



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 3, 2021 – 05:51 PM EDT

PDB ID : 3HI6
Title : Crystal structure of intermediate affinity I domain of integrin LFA-1 with the Fab fragment of its antibody AL-57
Authors : Zhang, H.; Wang, J.
Deposited on : 2009-05-19
Resolution : 2.30 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) 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 : 2.23.2
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) : 2.23.2

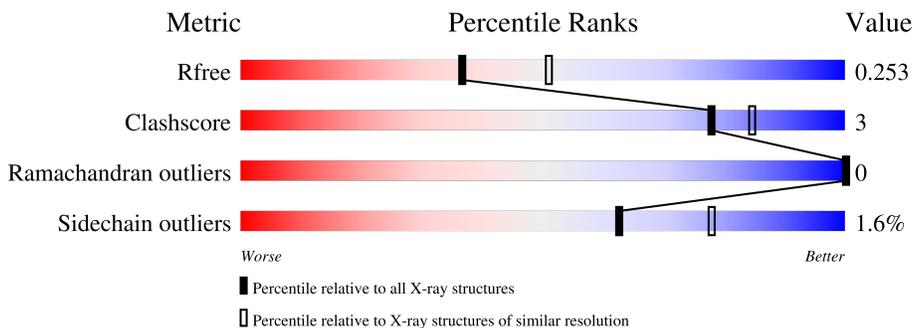
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	180	
1	B	180	
2	H	220	
2	X	220	
3	L	212	
3	Y	212	

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 10097 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
			Total	C	N	O	S			
1	A	180	1447	934	230	277	6	0	0	0
1	B	180	1454	939	232	277	6	0	1	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	161	CYS	LEU	engineered mutation	UNP P20701
A	189	TRP	ARG	variant	UNP P20701
A	299	CYS	PHE	engineered mutation	UNP P20701
B	161	CYS	LEU	engineered mutation	UNP P20701
B	189	TRP	ARG	variant	UNP P20701
B	299	CYS	PHE	engineered mutation	UNP P20701

- Molecule 2 is a protein called Heavy chain of Fab fragment of AL-57 against alpha L I domain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	H	213	1622	1031	268	316	7	0	0	0
2	X	217	1645	1043	272	323	7	0	0	0

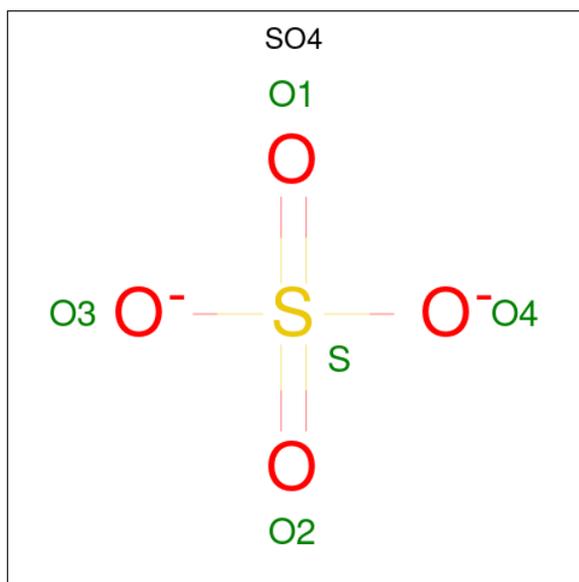
- Molecule 3 is a protein called light chain of Fab fragment of AL-57 against alpha L I domain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	L	210	1601	998	269	329	5	0	0	0
3	Y	209	1596	996	268	327	5	0	0	0

- Molecule 4 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Mn 1 1	0	0
4	B	1	Total Mn 1 1	0	0

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total O S 5 4 1	0	0
5	H	1	Total O S 5 4 1	0	0
5	H	1	Total O S 5 4 1	0	0
5	L	1	Total O S 5 4 1	0	0
5	X	1	Total O S 5 4 1	0	0
5	Y	1	Total O S 5 4 1	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	98	Total O 98 98	0	0
6	B	111	Total O 111 111	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	H	152	Total 152	O 152	0	0
6	L	128	Total 128	O 128	0	0
6	X	101	Total 101	O 101	0	0
6	Y	110	Total 110	O 110	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.

