



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2014 – 05:07 AM GMT

PDB ID : 1MFB  
Title : HIGH RESOLUTION STRUCTURES OF ANTIBODY FAB FRAGMENT COMPLEXED WITH CELL-SURFACE OLIGOSACCHARIDE OF PATHOGENIC SALMONELLA  
Authors : Zdanov, A.; Cygler, M.  
Deposited on : 1993-10-25  
Resolution : 2.10 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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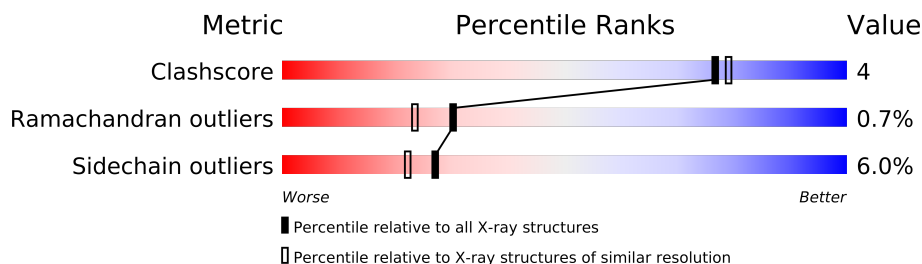
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	21963
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.10 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	79885	3649 (2.10-2.10)
Ramachandran outliers	78287	3610 (2.10-2.10)
Sidechain outliers	78261	3611 (2.10-2.10)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	L	215	
2	H	219	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3505 atoms, of which 0 are hydrogen and 0 are deuterium.

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 IGG1-LAMBDA SE155-4 FAB (LIGHT CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	212	Total	C	N	O	S	0	0	0
			1580	985	268	320	7			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	28	THR	ALA	CONFLICT	GB 387376
L	31	SER	THR	CONFLICT	GB 387376
L	32	GLY	SER	CONFLICT	GB 387376
L	34	HIS	TYR	CONFLICT	GB 387376
L	52	ASP	GLY	CONFLICT	GB 387376
L	82	PRO	THR	CONFLICT	GB 387376
L	94	CYS	TYR	CONFLICT	GB 387376
L	95	ASN	SER	CONFLICT	GB 387376
L	99	ILE	VAL	CONFLICT	GB 387376

- Molecule 2 is a protein called IGG1-LAMBDA SE155-4 FAB (HEAVY CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	212	Total	C	N	O	S	0	0	1
			1595	1018	266	303	8			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	?	-	ALA	DELETION	GB 208365
H	468	ARG	ASP	CONFLICT	GB 208365

- Molecule 3 is a polymer of unknown type called SUGAR (7-MER).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	H	7	Total	C	O	0	0
			74	42	32		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	?	-	ALA	DELETION	GB 208365
H	468	ARG	ASP	CONFLICT	GB 208365

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	H	122	Total	O	0	0
			122	122		
4	L	134	Total	O	0	0
			134	134		

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

Note EDS was not executed.

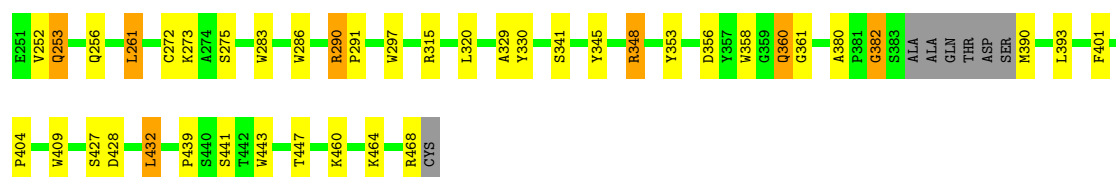
- Molecule 1: IGG1-LAMBDA SE155-4 FAB (LIGHT CHAIN)

Chain L: 



- Molecule 2: IGG1-LAMBDA SE155-4 FAB (HEAVY CHAIN)

Chain H: 



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	47.30Å 129.00Å 79.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.10	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.10)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, $R_{free}$	0.160 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3505	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GLA, RAM, ABE, MAN

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	L	0.76	0/1618	1.42	17/2211 (0.8%)
2	H	0.79	0/1642	1.48	26/2246 (1.2%)
All	All	0.78	0/3260	1.45	43/4457 (1.0%)

There are no bond length outliers.

