



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 10:39 AM GMT

PDB ID : 3MLX  
Title : Crystal structure of anti-HIV-1 V3 Fab 3074 in complex with an MN V3 peptide  
Authors : Kong, X.-P.  
Deposited on : 2010-04-18  
Resolution : 1.90 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](mailto: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.

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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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

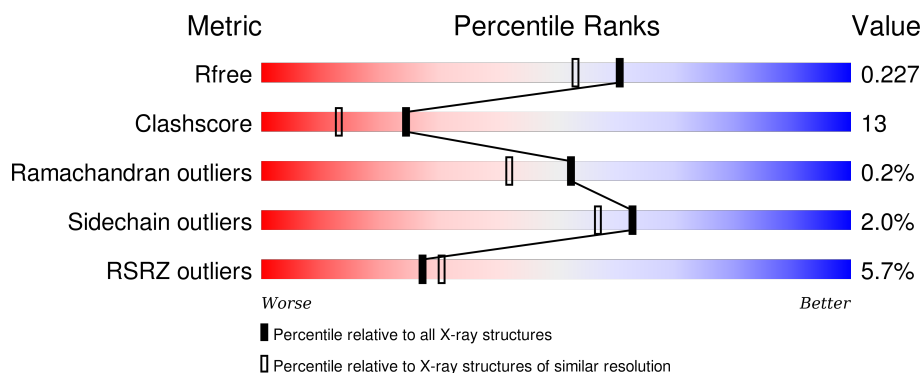
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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))
$R_{free}$	91344	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (1.90-1.90)

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  $\geq 3$ , 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.

Mol	Chain	Length	Quality of chain
1	L	211	<div> <div>0%</div> <div>85%</div> <div>14%</div> <div>•</div> </div>
1	M	211	<div> <div>3%</div> <div>83%</div> <div>16%</div> <div>•</div> </div>
2	H	228	<div> <div>6%</div> <div>75%</div> <div>23%</div> <div>•</div> </div>
2	I	228	<div> <div>9%</div> <div>75%</div> <div>25%</div> </div>
3	P	23	<div> <div>22%</div> <div>30%</div> <div>22%</div> <div>9%</div> <div>39%</div> </div>

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Mol	Chain	Length	Quality of chain
3	Q	23	<div><div></div><div></div><div></div><div></div></div>

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7531 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 Human monoclonal anti-HIV-1 gp120 V3 antibody 3074 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	211	Total	C	N	O	S	0	0	0
			1567	978	267	317	5			
1	M	211	Total	C	N	O	S	0	0	0
			1567	978	267	317	5			

- Molecule 2 is a protein called Human monoclonal anti-HIV-1 gp120 V3 antibody 3074 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	228	Total	C	N	O	S	0	0	0
			1709	1080	281	342	6			
2	I	228	Total	C	N	O	S	0	0	0
			1709	1080	281	342	6			

- Molecule 3 is a protein called HIV-1 gp120 third variable region (V3) crown.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	P	14	Total	C	N	O	0	0	0
			114	74	23	17			
3	Q	14	Total	C	N	O	0	0	0
			114	74	23	17			

- Molecule 4 is water.


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	L	175	Total	O	0	0
			175	175		
4	H	218	Total	O	0	0
			218	218		
4	P	12	Total	O	0	0
			12	12		

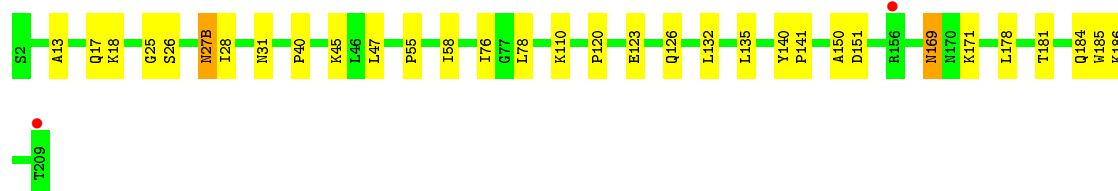
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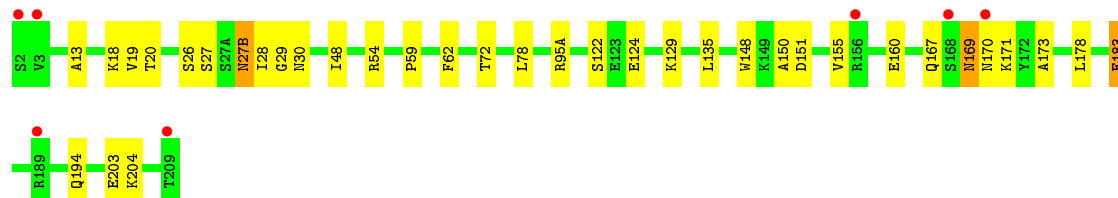
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	M	148	Total 148	O 148	0	0
4	I	193	Total 193	O 193	0	0
4	Q	5	Total 5	O 5	0	0

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.

