



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 07:28 am GMT

PDB ID : 2HKF  
Title : Crystal structure of the Complex Fab M75- Peptide  
Authors : Kral, V.; Mader, P.; Stouracova, R.; Fabry, M.; Horejsi, M.; Brynda, J.  
Deposited on : 2006-07-04  
Resolution : 2.01 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](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.

---

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

MolProbity : 4.02b-467  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : recalc28949

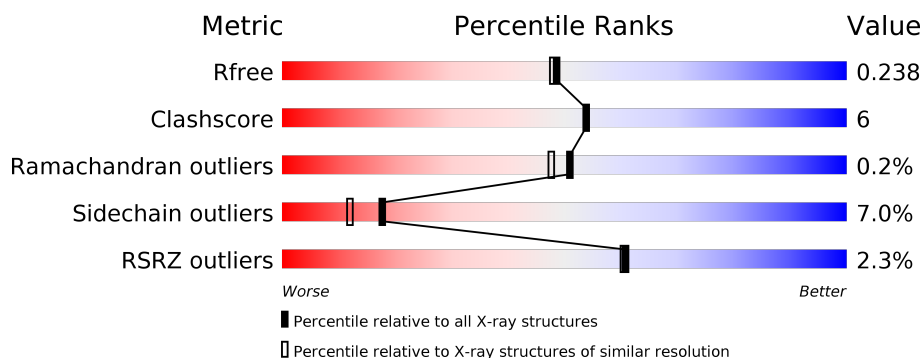
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.01 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))
$R_{free}$	100719	6609 (2.00-2.00)
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (2.00-2.00)

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	219	<div> <div>84%</div> <div>13%</div> <div>.</div> </div>
2	H	218	<div> <div>4%</div> <div>78%</div> <div>15%</div> <div>.</div> <div>.</div> </div>
3	P	9	<div> <div>11%</div> <div>78%</div> <div>22%</div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3666 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 Immunoglobulin Light chain Fab fragment.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	219	Total	C	N	O	S	0	3	0
			1705	1063	289	344	9			

- Molecule 2 is a protein called Immunoglobulin Heavy chain Fab fragment.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	210	Total	C	N	O	S	0	1	0
			1597	1008	264	315	10			

- Molecule 3 is a protein called Carbonic anhydrase 9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	P	9	Total	C	N	O	0	0	0
			61	36	9	16			

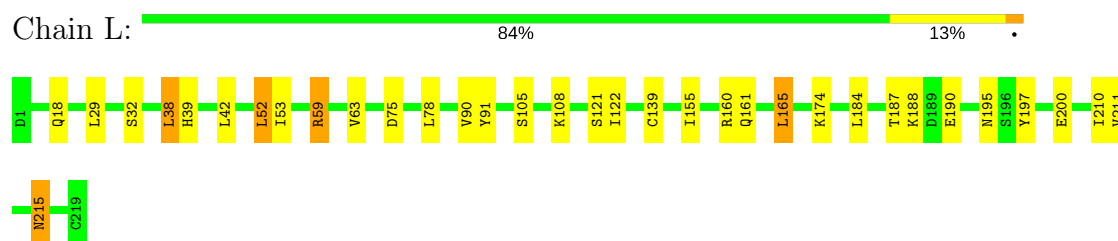
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	H	119	Total	O	0	0
			119	119		
4	L	175	Total	O	0	0
			175	175		
4	P	9	Total	O	0	0
			9	9		

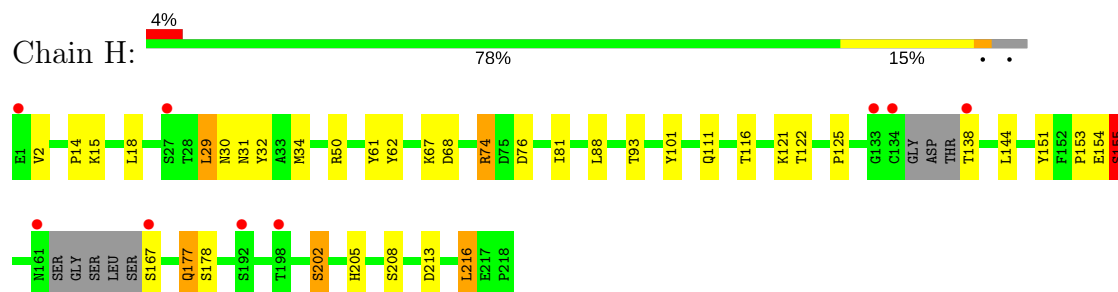
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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 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.

