



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 2, 2018 – 11:43 AM EST

PDB ID : 5OJF
Title : Crystal Structure of KLC2-TPR domain (fragment [A1-B6])
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Deposited on : 2017-07-21
Resolution : 3.40 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

<http://wwpdb.org/validation/2016/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)	:	1.9-1692
EDS	:	rb-20030736
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20030736

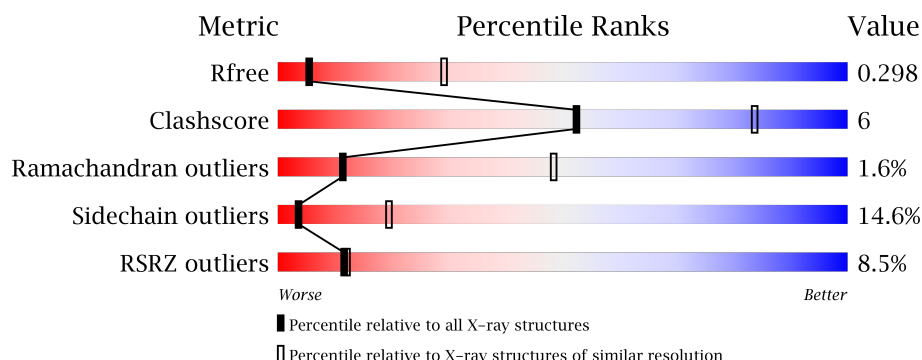
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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}	100719	1679 (3.50-3.30)
Clashscore	112137	1832 (3.50-3.30)
Ramachandran outliers	110173	1789 (3.50-3.30)
Sidechain outliers	110143	1789 (3.50-3.30)
RSRZ outliers	101464	1709 (3.50-3.30)

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. 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	314	<div> <div>7%</div> <div>63% 18% 17%</div> </div>
1	B	314	<div> <div>5%</div> <div>61% 20% 17%</div> </div>
1	C	314	<div> <div>10%</div> <div>61% 19% 17%</div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 6255 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 Kinesin light chain 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	262	Total	C	N	O	S	0	0	0
			2085	1305	381	392	7			
1	B	262	Total	C	N	O	S	0	0	0
			2085	1305	381	392	7			
1	C	262	Total	C	N	O	S	0	0	0
			2085	1305	381	392	7			

There are 57 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	171	MET	-	initiating methionine	UNP Q91YS4
A	172	GLY	-	expression tag	UNP Q91YS4
A	173	SER	-	expression tag	UNP Q91YS4
A	174	SER	-	expression tag	UNP Q91YS4
A	175	HIS	-	expression tag	UNP Q91YS4
A	176	HIS	-	expression tag	UNP Q91YS4
A	177	HIS	-	expression tag	UNP Q91YS4
A	178	HIS	-	expression tag	UNP Q91YS4
A	179	HIS	-	expression tag	UNP Q91YS4
A	180	HIS	-	expression tag	UNP Q91YS4
A	181	SER	-	expression tag	UNP Q91YS4
A	182	SER	-	expression tag	UNP Q91YS4
A	183	GLY	-	expression tag	UNP Q91YS4
A	184	LEU	-	expression tag	UNP Q91YS4
A	185	VAL	-	expression tag	UNP Q91YS4
A	186	PRO	-	expression tag	UNP Q91YS4
A	187	ARG	-	expression tag	UNP Q91YS4
A	188	GLY	-	expression tag	UNP Q91YS4
A	189	SER	-	expression tag	UNP Q91YS4
B	171	MET	-	initiating methionine	UNP Q91YS4
B	172	GLY	-	expression tag	UNP Q91YS4
B	173	SER	-	expression tag	UNP Q91YS4
B	174	SER	-	expression tag	UNP Q91YS4