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	151	TRP	CD1-CG-CD2	9.08	113.56	106.30
2	H	348	ARG	NE-CZ-NH1	8.83	124.72	120.30
1	L	56	ARG	NE-CZ-NH1	8.75	124.68	120.30
2	H	297	TRP	CD1-CG-CD2	8.73	113.28	106.30
2	H	443	TRP	CD1-CG-CD2	8.67	113.24	106.30
2	H	286	TRP	CD1-CG-CD2	8.26	112.91	106.30
2	H	358	TRP	CD1-CG-CD2	8.25	112.90	106.30
2	H	283	TRP	CD1-CG-CD2	8.11	112.79	106.30
1	L	188	TRP	CD1-CG-CD2	8.08	112.76	106.30
2	H	283	TRP	CE2-CD2-CG	-8.02	100.88	107.30
1	L	98	TRP	CD1-CG-CD2	7.82	112.55	106.30
1	L	93	TRP	CD1-CG-CD2	7.78	112.53	106.30
1	L	93	TRP	CE2-CD2-CG	-7.78	101.08	107.30
2	H	358	TRP	CE2-CD2-CG	-7.75	101.10	107.30
1	L	151	TRP	CE2-CD2-CG	-7.72	101.12	107.30
2	H	348	ARG	NE-CZ-NH2	-7.71	116.45	120.30
2	H	409	TRP	CD1-CG-CD2	7.59	112.37	106.30
2	H	443	TRP	CE2-CD2-CG	-7.54	101.27	107.30
1	L	188	TRP	CE2-CD2-CG	-7.47	101.33	107.30
1	L	37	TRP	CD1-CG-CD2	7.36	112.19	106.30
2	H	286	TRP	CE2-CD2-CG	-7.25	101.50	107.30
2	H	297	TRP	CE2-CD2-CG	-7.19	101.55	107.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	98	TRP	CE2-CD2-CG	-6.88	101.80	107.30
1	L	37	TRP	CE2-CD2-CG	-6.70	101.94	107.30
2	H	409	TRP	CE2-CD2-CG	-6.47	102.12	107.30
1	L	93	TRP	CG-CD2-CE3	6.34	139.60	133.90
2	H	432	LEU	CA-CB-CG	6.05	129.22	115.30
2	H	358	TRP	CG-CD2-CE3	5.84	139.16	133.90
1	L	63	ARG	NE-CZ-NH1	5.79	123.20	120.30
2	H	286	TRP	CG-CD1-NE1	-5.78	104.32	110.10
1	L	93	TRP	CB-CG-CD1	-5.78	119.49	127.00
2	H	330	TYR	CB-CG-CD1	-5.76	117.55	121.00
1	L	180	TYR	CB-CG-CD1	-5.72	117.57	121.00
2	H	353	TYR	CB-CG-CD2	-5.71	117.58	121.00
2	H	297	TRP	CG-CD1-NE1	-5.52	104.58	110.10
1	L	151	TRP	CG-CD1-NE1	-5.43	104.67	110.10
2	H	443	TRP	CG-CD1-NE1	-5.38	104.72	110.10
2	H	382	GLY	N-CA-C	-5.36	99.70	113.10
2	H	315	ARG	CB-CG-CD	-5.35	97.70	111.60
2	H	315	ARG	NE-CZ-NH2	-5.29	117.66	120.30
2	H	283	TRP	CG-CD2-CE3	5.21	138.59	133.90
1	L	188	TRP	CG-CD1-NE1	-5.03	105.07	110.10
2	H	358	TRP	CB-CG-CD1	-5.02	120.48	127.00

There are no chirality outliers.

There are no planarity outliers.

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L	1580	0	1511	8	0
2	H	1595	0	1547	16	0
3	H	74	0	66	0	0
4	H	122	0	0	1	0
4	L	134	0	0	1	0
All	All	3505	0	3124	24	0



Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 4.

