



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 21, 2025 – 11:42 PM EDT

PDB ID : 7KIQ / pdb_00007kiq
Title : Crystal structure of the mouse lipin-2 M-Lip domain
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Deposited on : 2020-10-24
Resolution : 2.52 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.006 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.42

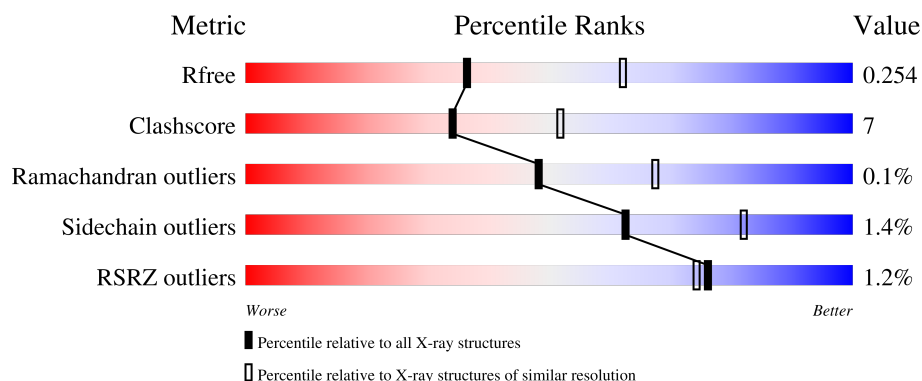
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION





The reported resolution of this entry is 2.52 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}	164625	6935 (2.54-2.50)
Clashscore	180529	7778 (2.54-2.50)
Ramachandran outliers	177936	7674 (2.54-2.50)
Sidechain outliers	177891	7676 (2.54-2.50)
RSRZ outliers	164620	6935 (2.54-2.50)

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 $\leq 5\%$. 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	91	 80% 8% 12%
1	B	91	 73% 16% 10%
1	C	91	 77% 18% 5%
1	D	91	 75% 13% 12%
1	E	91	 75% 16% 9%

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Mol	Chain	Length	Quality of chain
1	F	91	<div><div></div><div>73%15%10%</div></div>
1	G	91	<div><div>2%</div><div></div><div>67%21%12%</div></div>
1	H	91	<div><div>2%</div><div></div><div>70%18%12%</div></div>
1	I	91	<div><div>2%</div><div></div><div>77%11%12%</div></div>
1	J	91	<div><div>3%</div><div></div><div>66%18%16%</div></div>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6814 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 Phosphatidate phosphatase LPIN2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	80	Total	C	N	O	S	0	0	0
			645	422	104	116	3			
1	B	82	Total	C	N	O	S	0	0	0
			662	432	107	120	3			
1	C	87	Total	C	N	O	S	0	0	0
			700	453	113	130	4			
1	D	80	Total	C	N	O	S	0	0	0
			648	423	105	117	3			
1	E	83	Total	C	N	O	S	0	0	0
			670	437	108	121	4			
1	F	82	Total	C	N	O	S	0	0	0
			662	432	107	120	3			
1	G	80	Total	C	N	O	S	0	0	0
			648	423	105	117	3			
1	H	80	Total	C	N	O	S	0	0	0
			652	426	105	117	4			
1	I	80	Total	C	N	O	S	0	0	0
			644	420	104	117	3			
1	J	76	Total	C	N	O	S	0	0	0
			619	407	100	109	3			

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		
2	B	1	Total	Ca	0	0
			1	1		
2	C	1	Total	Ca	0	0
			1	1		
2	D	1	Total	Ca	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	E	1	Total 1	Ca 1	0	0
2	F	1	Total 1	Ca 1	0	0
2	G	1	Total 1	Ca 1	0	0
2	H	1	Total 1	Ca 1	0	0
2	I	1	Total 1	Ca 1	0	0
2	J	1	Total 1	Ca 1	0	0


- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	36	Total 36	O 36	0	0
3	B	30	Total 30	O 30	0	0
3	C	35	Total 35	O 35	0	0
3	D	26	Total 26	O 26	0	0
3	E	32	Total 32	O 32	0	0
3	F	17	Total 17	O 17	0	0
3	G	21	Total 21	O 21	0	0
3	H	26	Total 26	O 26	0	0
3	I	22	Total 22	O 22	0	0
3	J	9	Total 9	O 9	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: Phosphatidate phosphatase LPIN2

