



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 17, 2024 – 09:01 AM EDT

PDB ID : 3EOB
Title : Crystal structure the Fab fragment of Efalizumab in complex with LFA-1 I domain, Form II
Authors : Li, S.; Ding, J.
Deposited on : 2008-09-26
Resolution : 3.60 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) : 1.20.1
EDS : 2.37.1
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) : 2.37.1

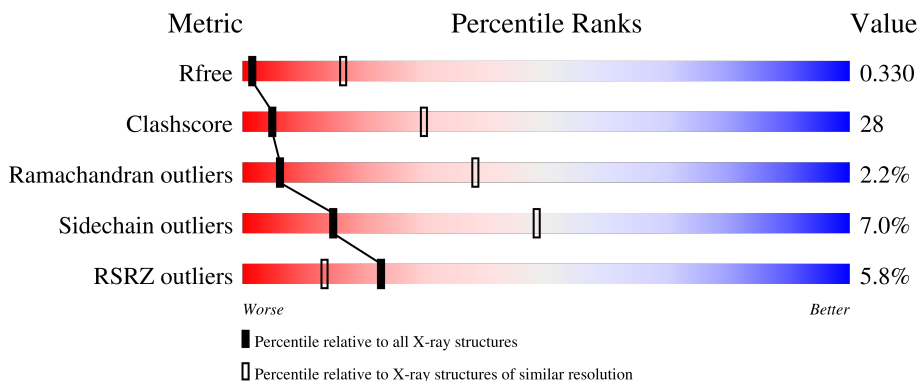
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.60 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	1257 (3.70-3.50)
Clashscore	141614	1353 (3.70-3.50)
Ramachandran outliers	138981	1307 (3.70-3.50)
Sidechain outliers	138945	1307 (3.70-3.50)
RSRZ outliers	127900	1161 (3.70-3.50)

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	214	
1	L	214	
2	B	220	
2	H	220	
3	I	181	

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Mol	Chain	Length	Quality of chain
3	J	181	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into four segments: a small red segment (2%), a large green segment (47%), a large yellow segment (46%), and a small orange segment (6%).</p>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 9454 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 Efalizumab Fab fragment, light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	L	214	Total 1647	C 1030	N 276	O 335	S 6	0	0	0
1	A	214	Total 1647	C 1030	N 276	O 335	S 6	0	0	0

- Molecule 2 is a protein called Efalizumab Fab fragment, heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	H	215	Total 1641	C 1043	N 273	O 318	S 7	0	0	0
2	B	215	Total 1641	C 1043	N 273	O 318	S 7	0	0	0

- Molecule 3 is a protein called Integrin alpha-L.

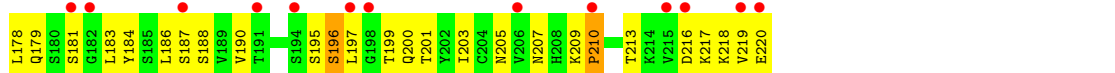
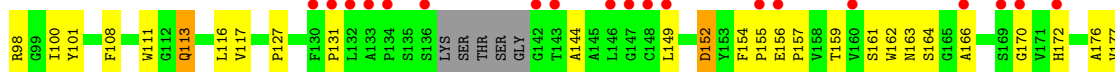
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	I	179	Total 1438	C 929	N 231	O 274	S 4	0	0	0
3	J	179	Total 1438	C 929	N 231	O 274	S 4	0	0	0

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

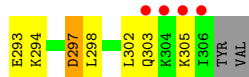
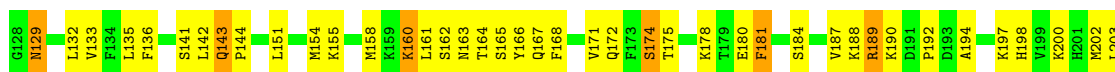
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	I	1	Total 1	Zn 1	0	0
4	J	1	Total 1	Zn 1	0	0



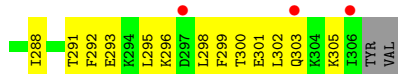
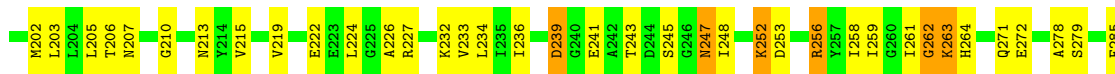
- Molecule 2: Efalizumab Fab fragment, heavy chain



- Molecule 3: Integrin alpha-L



- Molecule 3: Integrin alpha-L



4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	111.10Å 111.10Å 470.73Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 3.60 47.84 – 3.60	Depositor EDS
% Data completeness (in resolution range)	97.7 (50.00-3.60) 97.8 (47.84-3.60)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	0.20	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.18 (at 3.57Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.267 , 0.333 0.267 , 0.330	Depositor DCC
R_{free} test set	1031 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	99.2	Xtrriage
Anisotropy	0.022	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 85.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	9454	wwPDB-VP
Average B, all atoms (Å ²)	97.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.89% 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:
ZN

