

wwPDB X-ray Structure Validation Summary Report (i)

Aug 28, 2023 - 03:20 AM EDT

PDB ID	:	3KUS
Title	:	Crystal structure of the MLLE domain of poly(A)-binding protein in complex
		with the binding region of Paip2
Authors	:	Kozlov, G.; Gehring, K.
Deposited on	:	2009-11-27
Resolution	:	1.40 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 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:

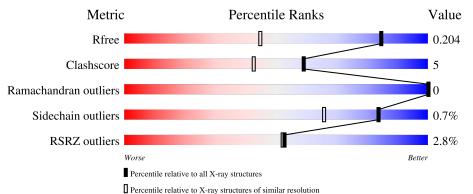
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 1.40 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	1714 (1.40-1.40)
Clashscore	141614	1812 (1.40-1.40)
Ramachandran outliers	138981	1763 (1.40-1.40)
Sidechain outliers	138945	1762 (1.40-1.40)
RSRZ outliers	127900	1674 (1.40-1.40)

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		
1	А	88	86%		7% 7%
1	В	88	% 73%	7%	20%
2	С	15	7%		27%
2	D	15	87%		7% 7%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard



residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	GOL	А	1	-	-	Х	-



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 1503 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.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	82	Total	С	Ν	0	S	0	9	Ο
1	Л	02	627	393	107	122	5	0	2	0
1	В	70	Total	С	Ν	0	S	0	1	0
1	D	70	536	339	92	101	4	0	1	0

• Molecule 1 is a protein called Polyadenylate-binding protein 1.

Chain	Residue	Modelled	Actual	Comment	Reference
А	539	GLY	-	expression tag	UNP P11940
А	540	PRO	-	expression tag	UNP P11940
А	541	LEU	-	expression tag	UNP P11940
А	542	GLY	-	expression tag	UNP P11940
А	543	SER	-	expression tag	UNP P11940
В	539	GLY	-	expression tag	UNP P11940
В	540	PRO	-	expression tag	UNP P11940
В	541	LEU	-	expression tag	UNP P11940
В	542	GLY	-	expression tag	UNP P11940
В	543	SER	-	expression tag	UNP P11940

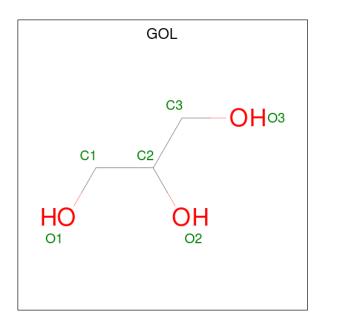
There are 10 discrepancies between the modelled and reference sequences:

• Molecule 2 is a protein called PAIP2 protein.

Mol	Chain	Residues	1	Ator	ns		ZeroOcc	AltConf	Trace
9	С	11	Total	С	Ν	0	0	0	0
	U	11	83	54	14	15	0	0	0
9	Л	14	Total	С	Ν	0	0	0	0
	D	14	108	69	19	20	0	U	0

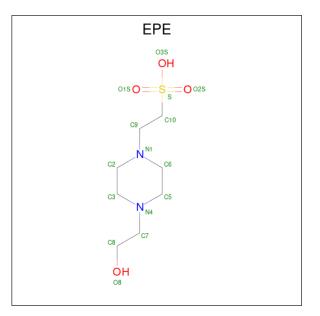
• Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	А	1	Total 6	C 3	O 3	0	0

• Molecule 4 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: $C_8H_{18}N_2O_4S$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
4	В	1	Total	С	Ν	0	S	0	0
T	D	Ĩ	15	8	2	4	1		0

• Molecule 5 is water.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	63	$\begin{array}{cc} \text{Total} & \text{O} \\ 63 & 63 \end{array}$	0	0
5	В	50	Total O 50 50	0	0
5	С	7	Total O 7 7	0	0
5	D	8	Total O 8 8	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.

- Chain A: 86% 7% 7% GLY PRO LEU GLY SER SER • Molecule 1: Polyadenylate-binding protein 1 Chain B: 73% 7% 20% GLY CEU CEU GLY SER PRO PRO LEU ALA SER MET CEU • Molecule 2: PAIP2 protein Chain C: 73% 27% • Molecule 2: PAIP2 protein 20% Chain D: 87% 7% 7%
- Molecule 1: Polyadenylate-binding protein 1



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants	26.40Å 31.61Å 48.21Å	Depositor
a, b, c, α , β , γ	100.12° 92.26° 98.90°	Depositor
Resolution (Å)	47.35 - 1.40	Depositor
Resolution (A)	30.70 - 1.40	EDS
% Data completeness	95.7 (47.35 - 1.40)	Depositor
(in resolution range)	95.7 (30.70-1.40)	EDS
R _{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$4.34 (at 1.40 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.178 , 0.205	Depositor
II, II, <i>free</i>	0.177 , 0.204	DCC
R_{free} test set	1438 reflections (5.03%)	wwPDB-VP
Wilson B-factor $(Å^2)$	11.6	Xtriage
Anisotropy	0.073	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.40 , 47.1	EDS
L-test for twinning ²	$ \langle L \rangle = 0.50, \langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	1503	wwPDB-VP
Average B, all atoms $(Å^2)$	10.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 11.15% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities 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: EPE, GOL