All (24) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:H:253:GLN:HB2	2:H:275:SER:HB2	1.75	0.69
2:H:256:GLN:HE22	2:H:345:TYR:HA	1.62	0.63
2:H:256:GLN:HG2	2:H:272:CYS:SG	2.41	0.61
1:L:23:ARG:HH11	1:L:72:LYS:HD3	1.67	0.59
1:L:23:ARG:HB3	1:L:72:LYS:HG2	1.87	0.57
1:L:192:SER:O	1:L:210:SER:HA	2.09	0.53
2:H:390:MET:HG2	2:H:439:PRO:HA	1.91	0.51
2:H:380:ALA:HB3	2:H:468:ARG:HG3	1.94	0.49
2:H:256:GLN:NE2	2:H:361:GLY:H	2.11	0.48
1:L:95:ASN:HB2	4:L:830:HOH:O	2.13	0.48
2:H:360:GLN:NE2	2:H:360:GLN:H	2.12	0.48
2:H:447:THR:HG23	2:H:464:LYS:HG3	1.97	0.47
2:H:290:ARG:HH21	2:H:341:SER:HB2	1.78	0.47
2:H:252:VAL:HG21	2:H:348:ARG:NH2	2.33	0.44
1:L:153:VAL:HG23	1:L:158:VAL:HG21	2.00	0.44
2:H:329:ALA:HB1	4:H:657:HOH:O	2.17	0.43
1:L:23:ARG:NH1	1:L:72:LYS:HD3	2.32	0.43
1:L:93:TRP:CZ2	1:L:96:ASN:HA	2.54	0.43
2:H:252:VAL:HA	2:H:275:SER:O	2.19	0.42
2:H:360:GLN:H	2:H:360:GLN:HE21	1.67	0.42
2:H:382:GLY:HA2	2:H:468:ARG:HB2	2.00	0.42
2:H:261:LEU:HD21	2:H:401:PHE:HZ	1.85	0.42
2:H:348:ARG:HD2	2:H:356:ASP:OD1	2.20	0.41
1:L:189:GLU:HA	1:L:211:ARG:HD2	2.03	0.41

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

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	L	210/215 (98%)	202 (96%)	7 (3%)	1 (0%)	38 33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	H	208/219 (95%)	196 (94%)	10 (5%)	2 (1%)	22	14
All	All	418/434 (96%)	398 (95%)	17 (4%)	3 (1%)	30	23

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	109	LEU
2	H	291	PRO
2	H	427	SER

### 5.3.2 Protein sidechains ⓘ

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	L	176/183 (96%)	167 (95%)	9 (5%)	33	29
2	H	175/184 (95%)	163 (93%)	12 (7%)	22	17
All	All	351/367 (96%)	330 (94%)	21 (6%)	27	22

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	45	LEU
1	L	54	ASN
1	L	92	LEU
1	L	125	SER
1	L	147	VAL
1	L	162	MET
1	L	192	SER
1	L	203	HIS
1	L	207	LYS
2	H	253	GLN
2	H	261	LEU
2	H	273	LYS
2	H	290	ARG
2	H	320	LEU
2	H	360	GLN

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Mol	Chain	Res	Type
2	H	393	LEU
2	H	404	PRO
2	H	428	ASP
2	H	432	LEU
2	H	441	SER
2	H	460	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	36	ASN
1	L	54	ASN
1	L	191	HIS
1	L	197	GLN
2	H	256	GLN
2	H	289	GLN
2	H	305	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

7 carbohydrates are modelled in this entry.

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	$\# Z  > 2$
3	GLA	H	511	3	10,11,12	0.67	0	11,15,17	1.05	1 (9%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	MAN	H	512	3	10,11,12	0.69	0	11,15,17	0.88	0
3	ABE	H	513	3	8,9,10	1.16	1 (12%)	8,12,14	0.67	0
3	RAM	H	514	3	11,11,11	1.00	0	16,16,16	1.16	1 (6%)
3	GLA	H	521	3	10,11,12	1.01	0	11,15,17	1.22	2 (18%)
3	MAN	H	522	3	10,11,12	0.74	0	11,15,17	0.65	0
3	RAM	H	524	3	9,10,11	0.85	0	10,14,16	1.23	2 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GLA	H	511	3	-	0/2/19/22	0/1/1/1
3	MAN	H	512	3	-	0/2/19/22	0/1/1/1
3	ABE	H	513	3	-	0/0/13/16	0/1/1/1
3	RAM	H	514	3	-	0/0/20/20	0/1/1/1
3	GLA	H	521	3	-	0/2/19/22	0/1/1/1
3	MAN	H	522	3	-	0/2/19/22	0/1/1/1
3	RAM	H	524	3	-	0/0/17/20	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	513	ABE	C4-C5	2.72	1.58	1.52

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	514	RAM	C6-C5-C4	2.85	117.69	113.06
3	H	521	GLA	C6-C5-C4	2.24	118.42	113.00
3	H	521	GLA	O4-C4-C3	-2.16	105.52	110.35
3	H	524	RAM	O5-C5-C4	-2.14	107.00	110.22
3	H	524	RAM	C4-C3-C2	-2.08	107.72	110.50
3	H	511	GLA	C6-C5-C4	2.01	117.85	113.00

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 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

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers

EDS was not executed - this section will therefore be empty.