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	0.48	0/1682	0.73	2/2280 (0.1%)
1	L	0.45	0/1682	0.73	0/2280
2	B	0.54	2/1684 (0.1%)	0.75	1/2291 (0.0%)
2	H	0.58	2/1684 (0.1%)	0.78	2/2291 (0.1%)
3	I	0.63	3/1465 (0.2%)	0.83	4/1970 (0.2%)
3	J	0.60	0/1465	0.85	1/1970 (0.1%)
All	All	0.55	7/9662 (0.1%)	0.78	10/13082 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	H	0	1
3	I	0	1
All	All	0	2

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	I	241	GLU	CG-CD	7.92	1.63	1.51
3	I	141	SER	CA-CB	-7.37	1.41	1.52
2	H	57	GLU	CB-CG	7.21	1.65	1.52
2	H	57	GLU	CG-CD	6.78	1.62	1.51
2	B	57	GLU	CB-CG	6.61	1.64	1.52

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	J	239	ASP	CB-CG-OD1	-9.41	109.83	118.30
3	I	141	SER	CA-CB-OG	-8.05	89.47	111.20
3	I	239	ASP	CB-CG-OD1	-7.86	111.22	118.30
2	H	61	ASN	N-CA-C	-6.77	92.71	111.00
2	B	61	ASN	N-CA-C	-6.25	94.13	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	H	103	TYR	Sidechain
3	I	261	ILE	Peptide

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	1647	0	1608	69	1
1	L	1647	0	1608	105	0
2	B	1641	0	1591	88	0
2	H	1641	0	1591	99	0
3	I	1438	0	1449	90	0
3	J	1438	0	1449	97	0
4	I	1	0	0	0	0
4	J	1	0	0	0	0
All	All	9454	0	9296	516	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 28.

The worst 5 of 516 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:115:VAL:HG21	1:A:196:VAL:HG21	1.38	1.05
1:L:1:ASP:O	1:L:2:ILE:HG13	1.59	1.03
1:L:175:LEU:HD23	1:L:176:SER:N	1.78	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:143:GLN:HG3	3:J:144:PRO:HD2	1.49	0.94
1:L:80:PRO:HA	1:L:106:ILE:HD13	1.50	0.94

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)
1:A:1:ASP:OD2	1:A:1:ASP:OD2[9_554]	2.06	0.14

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	212/214 (99%)	193 (91%)	17 (8%)	2 (1%)	17	57
1	L	212/214 (99%)	182 (86%)	22 (10%)	8 (4%)	3	27
2	B	211/220 (96%)	183 (87%)	22 (10%)	6 (3%)	5	34
2	H	211/220 (96%)	191 (90%)	16 (8%)	4 (2%)	8	42
3	I	177/181 (98%)	157 (89%)	16 (9%)	4 (2%)	6	38
3	J	177/181 (98%)	158 (89%)	16 (9%)	3 (2%)	9	45
All	All	1200/1230 (98%)	1064 (89%)	109 (9%)	27 (2%)	6	38

5 of 27 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	2	ILE
1	L	28	THR
2	H	152	ASP
2	B	152	ASP
2	B	196	SER

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	189/189 (100%)	172 (91%)	17 (9%)	9	39
1	L	189/189 (100%)	178 (94%)	11 (6%)	20	55
2	B	182/186 (98%)	176 (97%)	6 (3%)	38	69
2	H	182/186 (98%)	168 (92%)	14 (8%)	13	45
3	I	159/161 (99%)	148 (93%)	11 (7%)	15	49
3	J	159/161 (99%)	144 (91%)	15 (9%)	8	38
All	All	1060/1072 (99%)	986 (93%)	74 (7%)	15	48

5 of 74 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	113	GLN
3	J	263	LYS
3	J	129	ASN
3	J	189	ARG
2	H	177	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	205	ASN
3	J	129	ASN
3	J	266	GLN
3	I	247	ASN
3	I	167	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](#)

Of 2 ligands modelled in this entry, 2 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 [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, 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	214/214 (100%)	0.56	23 (10%) 6 3	54, 102, 134, 155	0
1	L	214/214 (100%)	0.15	5 (2%) 60 44	72, 101, 129, 144	0
2	B	215/220 (97%)	0.67	32 (14%) 2 1	52, 104, 132, 159	0
2	H	215/220 (97%)	0.15	4 (1%) 66 51	53, 95, 121, 136	0
3	I	179/181 (98%)	0.12	4 (2%) 62 45	26, 91, 122, 137	0
3	J	179/181 (98%)	0.08	3 (1%) 70 55	26, 86, 118, 137	0
All	All	1216/1230 (98%)	0.30	71 (5%) 23 13	26, 96, 130, 159	0

The worst 5 of 71 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	I	306	ILE	8.9
3	I	304	LYS	7.9
1	A	129	THR	5.6
1	A	214	CYS	4.9
2	B	142	GLY	4.8

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, 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(Å ²)	Q<0.9
4	ZN	I	1	1/1	0.84	0.28	99,99,99,99	0
4	ZN	J	2	1/1	0.97	0.25	99,99,99,99	0

6.5 Other polymers [i](#)

There are no such residues in this entry.