



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 1MQA / pdb_00001mqa
Title : Crystal structure of high affinity alphaL I domain in the absence of ligand or metal
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Deposited on : 2002-09-15
Resolution : 2.50 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 ⓘ 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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

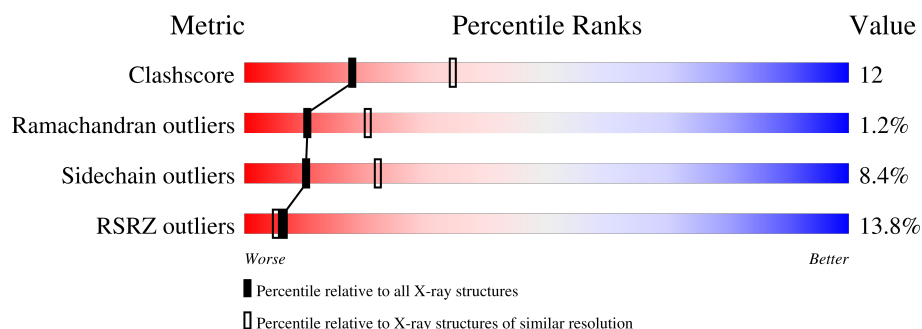
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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))
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	180	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1419 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	174	Total	C	N	O	S	0	0	0
			1388	894	221	266	7			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	127	MET	-	cloning artifact	UNP P20701
A	287	CYS	LYS	engineered mutation	UNP P20701
A	294	CYS	LYS	engineered mutation	UNP P20701

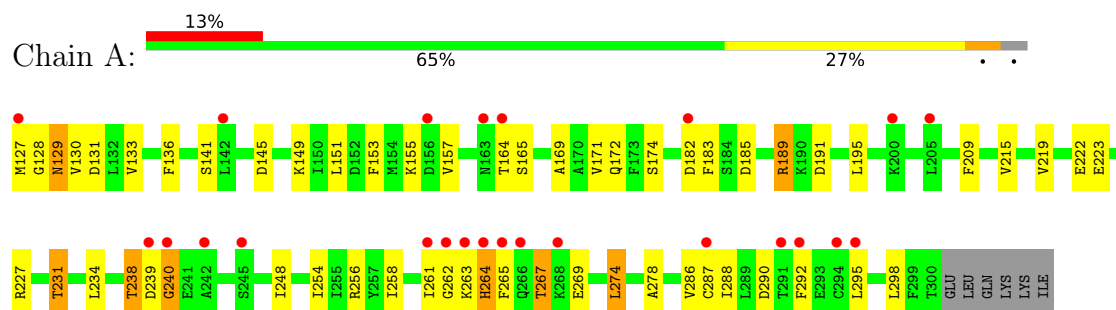
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	31	Total	O	0	0
			31	31		

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: Integrin alpha-L



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	61.86Å 121.32Å 54.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.36 – 2.50 40.36 – 2.50	Depositor EDS
% Data completeness (in resolution range)	90.9 (40.36-2.50) 90.9 (40.36-2.50)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	0.18	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.01 (at 2.48Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.249 , 0.283 0.236 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	28.6	Xtriage
Anisotropy	0.658	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 42.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	1419	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.46% 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 [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	0.37	0/1415	0.93	3/1906 (0.2%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	262	GLY	N-CA-C	-8.99	102.31	111.85
1	A	238	THR	N-CA-C	7.12	117.43	108.45
1	A	240	GLY	N-CA-C	-5.14	108.57	114.69

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	1388	0	1378	34	0
2	A	31	0	0	2	0
All	All	1419	0	1378	34	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 12.

