

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

## Oct 17, 2021 - 03:36 AM EDT

PDB ID	:	1MJN
Title	:	Crystal Structure of the intermediate affinity aL I domain mutant
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Deposited on	:	2002-08-28
Resolution	:	1.30  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 following versions of software and data (see references (1)) were used in the production of this report:

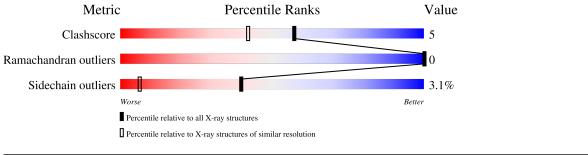
0 ( )	:	4.02b-467 NOT EXECUTED NOT EXECUTED
		20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

# 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.30 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	Similar resolution		
Metric	$(\# {\rm Entries})$	$(\# { m Entries},  { m resolution}  { m range}({ m \AA}))$		
Clashscore	141614	1101 (1.30-1.30)		
Ramachandran outliers	138981	1058 (1.30-1.30)		
Sidechain outliers	138945	1058 (1.30-1.30)		

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 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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain		
1	Δ	179	/030	1.70/	
1	Л	119	85%	12%	••



#### $1 \mathrm{MJN}$

# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 1757 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 Integrin alpha-L.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	179	Total 1434	C 921	N 231	0 275	${f S}7$	0	1	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	161	CYS	LEU	engineered mutation	UNP P20701
А	299	CYS	PHE	engineered mutation	UNP P20701

• Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	$\begin{array}{ccc} \text{Total} & \text{M}_{2} \\ 1 & 1 \end{array}$	g 0	0

• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	322	Total         O           322         322	0	0

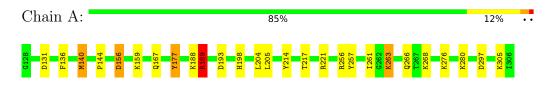


# 3 Residue-property plots (i)

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. 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.

Note EDS was not executed.

• Molecule 1: Integrin alpha-L





# 4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source	
Space group	P 21 21 21	Depositor	
Cell constants	40.37Å 57.40Å 66.91Å	Depositor	
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor	
Resolution (Å)	50.00 - 1.30	Depositor	
% Data completeness	(Not available) (50.00-1.30)	Depositor	
(in resolution range)	(1007 available) (50.00-1.50)		
$R_{merge}$	0.09	Depositor	
$R_{sym}$	0.09	Depositor	
Refinement program	SHELXL-97	Depositor	
$R, R_{free}$	0.156 , $0.202$	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	1757	wwPDB-VP	
Average B, all atoms $(Å^2)$	15.0	wwPDB-VP	



# 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: MG

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		lengths	Bond angles		
	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.63	0/1466	1.42	20/1969~(1.0%)	

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	177	TYR	CB-CG-CD1	15.03	130.02	121.00
1	А	177	TYR	CB-CG-CD2	-14.70	112.18	121.00
1	А	256	ARG	NE-CZ-NH1	9.07	124.84	120.30
1	А	214	TYR	CB-CG-CD1	-8.54	115.88	121.00
1	А	257	TYR	CB-CG-CD2	-8.45	115.93	121.00
1	А	189	ARG	NE-CZ-NH1	8.19	124.40	120.30
1	А	297	ASP	CB-CG-OD1	7.38	124.94	118.30
1	А	136	PHE	CB-CG-CD1	5.98	124.99	120.80
1	А	204	LEU	C-N-CA	5.95	136.57	121.70
1	А	156	ASP	CB-CG-OD1	-5.83	113.05	118.30
1	А	205	LEU	C-N-CA	5.70	135.96	121.70
1	А	205	LEU	O-C-N	-5.64	113.68	122.70
1	А	131	ASP	CB-CG-OD1	5.63	123.37	118.30
1	А	193	ASP	O-C-N	-5.34	114.16	122.70
1	А	140[A]	MET	CA-CB-CG	5.30	122.31	113.30
1	А	140[B]	MET	CA-CB-CG	5.30	122.31	113.30
1	А	156	ASP	CB-CG-OD2	5.18	122.96	118.30
1	А	189	ARG	CB-CG-CD	5.16	125.01	111.60
1	А	189	ARG	CG-CD-NE	5.10	122.51	111.80
1	А	189	ARG	CA-CB-CG	5.06	124.54	113.40

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	1434	0	1436	14	0
2	А	1	0	0	0	0
3	А	322	0	0	11	0
All	All	1757	0	1436	14	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.

All (14) 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:263:LYS:O	1:A:266:GLN:HG3	1.87	0.75
1:A:217:THR:O	1:A:221:ARG:HD3	1.95	0.67
1:A:188:LYS:HE3	1:A:189:ARG:NH1	2.12	0.65
1:A:268:LYS:HD3	3:A:2260:HOH:O	2.04	0.57
1:A:280:LYS:HE2	3:A:2259:HOH:O	2.04	0.57
1:A:140[B]:MET:HG2	3:A:2196:HOH:O	2.05	0.56
1:A:263:LYS:HG3	3:A:2096:HOH:O	2.10	0.52
1:A:305:LYS:HE3	3:A:2246:HOH:O	2.11	0.50
1:A:144:PRO:HG2	3:A:2092:HOH:O	2.13	0.48
1:A:140[A]:MET:HG3	3:A:2196:HOH:O	2.16	0.44
1:A:159:LYS:NZ	3:A:2161:HOH:O	2.50	0.43
1:A:156:ASP:HB2	3:A:2272:HOH:O	2.18	0.42
1:A:276:LYS:HE3	3:A:2115:HOH:O	2.20	0.42
1:A:167:GLN:NE2	3:A:2299:HOH:O	2.54	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	Percer	ntiles
1	А	178/179~(99%)	173~(97%)	5(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.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	А	160/159~(101%)	155~(97%)	5(3%)	40 6

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	177	TYR
1	А	189	ARG
1	А	198	HIS
1	А	261	ILE
1	А	263	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	207	ASN

### 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 (i)

## 6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

### 6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

#### 6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

