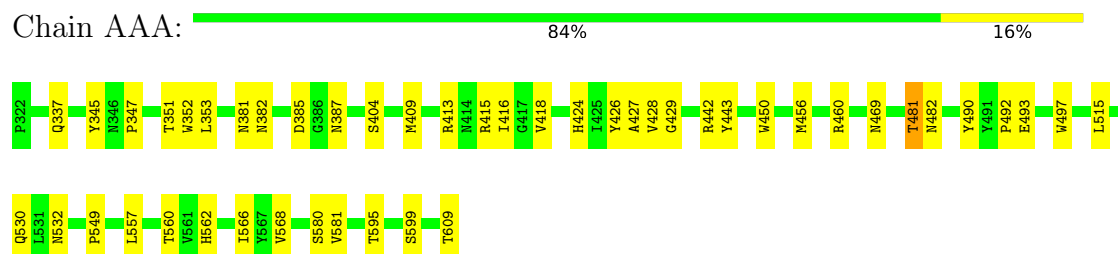
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	AAA	9	Total	O	0	0
			9	9		

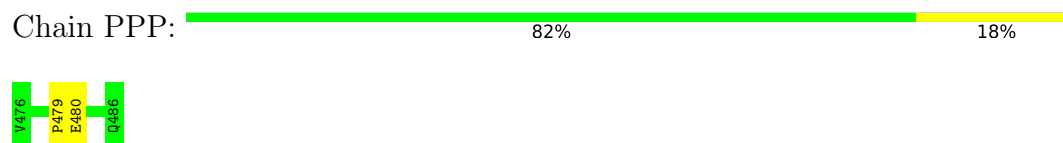
### 3 Residue-property plots [i](#)

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. 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. 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



- Molecule 2: VAL-ILE-ASN-PRO-GLU-THR-GLY-GLU-GLN-ILE-GLN



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	75.30Å 75.30Å 127.54Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	17.00 – 2.75 17.81 – 2.75	Depositor EDS
% Data completeness (in resolution range)	99.5 (17.00-2.75) 100.0 (17.81-2.75)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.19 (at 2.74Å)	Xtriage
Refinement program	REFMAC 5.8.0257	Depositor
R, $R_{free}$	0.181 , 0.258 0.190 , 0.257	Depositor DCC
$R_{free}$ test set	560 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	73.8	Xtriage
Anisotropy	0.002	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.039 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	2334	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.56% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>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

### 5.1 Standard geometry

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

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	AAA	0.64	0/2296	0.86	0/3124
2	PPP	0.65	0/85	0.77	0/115
All	All	0.64	0/2381	0.85	0/3239

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

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	AAA	2239	0	2143	27	0
2	PPP	85	0	81	2	0
3	AAA	1	0	0	0	0
4	AAA	9	0	0	0	0
All	All	2334	0	2224	27	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 6.