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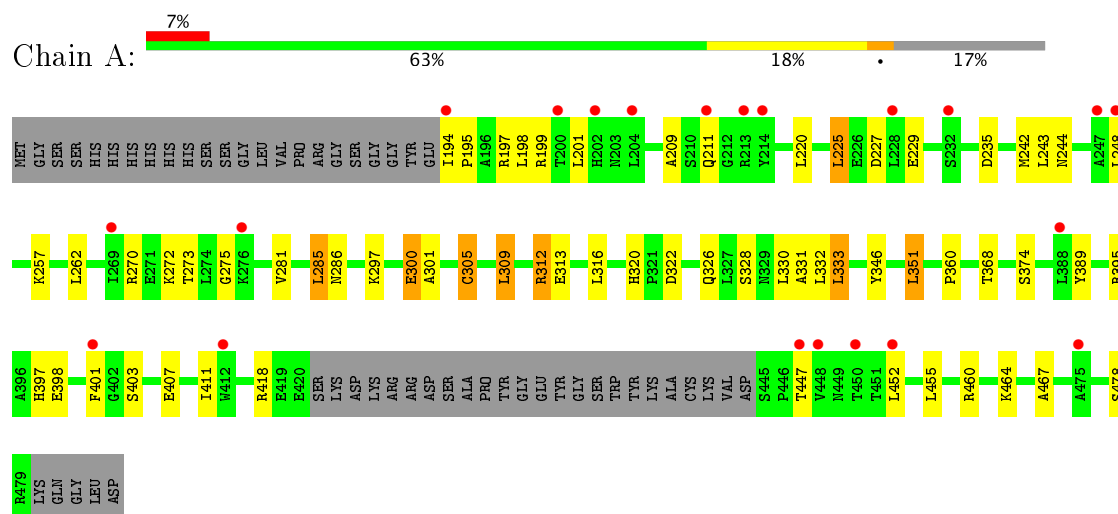
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Chain	Residue	Modelled	Actual	Comment	Reference
B	175	HIS	-	expression tag	UNP Q91YS4
B	176	HIS	-	expression tag	UNP Q91YS4
B	177	HIS	-	expression tag	UNP Q91YS4
B	178	HIS	-	expression tag	UNP Q91YS4
B	179	HIS	-	expression tag	UNP Q91YS4
B	180	HIS	-	expression tag	UNP Q91YS4
B	181	SER	-	expression tag	UNP Q91YS4
B	182	SER	-	expression tag	UNP Q91YS4
B	183	GLY	-	expression tag	UNP Q91YS4
B	184	LEU	-	expression tag	UNP Q91YS4
B	185	VAL	-	expression tag	UNP Q91YS4
B	186	PRO	-	expression tag	UNP Q91YS4
B	187	ARG	-	expression tag	UNP Q91YS4
B	188	GLY	-	expression tag	UNP Q91YS4
B	189	SER	-	expression tag	UNP Q91YS4
C	171	MET	-	initiating methionine	UNP Q91YS4
C	172	GLY	-	expression tag	UNP Q91YS4
C	173	SER	-	expression tag	UNP Q91YS4
C	174	SER	-	expression tag	UNP Q91YS4
C	175	HIS	-	expression tag	UNP Q91YS4
C	176	HIS	-	expression tag	UNP Q91YS4
C	177	HIS	-	expression tag	UNP Q91YS4
C	178	HIS	-	expression tag	UNP Q91YS4
C	179	HIS	-	expression tag	UNP Q91YS4
C	180	HIS	-	expression tag	UNP Q91YS4
C	181	SER	-	expression tag	UNP Q91YS4
C	182	SER	-	expression tag	UNP Q91YS4
C	183	GLY	-	expression tag	UNP Q91YS4
C	184	LEU	-	expression tag	UNP Q91YS4
C	185	VAL	-	expression tag	UNP Q91YS4
C	186	PRO	-	expression tag	UNP Q91YS4
C	187	ARG	-	expression tag	UNP Q91YS4
C	188	GLY	-	expression tag	UNP Q91YS4
C	189	SER	-	expression tag	UNP Q91YS4

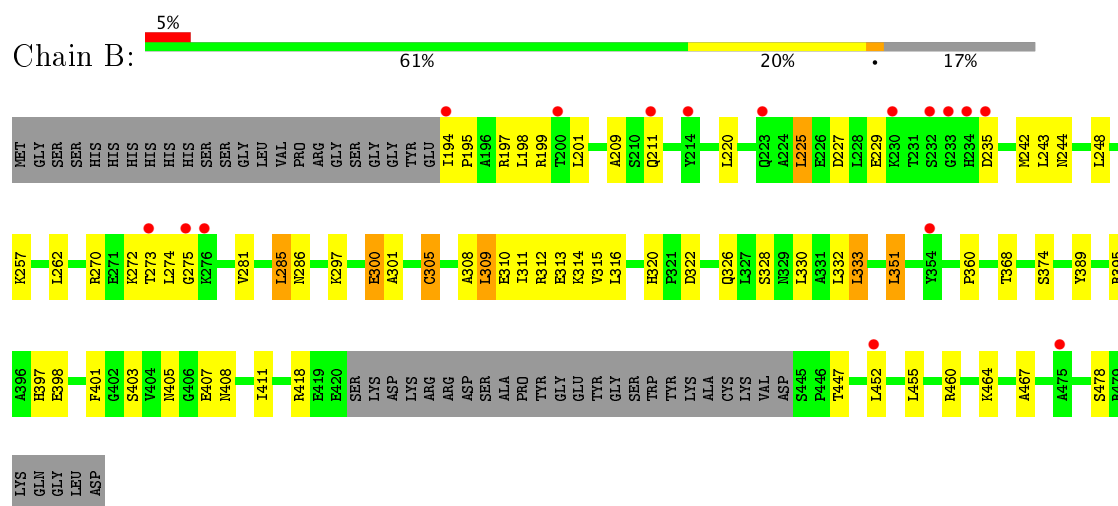
3 Residue-property plots [i](#)