All (34) 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:133:VAL:HG22	1:A:169:ALA:HB3	1.81	0.61
1:A:151:LEU:O	1:A:155:LYS:HG3	2.00	0.61
1:A:288:ILE:HG22	1:A:290:ASP:H	1.65	0.60
1:A:267:THR:HG22	1:A:269:GLU:H	1.67	0.60
1:A:254:ILE:O	1:A:256:ARG:HG3	2.03	0.58
1:A:239:ASP:O	1:A:265:PHE:HZ	1.86	0.57
1:A:129:ASN:H	1:A:129:ASN:ND2	2.04	0.55
1:A:258:ILE:HG22	1:A:278:ALA:HB2	1.88	0.55
1:A:295:LEU:HA	1:A:298:LEU:HD13	1.88	0.55
1:A:263:LYS:NZ	1:A:263:LYS:HB3	2.22	0.54
1:A:240:GLY:HA3	1:A:274:LEU:HD12	1.90	0.54
1:A:264:HIS:ND1	1:A:264:HIS:N	2.56	0.53
1:A:129:ASN:HD22	1:A:129:ASN:N	2.07	0.53
1:A:136:PHE:CZ	1:A:172:GLN:HB2	2.44	0.52
1:A:153:PHE:O	1:A:157:VAL:HG23	2.08	0.52
1:A:129:ASN:ND2	1:A:129:ASN:N	2.56	0.52
1:A:258:ILE:CG2	1:A:286:VAL:HG22	2.40	0.52
1:A:185:ASP:O	1:A:189:ARG:HG2	2.11	0.51
1:A:129:ASN:HA	1:A:165:SER:HB2	1.95	0.48
1:A:127:MET:HE1	1:A:231:THR:HG21	1.95	0.48
1:A:287:CYS:SG	1:A:292:PHE:HA	2.54	0.48
1:A:129:ASN:HB2	1:A:227:ARG:CZ	2.45	0.47
1:A:195:LEU:HA	2:A:30:HOH:O	2.15	0.47
1:A:171:VAL:HG21	1:A:219:VAL:HG21	1.97	0.47
1:A:127:MET:CE	1:A:231:THR:HG21	2.45	0.47
1:A:209:PHE:HD1	1:A:248:ILE:HG23	1.80	0.46
1:A:127:MET:HB3	1:A:128:GLY:H	1.50	0.46
1:A:215:VAL:HG11	1:A:234:LEU:HD13	1.98	0.45
1:A:239:ASP:O	1:A:265:PHE:CZ	2.69	0.44
1:A:191:ASP:O	1:A:195:LEU:HG	2.20	0.42
1:A:149:LYS:HB2	1:A:149:LYS:HE3	1.84	0.42
1:A:238:THR:OG1	1:A:239:ASP:N	2.45	0.41
1:A:287:CYS:HB2	2:A:8:HOH:O	2.20	0.41
1:A:131:ASP:HB3	1:A:183:PHE:CZ	2.56	0.40

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	172/180 (96%)	159 (92%)	11 (6%)	2 (1%)	10	20

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	174	SER
1	A	267	THR

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	154/160 (96%)	141 (92%)	13 (8%)	10	22

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

Mol	Chain	Res	Type
1	A	129	ASN
1	A	130	VAL
1	A	141	SER
1	A	145	ASP
1	A	164	THR
1	A	182	ASP
1	A	189	ARG
1	A	222	GLU
1	A	223	GLU

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Mol	Chain	Res	Type
1	A	231	THR
1	A	261	ILE
1	A	264	HIS
1	A	274	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	129	ASN
1	A	247	ASN
1	A	271	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 oligosaccharides 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

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	174/180 (96%)	1.04	24 (13%) 6 5	12, 33, 69, 98	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	265	PHE	4.4
1	A	294	CYS	4.0
1	A	266	GLN	3.7
1	A	163	ASN	3.3
1	A	268	LYS	3.2
1	A	264	HIS	2.8
1	A	287	CYS	2.8
1	A	239	ASP	2.8
1	A	262	GLY	2.8
1	A	292	PHE	2.7
1	A	261	ILE	2.6
1	A	205	LEU	2.6
1	A	295	LEU	2.5
1	A	127	MET	2.4
1	A	142	LEU	2.3
1	A	291	THR	2.3
1	A	182	ASP	2.2
1	A	245	SER	2.2
1	A	263	LYS	2.2
1	A	156	ASP	2.1
1	A	242	ALA	2.1
1	A	240	GLY	2.0
1	A	164	THR	2.0
1	A	200	LYS	2.0

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 oligosaccharides 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.