All (27) 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:AAA:347:PRO:HG2	1:AAA:562:HIS:CD2	2.19	0.77
1:AAA:532:ASN:HD22	1:AAA:549:PRO:HB2	1.61	0.66
1:AAA:353:LEU:HD23	1:AAA:353:LEU:N	2.12	0.63
1:AAA:413:ARG:HD3	1:AAA:429:GLY:O	1.99	0.63
1:AAA:352:TRP:C	1:AAA:353:LEU:HD23	2.24	0.57
1:AAA:409:MET:HE1	1:AAA:413:ARG:HD2	1.87	0.57
1:AAA:345:TYR:CE2	1:AAA:347:PRO:HA	2.40	0.57
1:AAA:426:TYR:OH	1:AAA:442:ARG:HD3	2.11	0.51
1:AAA:381:ASN:O	1:AAA:387:ASN:HA	2.13	0.48
1:AAA:382:ASN:HA	1:AAA:387:ASN:CB	2.43	0.48
1:AAA:515:LEU:HD22	1:AAA:566:ILE:HG13	1.95	0.47
1:AAA:409:MET:HE2	1:AAA:413:ARG:HE	1.79	0.47
1:AAA:415:ARG:HH22	2:PPP:480:GLU:CD	2.18	0.46
1:AAA:532:ASN:ND2	1:AAA:549:PRO:HB2	2.27	0.46
1:AAA:382:ASN:HA	1:AAA:387:ASN:HB2	1.97	0.46
1:AAA:530:GLN:NE2	2:PPP:479:PRO:O	2.49	0.46
1:AAA:443:TYR:HB2	1:AAA:450:TRP:CD2	2.52	0.44
1:AAA:424:HIS:ND1	1:AAA:442:ARG:HD2	2.33	0.43
1:AAA:490:TYR:HB2	1:AAA:497:TRP:CE2	2.53	0.43
1:AAA:568:VAL:O	1:AAA:581:VAL:HA	2.19	0.43
1:AAA:456:MET:CE	1:AAA:460:ARG:HD2	2.49	0.42
1:AAA:418:VAL:HA	1:AAA:426:TYR:O	2.18	0.42
1:AAA:490:TYR:HB2	1:AAA:497:TRP:CZ2	2.54	0.42
1:AAA:490:TYR:CE2	1:AAA:492:PRO:HA	2.55	0.41
1:AAA:347:PRO:HG2	1:AAA:562:HIS:NE2	2.34	0.41
1:AAA:416:ILE:HD11	1:AAA:427:ALA:HB1	2.03	0.40
1:AAA:481:THR:HB	1:AAA:482:ASN:ND2	2.36	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	AAA	289/288 (100%)	269 (93%)	19 (7%)	1 (0%)	41	60
2	PPP	9/11 (82%)	9 (100%)	0	0	100	100
All	All	298/299 (100%)	278 (93%)	19 (6%)	1 (0%)	41	60

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AAA	385	ASP

### 5.3.2 Protein sidechains ⓘ

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	AAA	237/234 (101%)	224 (94%)	13 (6%)	21	37
2	PPP	10/10 (100%)	10 (100%)	0	100	100
All	All	247/244 (101%)	234 (95%)	13 (5%)	22	38

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	337	GLN
1	AAA	351	THR
1	AAA	404	SER
1	AAA	428	VAL
1	AAA	469	ASN
1	AAA	481	THR
1	AAA	493	GLU
1	AAA	557	LEU
1	AAA	560	THR
1	AAA	580	SER
1	AAA	595	THR
1	AAA	599	SER
1	AAA	609	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are



no such sidechains identified.

### 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 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.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

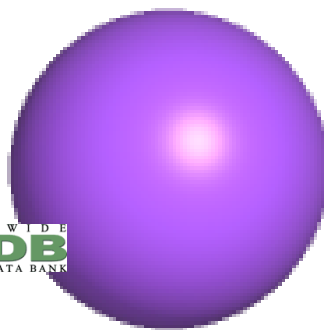
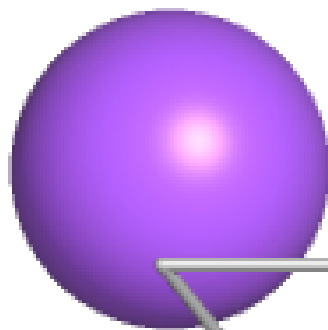
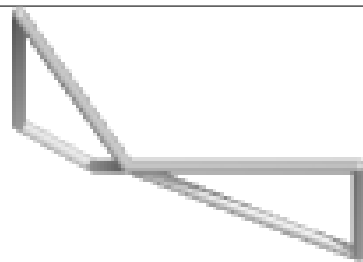
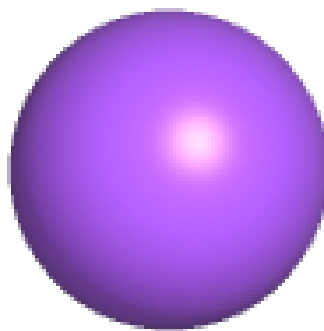
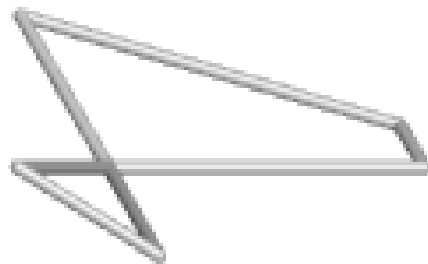
### 6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around NA AAA 701:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.