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: Kinesin light chain 2

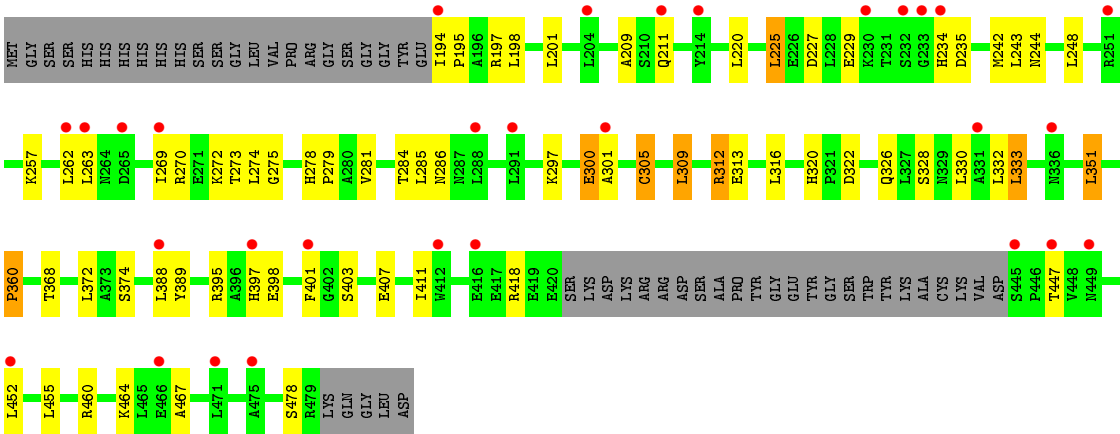


• Molecule 1: Kinesin light chain 2



• Molecule 1: Kinesin light chain 2





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	97.62Å 116.47Å 108.11Å 90.00° 99.51° 90.00°	Depositor
Resolution (Å)	20.00 – 3.40 48.14 – 3.39	Depositor EDS
% Data completeness (in resolution range)	99.9 (20.00-3.40) 99.2 (48.14-3.39)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.15 (at 3.40Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.232 , 0.264 0.258 , 0.298	Depositor DCC
R_{free} test set	821 reflections (4.99%)	DCC
Wilson B-factor (Å ²)	104.9	Xtriage
Anisotropy	0.184	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 116.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	6255	wwPDB-VP
Average B, all atoms (Å ²)	127.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 27.36 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 2.2291e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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](#)

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	0.54	0/2120	0.74	0/2861
1	B	0.53	0/2120	0.73	0/2861
1	C	0.52	0/2120	0.72	0/2861
All	All	0.53	0/6360	0.73	0/8583

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	2085	0	2102	24	0
1	B	2085	0	2102	27	0
1	C	2085	0	2102	28	0
All	All	6255	0	6306	79	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.

The worst 5 of 79 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:B:225:LEU:HD12	1:B:242:MET:HB3	1.61	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:225:LEU:HD12	1:A:242:MET:HB3	1.64	0.80
1:C:225:LEU:HD12	1:C:242:MET:HB3	1.62	0.78
1:A:309:LEU:HD12	1:A:326:GLN:HG3	1.70	0.73
1:B:309:LEU:HD12	1:B:326:GLN:HG3	1.85	0.58

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	258/314 (82%)	235 (91%)	19 (7%)	4 (2%)	11	48
1	B	258/314 (82%)	235 (91%)	19 (7%)	4 (2%)	11	48
1	C	258/314 (82%)	235 (91%)	19 (7%)	4 (2%)	11	48
All	All	774/942 (82%)	705 (91%)	57 (7%)	12 (2%)	11	48

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	360	PRO
1	A	478	SER
1	B	360	PRO
1	B	478	SER
1	C	360	PRO

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	219/261 (84%)	187 (85%)	32 (15%)	3	19
1	B	219/261 (84%)	187 (85%)	32 (15%)	3	19
1	C	219/261 (84%)	187 (85%)	32 (15%)	3	19
All	All	657/783 (84%)	561 (85%)	96 (15%)	3	19

5 of 96 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	273	THR
1	B	332	LEU
1	C	374	SER
1	B	285	LEU
1	B	309	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	202	HIS
1	B	337	GLN
1	C	337	GLN
1	A	405	ASN
1	C	326	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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, 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	262/314 (83%)	0.64	21 (8%) 13 13	74, 120, 169, 206	0
1	B	262/314 (83%)	0.60	16 (6%) 22 21	66, 121, 175, 213	0
1	C	262/314 (83%)	0.85	30 (11%) 5 6	82, 130, 178, 207	0
All	All	786/942 (83%)	0.70	67 (8%) 11 12	66, 124, 175, 213	0

The worst 5 of 67 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	416	GLU	5.2
1	C	471	LEU	5.0
1	B	232	SER	4.6
1	B	233	GLY	4.5
1	C	234	HIS	4.1

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.