- Molecule 1: Integrin alpha-L

Chain A:  91% 9%



- Molecule 1: Integrin alpha-L

Chain B:  92% 8%



- Molecule 2: Heavy chain of Fab fragment of AL-57 against alpha L I domain

Chain H:  87% 10%



- Molecule 2: Heavy chain of Fab fragment of AL-57 against alpha L I domain

Chain X:  93% 5%



- Molecule 3: light chain of Fab fragment of AL-57 against alpha L I domain

Chain L:  93% 6%



- Molecule 3: light chain of Fab fragment of AL-57 against alpha L I domain

Chain Y:  90% 8%



4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	133.78Å 133.78Å 161.05Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.30 38.62 – 2.30	Depositor EDS
% Data completeness (in resolution range)	94.5 (30.00-2.30) 94.5 (38.62-2.30)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.64 (at 2.31Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.170 , 0.226 0.221 , 0.253	Depositor DCC
R_{free} test set	3449 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	35.0	Xtrriage
Anisotropy	0.017	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 49.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.034 for h,-h-k,-l	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	10097	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.28% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MN, SO4

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	0.50	0/1476	0.59	0/1986
1	B	0.48	0/1487	0.61	0/2001
2	H	0.47	0/1666	0.60	0/2271
2	X	0.39	0/1689	0.56	0/2302
3	L	0.48	0/1633	0.59	0/2213
3	Y	0.42	0/1628	0.56	0/2208
All	All	0.46	0/9579	0.58	0/12981

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	1447	0	1440	9	0
1	B	1454	0	1447	8	0
2	H	1622	0	1563	12	0
2	X	1645	0	1581	10	0
3	L	1601	0	1557	6	0
3	Y	1596	0	1554	11	0
4	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	1	0	0	0	0
5	B	5	0	0	0	0
5	H	10	0	0	0	0
5	L	5	0	0	0	0
5	X	5	0	0	0	0
5	Y	5	0	0	0	0
6	A	98	0	0	1	1
6	B	111	0	0	1	0
6	H	152	0	0	2	1
6	L	128	0	0	1	0
6	X	101	0	0	1	0
6	Y	110	0	0	2	0
All	All	10097	0	9142	53	1

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 3.

All (53) 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)
3:Y:107:ARG:NH1	3:Y:110:ALA:HB2	2.01	0.75
3:Y:107:ARG:HH12	3:Y:110:ALA:HB2	1.52	0.74
3:Y:108:THR:HG22	6:Y:599:HOH:O	1.99	0.62
2:H:168:SER:H	2:X:199:LYS:HZ3	1.48	0.60
2:X:5:LEU:HD12	2:X:112:GLN:OE1	2.03	0.59
3:L:19:VAL:HG11	3:L:78:LEU:HD11	1.84	0.59
2:H:199:LYS:HE2	2:X:195:SER:HA	1.84	0.58
1:A:157:VAL:HG22	1:A:298:LEU:HD21	1.86	0.58
2:X:109:ILE:HD12	6:X:243:HOH:O	2.04	0.58
3:Y:107:ARG:NH1	3:Y:108:THR:O	2.38	0.56
2:H:48:VAL:HG13	2:H:64:VAL:HG11	1.88	0.56
3:L:72:THR:HG23	6:L:570:HOH:O	2.04	0.56
3:L:162:VAL:HG22	3:L:174:LEU:HD12	1.88	0.56
2:H:195:SER:HB2	2:H:199:LYS:HD3	1.89	0.54
2:X:11:LEU:HD23	2:X:123:THR:HG22	1.89	0.53
1:A:298:LEU:HD11	1:A:302:LEU:HD11	1.91	0.53
2:H:199:LYS:NZ	6:H:271:HOH:O	2.42	0.53
1:B:258:ILE:HG21	1:B:274:LEU:HD22	1.91	0.51
2:X:11:LEU:HD23	2:X:123:THR:CG2	2.40	0.51
2:H:155:GLU:CG	2:H:156:PRO:HA	2.41	0.51
2:H:40:ALA:HB3	2:H:43:LYS:HG3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:273:THR:HG22	1:B:277:PHE:CE2	2.49	0.48
1:A:289:LEU:C	1:A:289:LEU:HD23	2.33	0.48
1:B:158:MET:CE	1:B:186:TYR:CD1	2.97	0.48
3:Y:174:LEU:C	3:Y:174:LEU:HD23	2.34	0.48
1:B:158:MET:HE2	1:B:186:TYR:CE1	2.49	0.47
1:B:287:LYS:HE3	6:B:502:HOH:O	2.14	0.47
3:Y:119:PRO:HD3	3:Y:131:VAL:HG22	1.96	0.47
1:B:201:HIS:CE1	1:B:203:LEU:HD21	2.50	0.46
3:Y:2:ILE:N	6:Y:451:HOH:O	2.49	0.45
1:A:198:HIS:HD2	6:A:375:HOH:O	1.99	0.45
3:Y:105:ILE:O	3:Y:165:GLN:NE2	2.43	0.45
1:A:301:GLU:HG2	1:A:304:LYS:HZ2	1.82	0.45
1:B:236:ILE:HD12	1:B:258:ILE:CD1	2.47	0.44
1:A:133:VAL:HG23	1:A:220:PHE:CZ	2.52	0.44
2:H:155:GLU:HG3	2:H:156:PRO:HA	1.98	0.44
2:H:33:VAL:HG23	2:H:103:TRP:HB3	1.99	0.44
2:X:11:LEU:CD2	2:X:123:THR:HG22	2.48	0.44
3:L:6:GLN:O	3:L:99:GLN:NE2	2.39	0.43
2:H:30:SER:O	2:H:53:PRO:HB3	2.18	0.43
2:H:150:LYS:NZ	6:H:435:HOH:O	2.52	0.43
3:Y:48:ILE:HD12	3:Y:73:LEU:CD1	2.49	0.42
3:L:144:LYS:HB3	3:L:196:THR:HB	2.01	0.42
3:Y:50:ALA:O	3:Y:51:ALA:HB3	2.19	0.42
2:X:124:LYS:HZ3	2:X:151:ASP:HB3	1.85	0.42
1:A:160:LYS:CE	1:A:296:LYS:HA	2.50	0.41
1:B:133:VAL:HG23	1:B:220:PHE:CZ	2.55	0.41
2:H:25:SER:HB3	2:X:25:SER:HB3	2.03	0.41
1:A:158:MET:HE2	1:A:186:TYR:CE1	2.56	0.41
2:X:145:LEU:HD12	2:X:145:LEU:C	2.41	0.41
1:A:265:PHE:CD2	1:A:266:GLN:HG3	2.56	0.41
3:Y:200:LEU:HD13	3:Y:204:VAL:HG23	2.02	0.41
3:L:48:ILE:HD12	3:L:73:LEU:CD1	2.52	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:438:HOH:O	6:H:675:HOH:O[4_545]	1.83	0.37