Chain A: 



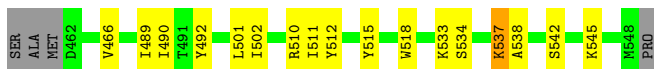
- Molecule 1: Phosphatidate phosphatase LPIN2

Chain B: 



- Molecule 1: Phosphatidate phosphatase LPIN2

Chain C: 




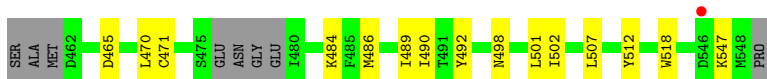
- Molecule 1: Phosphatidate phosphatase LPIN2

Chain D: 



- Molecule 1: Phosphatidate phosphatase LPIN2

Chain E: 



- Molecule 1: Phosphatidate phosphatase LPIN2

Chain F: 



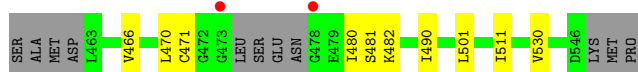
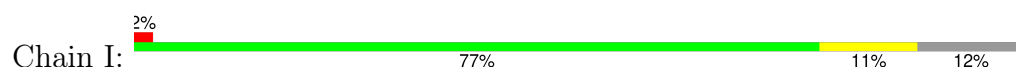
- Molecule 1: Phosphatidate phosphatase LPIN2



- Molecule 1: Phosphatidate phosphatase LPIN2



- Molecule 1: Phosphatidate phosphatase LPIN2



- Molecule 1: Phosphatidate phosphatase LPIN2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	70.71Å 84.61Å 97.51Å 90.00° 108.90° 90.00°	Depositor
Resolution (Å)	47.35 – 2.52 47.35 – 2.52	Depositor EDS
% Data completeness (in resolution range)	98.5 (47.35-2.52) 98.4 (47.35-2.52)	Depositor EDS
R_{merge}	0.26	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.09 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.14 _3260	Depositor
R, R_{free}	0.212 , 0.252 0.214 , 0.254	Depositor DCC
R_{free} test set	2353 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	44.7	Xtriage
Anisotropy	0.671	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 43.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.025 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6814	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.02% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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.

5 Model quality

5.1 Standard geometry

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

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	0.26	0/661	0.39	0/898
1	B	0.37	0/678	0.51	1/920 (0.1%)
1	C	0.28	0/717	0.41	0/973
1	D	0.26	0/664	0.38	0/901
1	E	0.26	0/686	0.41	0/930
1	F	0.37	0/678	0.53	1/920 (0.1%)
1	G	0.38	0/664	0.45	0/901
1	H	0.26	0/668	0.41	0/906
1	I	0.29	0/660	0.43	0/896
1	J	0.25	0/635	0.43	0/863
All	All	0.30	0/6711	0.44	2/9108 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	484	LYS	CD-CE-NZ	8.17	130.50	111.70
1	F	545	LYS	CD-CE-NZ	-5.25	99.63	111.70

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	A	645	0	649	5	0
1	B	662	0	666	13	0
1	C	700	0	697	15	0
1	D	648	0	650	7	0
1	E	670	0	675	12	0
1	F	662	0	666	14	0
1	G	648	0	650	18	0
1	H	652	0	656	13	0
1	I	644	0	642	5	0
1	J	619	0	626	9	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
3	A	36	0	0	0	0
3	B	30	0	0	0	0
3	C	35	0	0	1	0
3	D	26	0	0	1	0
3	E	32	0	0	1	0
3	F	17	0	0	0	0
3	G	21	0	0	0	0
3	H	26	0	0	0	0
3	I	22	0	0	1	0
3	J	9	0	0	0	0
All	All	6814	0	6577	98	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 7.