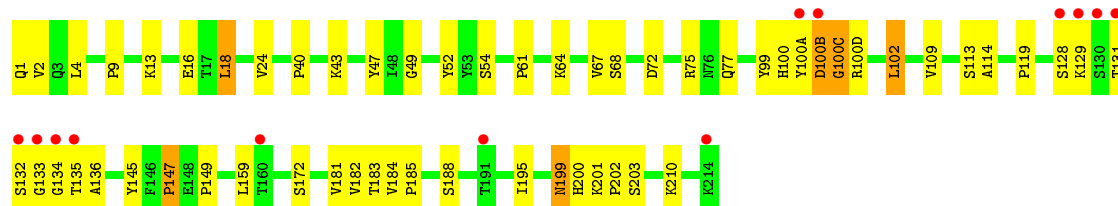
- Chain L:  85% 14%



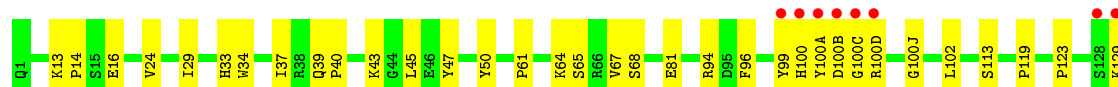
- Chain M: 



- Chain H: 

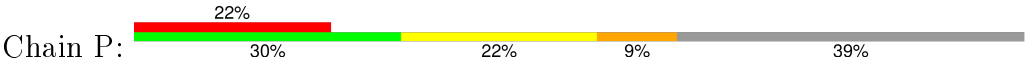


- Chain I: 





● Molecule 3: HIV-1 gp120 third variable region (V3) crown



● Molecule 3: HIV-1 gp120 third variable region (V3) crown



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	59.87Å 128.80Å 60.19Å 90.00° 92.66° 90.00°	Depositor
Resolution (Å)	50.00 – 1.90 30.53 – 1.86	Depositor EDS
% Data completeness (in resolution range)	93.7 (50.00-1.90) 91.3 (30.53-1.86)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.92 (at 1.87Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.192 , 0.228 0.192 , 0.227	Depositor DCC
$R_{free}$ test set	6794 reflections (10.12%)	DCC
Wilson B-factor (Å <sup>2</sup> )	20.7	Xtriage
Anisotropy	0.473	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 40.0	EDS
Estimated twinning fraction	0.002 for l,k,-h 0.032 for h,-k,-l 0.021 for l,-k,h	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 71813 reflections (0.001%)	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7531	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.21% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	L	0.31	0/1605	0.64	0/2192
1	M	0.31	0/1605	0.64	0/2192
2	H	0.32	0/1754	0.67	0/2391
2	I	0.33	0/1754	0.65	0/2391
3	P	0.34	0/117	0.53	0/156
3	Q	0.33	0/117	0.52	0/156
All	All	0.32	0/6952	0.65	0/9478

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	L	1567	0	1531	32	0
1	M	1567	0	1531	34	0
2	H	1709	0	1654	52	0
2	I	1709	0	1654	54	0
3	P	114	0	117	13	0
3	Q	114	0	117	8	0
4	H	218	0	0	6	0
4	I	193	0	0	2	0
4	L	175	0	0	3	0
4	M	148	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	P	12	0	0	0	0
4	Q	5	0	0	0	0
All	All	7531	0	6604	173	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 13.

The worst 5 of 173 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:M:27(B):ASN:HD22	1:M:28:ILE:H	0.92	0.90
1:M:27(B):ASN:ND2	1:M:28:ILE:H	1.74	0.85
1:L:27(B):ASN:HD22	1:L:28:ILE:H	1.23	0.85
2:I:156:SER:H	2:I:197:ASN:HD21	1.20	0.84
2:I:40:PRO:HG2	2:I:43:LYS:HB2	1.57	0.84

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	L	209/211 (99%)	202 (97%)	7 (3%)	0	100	100
1	M	209/211 (99%)	201 (96%)	8 (4%)	0	100	100
2	H	226/228 (99%)	214 (95%)	11 (5%)	1 (0%)	39	27
2	I	226/228 (99%)	213 (94%)	13 (6%)	0	100	100
3	P	12/23 (52%)	11 (92%)	0	1 (8%)	1	0
3	Q	12/23 (52%)	11 (92%)	1 (8%)	0	100	100
All	All	894/924 (97%)	852 (95%)	40 (4%)	2 (0%)	52	42

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	P	306	ARG
2	H	100(C)	GLY

### 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	177/177 (100%)	175 (99%)	2 (1%)	80	79
1	M	177/177 (100%)	172 (97%)	5 (3%)	51	41
2	H	195/195 (100%)	189 (97%)	6 (3%)	47	37
2	I	195/195 (100%)	194 (100%)	1 (0%)	92	92
3	P	11/19 (58%)	10 (91%)	1 (9%)	12	4
3	Q	11/19 (58%)	11 (100%)	0	100	100
All	All	766/782 (98%)	751 (98%)	15 (2%)	63	57

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	149	PRO
2	H	199	ASN
1	M	178	LEU
2	H	147	PRO
1	M	169	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
2	H	105	GLN
2	H	199	ASN
2	I	192	GLN
2	H	171	GLN
2	H	192	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 carbohydrates 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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	L	211/211 (100%)	-0.10	2 (0%) 85 87	16, 22, 33, 53	0
1	M	211/211 (100%)	0.01	7 (3%) 50 53	16, 24, 37, 52	0
2	H	228/228 (100%)	0.27	13 (5%) 27 30	15, 22, 47, 76	0
2	I	228/228 (100%)	0.46	21 (9%) 11 12	15, 23, 61, 80	0
3	P	14/23 (60%)	1.39	5 (35%) 0 0	21, 30, 58, 63	0
3	Q	14/23 (60%)	1.68	4 (28%) 1 0	26, 38, 58, 63	0
All	All	906/924 (98%)	0.21	52 (5%) 27 30	15, 23, 47, 80	0

The worst 5 of 52 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	131	THR	13.0
2	I	131	THR	12.9
2	H	132	SER	10.8
2	I	132	SER	9.8
2	I	130	SER	9.7

### 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 carbohydrates 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.