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	178/180 (99%)	169 (95%)	9 (5%)	0	100	100
1	B	179/180 (99%)	172 (96%)	7 (4%)	0	100	100
2	H	209/220 (95%)	205 (98%)	4 (2%)	0	100	100
2	X	213/220 (97%)	204 (96%)	9 (4%)	0	100	100
3	L	208/212 (98%)	202 (97%)	6 (3%)	0	100	100
3	Y	207/212 (98%)	199 (96%)	8 (4%)	0	100	100
All	All	1194/1224 (98%)	1151 (96%)	43 (4%)	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	A	160/160 (100%)	159 (99%)	1 (1%)	86	94
1	B	161/160 (101%)	159 (99%)	2 (1%)	71	84
2	H	180/187 (96%)	174 (97%)	6 (3%)	38	53
2	X	183/187 (98%)	181 (99%)	2 (1%)	73	86
3	L	183/185 (99%)	180 (98%)	3 (2%)	62	78
3	Y	183/185 (99%)	180 (98%)	3 (2%)	62	78
All	All	1050/1064 (99%)	1033 (98%)	17 (2%)	62	78

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	306	ILE
1	B	188	LYS
1	B	222	GLU
2	H	99	SER
2	H	112	GLN
2	H	142	THR
2	H	179	SER
2	H	206	ASP
2	H	220	SER
3	L	19	VAL
3	L	56	SER
3	L	90	GLN
2	X	99	SER
2	X	199	LYS
3	Y	20	THR
3	Y	99	GLN
3	Y	153	LEU

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

Mol	Chain	Res	Type
2	X	171	HIS

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 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 for Mogul analysis.

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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	SO4	H	222	-	4,4,4	0.17	0	6,6,6	0.34	0
5	SO4	H	221	-	4,4,4	0.15	0	6,6,6	0.44	0
5	SO4	Y	212	-	4,4,4	0.12	0	6,6,6	0.13	0
5	SO4	B	5	-	4,4,4	0.13	0	6,6,6	0.06	0
5	SO4	L	212	-	4,4,4	0.13	0	6,6,6	0.06	0
5	SO4	X	221	-	4,4,4	0.13	0	6,6,6	0.14	0

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

6.1 Protein, DNA and RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.