The worst 5 of 98 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:G:470:LEU:HD13	1:G:490:ILE:HD11	1.51	0.93
1:G:466:VAL:HG13	1:G:511:ILE:HD11	1.53	0.90
1:B:471:CYS:HB2	1:B:484:LYS:HE3	1.57	0.85
1:G:470:LEU:CD1	1:G:490:ILE:HD11	2.06	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:545:LYS:NZ	1:F:546:ASP:OD1	2.10	0.83

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	76/91 (84%)	75 (99%)	1 (1%)	0	100	100
1	B	78/91 (86%)	77 (99%)	1 (1%)	0	100	100
1	C	85/91 (93%)	85 (100%)	0	0	100	100
1	D	76/91 (84%)	75 (99%)	1 (1%)	0	100	100
1	E	79/91 (87%)	79 (100%)	0	0	100	100
1	F	78/91 (86%)	78 (100%)	0	0	100	100
1	G	76/91 (84%)	76 (100%)	0	0	100	100
1	H	76/91 (84%)	76 (100%)	0	0	100	100
1	I	76/91 (84%)	74 (97%)	1 (1%)	1 (1%)	10	18
1	J	72/91 (79%)	71 (99%)	1 (1%)	0	100	100
All	All	772/910 (85%)	766 (99%)	5 (1%)	1 (0%)	48	67

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	I	530	VAL

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	72/81 (89%)	71 (99%)	1 (1%)	62	82
1	B	74/81 (91%)	74 (100%)	0	100	100
1	C	78/81 (96%)	77 (99%)	1 (1%)	65	83
1	D	72/81 (89%)	71 (99%)	1 (1%)	62	82
1	E	75/81 (93%)	74 (99%)	1 (1%)	65	83
1	F	74/81 (91%)	71 (96%)	3 (4%)	26	47
1	G	72/81 (89%)	72 (100%)	0	100	100
1	H	73/81 (90%)	72 (99%)	1 (1%)	62	82
1	I	71/81 (88%)	70 (99%)	1 (1%)	62	82
1	J	69/81 (85%)	68 (99%)	1 (1%)	62	82
All	All	730/810 (90%)	720 (99%)	10 (1%)	62	82

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	542	SER
1	I	481	SER
1	J	545	LYS
1	E	547	LYS
1	F	514	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	529	GLN
1	B	488	HIS
1	B	529	GLN
1	G	529	GLN
1	H	529	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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 10 ligands modelled in this entry, 10 are 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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	80/91 (87%)	-0.06	0 100 100	32, 45, 68, 77	0
1	B	82/91 (90%)	0.15	0 100 100	33, 48, 72, 87	0
1	C	87/91 (95%)	0.11	0 100 100	33, 46, 75, 89	0
1	D	80/91 (87%)	0.09	0 100 100	35, 50, 71, 84	0
1	E	83/91 (91%)	0.17	1 (1%) 76 74	35, 49, 72, 86	0
1	F	82/91 (90%)	0.31	0 100 100	40, 56, 79, 103	0
1	G	80/91 (87%)	0.29	2 (2%) 58 56	39, 53, 78, 87	0
1	H	80/91 (87%)	0.27	2 (2%) 58 56	40, 53, 76, 95	0
1	I	80/91 (87%)	0.31	2 (2%) 58 56	42, 53, 71, 91	0
1	J	76/91 (83%)	0.31	3 (3%) 44 42	41, 55, 71, 85	0
All	All	810/910 (89%)	0.19	10 (1%) 76 74	32, 51, 74, 103	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	472	GLY	3.6
1	G	512	TYR	3.1
1	G	473	GLY	2.8
1	H	548	MET	2.7
1	I	473	GLY	2.7

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

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, 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(\AA^2)	Q<0.9
2	CA	C	601	1/1	0.71	0.12	114,114,114,114	0
2	CA	F	601	1/1	0.79	0.12	138,138,138,138	0
2	CA	J	601	1/1	0.82	0.18	98,98,98,98	0
2	CA	D	601	1/1	0.87	0.13	91,91,91,91	0
2	CA	A	601	1/1	0.91	0.10	77,77,77,77	0
2	CA	I	601	1/1	0.92	0.08	93,93,93,93	0
2	CA	E	601	1/1	0.94	0.07	57,57,57,57	0
2	CA	G	601	1/1	0.95	0.05	81,81,81,81	0
2	CA	H	601	1/1	0.95	0.16	76,76,76,76	0
2	CA	B	601	1/1	0.96	0.06	62,62,62,62	0

6.5 Other polymers [i](#)

There are no such residues in this entry.