



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 06:32 PM GMT

PDB ID : 1BAF
Title : 2.9 ANGSTROMS RESOLUTION STRUCTURE OF AN ANTI-DINITRO
PHENYL-SPIN-LABEL MONOCLONAL ANTIBODY FAB FRAGMENT
WITH BOUND HAPTEN
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Deposited on : 1992-01-16
Resolution : 2.90 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

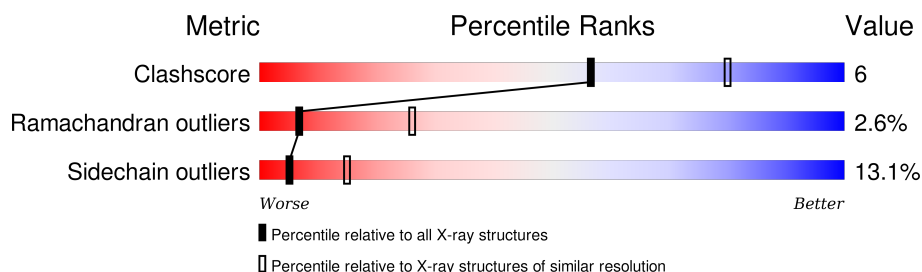
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	L	214	 68% 27% .
2	H	217	 68% 27% . .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4082 atoms, of which 740 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 IGG1-KAPPA AN02 FAB (LIGHT CHAIN).

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	L	214	2031	1033	378	272	338	10	0	0	0

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	17	GLU	GLN	CONFLICT	GB 437099
L	21	MET	ILE	CONFLICT	GB 437099
L	?	-	SER	DELETION	GB 437099
L	?	-	SER	DELETION	GB 437099
L	30	TYR	ARG	CONFLICT	GB 437099
L	31	TYR	PHE	CONFLICT	GB 437099
L	32	MET	LEU	CONFLICT	GB 437099
L	33	TYR	HIS	CONFLICT	GB 437099
L	39	PRO	SER	CONFLICT	GB 437099
L	41	SER	ALA	CONFLICT	GB 437099
L	44	ARG	LYS	CONFLICT	GB 437099
L	46	LEU	TRP	CONFLICT	GB 437099
L	52	ASN	LYS	CONFLICT	GB 437099
L	55	SER	PRO	CONFLICT	GB 437099
L	59	VAL	ALA	CONFLICT	GB 437099
L	76	ARG	SER	CONFLICT	GB 437099
L	84	THR	SER	CONFLICT	GB 437099
L	86	TYR	PHE	CONFLICT	GB 437099
L	88	GLN	HIS	CONFLICT	GB 437099
L	94	PRO	-	INSERTION	GB 437099
L	96	ILE	LEU	CONFLICT	GB 437099
L	100	VAL	ALA	CONFLICT	GB 437099

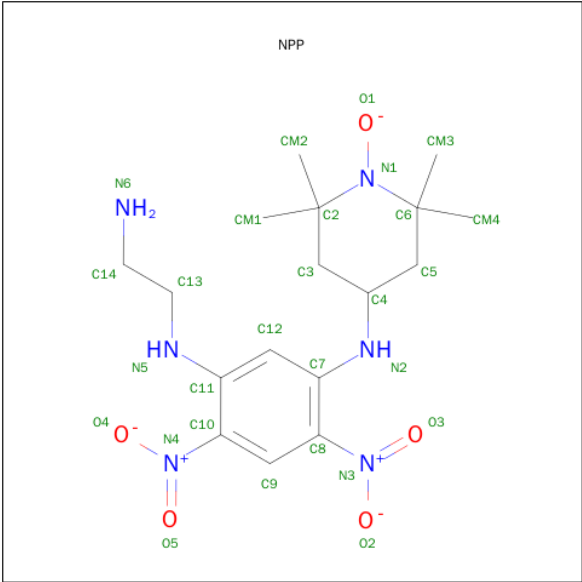
- Molecule 2 is a protein called IGG1-KAPPA AN02 FAB (HEAVY CHAIN).

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	H	217	Total	C	H	N	O	S	0	0	0
			2023	1048	362	278	327	8			

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	18	GLN	LEU	CONFLICT	GB 1513182
H	29	ILE	VAL	CONFLICT	GB 1513182
H	32	ASP	GLU	CONFLICT	GB 1513182
H	49	MET	LEU	CONFLICT	GB 1513182
H	52	MET	ILE	CONFLICT	GB 1513182
H	53	SER	ASN	CONFLICT	GB 1513182
H	59	ARG	SER	CONFLICT	GB 1513182
H	65	ARG	LYS	CONFLICT	GB 1513182
H	84	LYS	ASN	CONFLICT	GB 1513182
H	95	PHE	TYR	CONFLICT	GB 1513182
H	?	-	ASP	DELETION	GB 1513182
H	99	GLY	SER	CONFLICT	GB 1513182
H	101	PRO	-	INSERTION	GB 1513182
H	102	LEU	PHE	CONFLICT	GB 1513182
H	110	GLN	LEU	CONFLICT	GB 1513182
H	112	SER	THR	CONFLICT	GB 1513182
H	115	GLU	ALA	CONFLICT	GB 1513182
H	189	PRO	THR	CONFLICT	GB 1513182
H	190	ARG	TRP	CONFLICT	GB 1513182

- Molecule 3 is N-(2-AMINO-ETHYL)-4,6-DINITRO-N'-(2,2,6,6-TETRAMETHYL-1-OXY-PIPERIDIN-4-YL)-BENZENE-1,3-DIAMINE (three-letter code: NPP) (formula: C₁₇H₂₇N₆O₅).