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		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.43	0/641	0.50	0/863	
1	В	0.35	0/547	0.47	0/740	
2	С	0.39	0/85	0.41	0/115	
2	D	0.37	0/110	0.42	0/147	
All	All	0.39	0/1383	0.48	0/1865	

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	А	627	0	651	7	0
1	В	536	0	548	5	0
2	С	83	0	81	0	0
2	D	108	0	109	1	0
3	А	6	0	8	4	0
4	В	15	0	17	1	0
5	А	63	0	0	1	0
5	В	50	0	0	0	0
5	С	7	0	0	0	0

Continued on next page...



Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	8	0	0	1	0
All	All	1503	0	1414	13	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 5.

The worst 5 of 13 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:574:HIS:HD2	3:A:1:GOL:H2	1.44	0.81
1:A:574:HIS:HD2	3:A:1:GOL:C2	2.02	0.72
1:A:574:HIS:CD2	3:A:1:GOL:H2	2.26	0.70
1:A:592:GLU:HG2	1:A:596:MET:HE2	1.77	0.65
1:A:592:GLU:HG2	1:A:596:MET:CE	2.35	0.57

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	Perce	entiles
1	А	82/88~(93%)	82 (100%)	0	0	100	100
1	В	69/88~(78%)	69 (100%)	0	0	100	100
2	С	9/15~(60%)	9 (100%)	0	0	100	100
2	D	12/15~(80%)	12 (100%)	0	0	100	100
All	All	172/206~(84%)	172 (100%)	0	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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles		
1	А	69/71~(97%)	68~(99%)	1 (1%)	67 40		
1	В	58/71~(82%)	58 (100%)	0	100 100		
2	С	9/13~(69%)	9 (100%)	0	100 100		
2	D	12/13~(92%)	12 (100%)	0	100 100		
All	All	148/168~(88%)	147 (99%)	1 (1%)	84 66		

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type	
1	А	598	GLU	

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	А	595	HIS
1	В	595	HIS
1	В	618	GLN
1	А	574	HIS
1	А	556	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

2 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).

Mal	Mol Type Ch		Chain Res		Link Bond lengths			Bond angles		
IVIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
4	EPE	В	1	-	$15,\!15,\!15$	0.83	1 (6%)	18,20,20	2.09	5 (27%)
3	GOL	А	1	-	$5,\!5,\!5$	0.44	0	$5,\!5,\!5$	0.33	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
4	EPE	В	1	-	-	4/9/19/19	0/1/1/1
3	GOL	А	1	-	-	1/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
4	В	1	EPE	C10-S	2.85	1.81	1.77

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
4	В	1	EPE	C5-N4-C3	5.39	120.97	108.83
4	В	1	EPE	O1S-S-C10	4.03	111.77	106.92
4	В	1	EPE	C7-N4-C3	3.29	119.66	111.23
4	В	1	EPE	C7-N4-C5	3.18	119.36	111.23
4	В	1	EPE	O2S-S-C10	2.05	109.38	106.92



There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	В	1	EPE	S-C10-C9-N1
4	В	1	EPE	N4-C7-C8-O8
4	В	1	EPE	C10-C9-N1-C2
4	В	1	EPE	C10-C9-N1-C6
3	А	1	GOL	O1-C1-C2-C3

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	В	1	EPE	1	0
3	А	1	GOL	4	0

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	$\langle RSRZ \rangle$	# RSRZ > 2	$OWAB(Å^2)$	Q<0.9
1	А	82/88~(93%)	0.27	0 100 100	3, 6, 15, 18	0
1	В	70/88~(79%)	0.24	1 (1%) 75 74	5, 9, 15, 18	0
2	\mathbf{C}	11/15~(73%)	0.46	1 (9%) 9 8	7, 11, 14, 14	0
2	D	14/15~(93%)	0.80	$3\ (21\%)\ 0\ 0$	9, 14, 18, 19	0
All	All	177/206~(85%)	0.31	5 (2%) 53 52	3, 9, 16, 19	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	622	ALA	5.1
2	С	121	GLY	3.6
2	D	110	ASN	3.3
2	D	123	LYS	3.1
2	D	122	VAL	2.7

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,



Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	Q<0.9
3	GOL	А	1	6/6	0.65	0.28	$20,\!23,\!27,\!28$	0
4	EPE	В	1	15/15	0.94	0.29	34,36,36,36	10

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.

6.5 Other polymers (i)

There are no such residues in this entry.