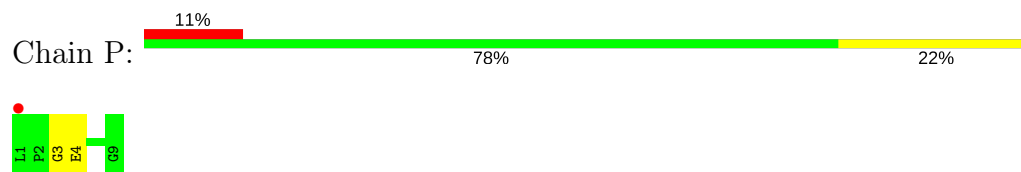
- Molecule 1: Immunoglobulin Light chain Fab fragment



- Molecule 2: Immunoglobulin Heavy chain Fab fragment



- Molecule 3: Carbonic anhydrase 9



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	40.39Å 43.15Å 58.02Å 85.03° 88.47° 85.67°	Depositor
Resolution (Å)	28.87 – 2.01 28.90 – 2.01	Depositor EDS
% Data completeness (in resolution range)	93.6 (28.87-2.01) 91.8 (28.90-2.01)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.46 (at 2.01Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.176 , 0.242 0.170 , 0.238	Depositor DCC
$R_{free}$ test set	1240 reflections (5.36%)	DCC
Wilson B-factor (Å <sup>2</sup> )	18.6	Xtriage
Anisotropy	0.242	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 36.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	3666	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	9.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.76% 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, 0.333 respectively for untwinned datasets, and 0.375, 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	0.57	0/1756	0.71	1/2383 (0.0%)
2	H	0.56	0/1640	0.67	2/2239 (0.1%)
3	P	0.61	0/62	0.61	0/82
All	All	0.57	0/3458	0.69	3/4704 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	74	ARG	NE-CZ-NH2	-5.75	117.42	120.30
2	H	74	ARG	NE-CZ-NH1	5.30	122.95	120.30
1	L	38	LEU	CA-CB-CG	-5.04	103.70	115.30

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	1705	0	1636	20	0
2	H	1597	0	1555	22	0
3	P	61	0	50	2	0
4	H	119	0	0	3	0
4	L	175	0	0	4	0
4	P	9	0	0	0	0
All	All	3666	0	3241	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.