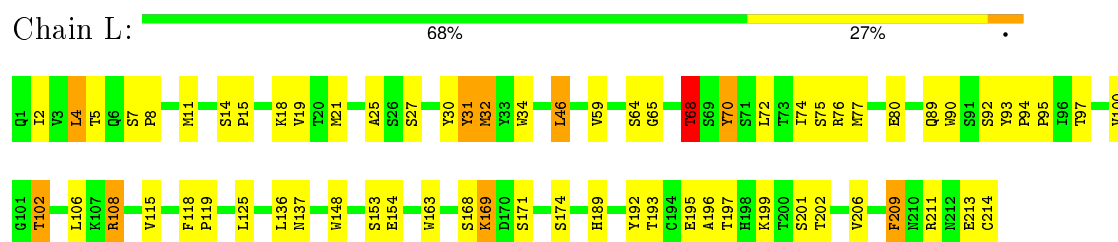
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	L	1	28	17	6	5	0	0

3 Residue-property plots

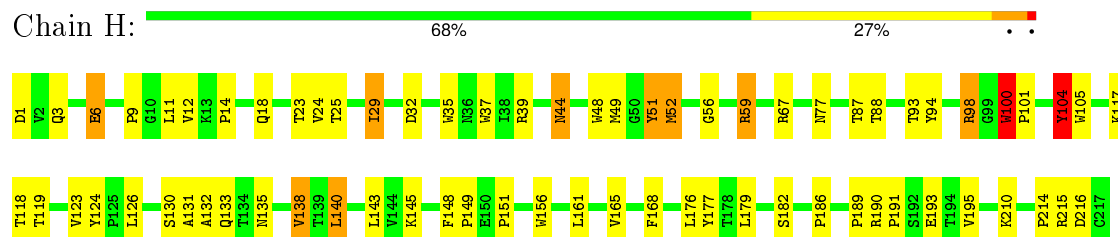
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 ($\text{RSRZ} > 2$). 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-KAPPA AN02 FAB (LIGHT CHAIN)



- Molecule 2: IGG1-KAPPA AN02 FAB (HEAVY CHAIN)



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	73.23 Å 73.23 Å 373.80 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	8.00 – 2.90	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-2.90)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.195 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4082	wwPDB-VP
Average B, all atoms (Å ²)	16.0	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: NPP

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	0.83	0/1693	1.60	22/2303 (1.0%)
2	H	0.85	0/1707	1.68	31/2337 (1.3%)
All	All	0.84	0/3400	1.64	53/4640 (1.1%)

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

There are no bond length outliers.

The worst 5 of 53 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	H	156	TRP	CD1-CG-CD2	9.83	114.17	106.30
1	L	32	MET	CA-CB-CG	-9.73	96.76	113.30
2	H	37	TRP	CD1-CG-CD2	8.69	113.25	106.30
2	H	67	ARG	NE-CZ-NH2	-8.49	116.06	120.30
1	L	34	TRP	CD1-CG-CD2	8.04	112.73	106.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	H	104	TYR	Sidechain

5.2 Too-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 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	L	1653	378	1582	25	0
2	H	1661	362	1617	18	0
3	L	28	0	27	2	0
All	All	3342	740	3226	40	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 6.

The worst 5 of 40 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)
2:H:3:GLN:HB3	2:H:25:THR:HB	1.56	0.87
2:H:190:ARG:HD2	2:H:191:PRO:HA	1.78	0.64
1:L:25:ALA:HB3	1:L:68:THR:HA	1.80	0.63
1:L:65:GLY:HA3	1:L:70:TYR:CD2	2.34	0.63
2:H:186:PRO:HB2	2:H:189:PRO:HD2	1.81	0.62

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	212/214 (99%)	193 (91%)	16 (8%)	3 (1%)	14 44
2	H	215/217 (99%)	189 (88%)	18 (8%)	8 (4%)	4 17
All	All	427/431 (99%)	382 (90%)	34 (8%)	11 (3%)	7 26

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	44	ASN
2	H	118	THR
2	H	131	ALA
1	L	211	ARG
1	L	201	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	L	190/190 (100%)	167 (88%)	23 (12%)	6	18
2	H	192/192 (100%)	165 (86%)	27 (14%)	4	12
All	All	382/382 (100%)	332 (87%)	50 (13%)	5	15

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	214	CYS
2	H	14	PRO
2	H	179	LEU
2	H	1	ASP
2	H	11	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	137	ASN
2	H	78	GLN

5.3.3 RNA [i](#)

There are no RNA molecules 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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

1 ligand is 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	NPP	L	250	-	25,29,29	1.97	8 (32%)	34,44,44	1.75	9 (26%)

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	NPP	L	250	-	-	0/14/38/38	0/2/2/2

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L	250	NPP	C7-C8	-2.57	1.38	1.40
3	L	250	NPP	C9-C8	-2.41	1.34	1.39
3	L	250	NPP	C5-C4	-2.33	1.49	1.52
3	L	250	NPP	C9-C10	-2.33	1.34	1.39
3	L	250	NPP	C2-N1	2.12	1.53	1.49

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	L	250	NPP	C6-C5-C4	-3.63	110.63	113.85
3	L	250	NPP	CM3-C6-C5	-3.56	103.66	110.29
3	L	250	NPP	C8-C7-N2	-3.37	119.75	123.39
3	L	250	NPP	C2-C3-C4	-3.24	110.97	113.85
3	L	250	NPP	C5-C4-C3	-2.94	106.09	108.72

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	L	250	NPP	2	0

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 ⓘ

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.