All (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:68:ASP:HA	4:H:312:HOH:O	1.59	1.01
2:H:74:ARG:HD3	2:H:76:ASP:OD1	1.60	1.01
2:H:74:ARG:CD	2:H:76:ASP:OD1	2.24	0.84
1:L:52:LEU:HB3	1:L:53:ILE:HD12	1.63	0.79
1:L:187:THR:OG1	1:L:190:GLU:HG3	1.84	0.78
1:L:165[B]:LEU:HD11	2:H:177:GLN:HB2	1.78	0.64
1:L:155:ILE:HD12	1:L:197:TYR:CD1	2.34	0.63
2:H:144:LEU:HB3	2:H:216:LEU:HD22	1.88	0.54
2:H:177:GLN:HG2	4:H:224:HOH:O	2.07	0.54
2:H:205:HIS:HD2	2:H:208:SER:OG	1.91	0.53
1:L:195:ASN:ND2	1:L:215:ASN:OD1	2.42	0.52
1:L:165[B]:LEU:CD1	2:H:177:GLN:HB2	2.39	0.52
2:H:153:PRO:O	2:H:205:HIS:HE1	1.92	0.52
2:H:202:SER:HB3	2:H:213:ASP:OD2	2.09	0.52
2:H:74:ARG:HD2	2:H:76:ASP:OD1	2.09	0.51
1:L:165[A]:LEU:HD23	4:L:227:HOH:O	2.11	0.50
1:L:155:ILE:HD12	1:L:197:TYR:CE1	2.47	0.50
2:H:93:THR:HG23	2:H:116:THR:HA	1.94	0.48
1:L:200:GLU:HG2	1:L:211:VAL:HG22	1.95	0.47
2:H:14:PRO:O	2:H:15:LYS:HB2	2.13	0.47
2:H:205:HIS:CD2	2:H:208:SER:OG	2.68	0.47
2:H:50:ARG:HD3	2:H:61:TYR:CD1	2.50	0.47
1:L:161:GLN:HG3	4:L:359:HOH:O	2.15	0.46
1:L:53:ILE:HD13	1:L:78:LEU:CD1	2.46	0.46
1:L:59:ARG:HG2	1:L:63:VAL:HB	1.98	0.45
1:L:38:LEU:HG	1:L:39:HIS:N	2.28	0.45
2:H:155:SER:HB3	4:H:313:HOH:O	2.17	0.45
1:L:160:ARG:HG2	1:L:184:LEU:HD11	1.98	0.44
1:L:75:ASP:HB2	4:L:366:HOH:O	2.17	0.44
1:L:90:VAL:HG22	1:L:108:LYS:HD3	1.99	0.44
1:L:210:ILE:HD11	4:L:324:HOH:O	2.17	0.44
2:H:34:MET:HG3	2:H:81:ILE:CD1	2.48	0.44
1:L:53:ILE:HD13	1:L:78:LEU:HD13	2.00	0.43
1:L:42:LEU:HD13	1:L:91:TYR:CZ	2.54	0.43
2:H:125:PRO:HB3	2:H:151:TYR:HB3	2.00	0.42
2:H:31:ASN:O	3:P:4:GLU:HA	2.19	0.42
2:H:32:TYR:HB3	3:P:3:GLY:O	2.20	0.42

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:62:TYR:HB2	2:H:67:LYS:HG3	2.02	0.42
2:H:29:LEU:HB3	2:H:30:ASN:H	1.67	0.42
1:L:122:ILE:HG13	1:L:139[B]:CYS:SG	2.61	0.40

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	220/219 (100%)	215 (98%)	5 (2%)	0	100	100
2	H	205/218 (94%)	198 (97%)	6 (3%)	1 (0%)	32	26
3	P	7/9 (78%)	7 (100%)	0	0	100	100
All	All	432/446 (97%)	420 (97%)	11 (2%)	1 (0%)	51	48

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	155	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	201/198 (102%)	189 (94%)	12 (6%)	22	17

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	H	183/188 (97%)	167 (91%)	16 (9%)	12	7
3	P	6/7 (86%)	6 (100%)	0	100	100
All	All	390/393 (99%)	362 (93%)	28 (7%)	18	11

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	18	GLN
1	L	29	LEU
1	L	32	SER
1	L	52	LEU
1	L	59	ARG
1	L	105	SER
1	L	121	SER
1	L	165[A]	LEU
1	L	165[B]	LEU
1	L	174	LYS
1	L	188	LYS
1	L	215	ASN
2	H	2	VAL
2	H	18	LEU
2	H	29	LEU
2	H	88	LEU
2	H	101	TYR
2	H	111	GLN
2	H	121	LYS
2	H	122	THR
2	H	138	THR
2	H	154	GLU
2	H	155	SER
2	H	167	SER
2	H	177	GLN
2	H	178	SER
2	H	202	SER
2	H	216	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	35	ASN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
2	H	103	ASN
2	H	197	GLN
2	H	205	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 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	219/219 (100%)	-0.20	0 <span>100</span> <span>100</span>	3, 8, 14, 28	0
2	H	210/218 (96%)	0.19	9 (4%) <span>36</span> <span>36</span>	3, 8, 19, 30	0
3	P	9/9 (100%)	0.20	1 (11%) <span>6</span> <span>6</span>	3, 6, 16, 16	0
All	All	438/446 (98%)	-0.00	10 (2%) <span>61</span> <span>60</span>	3, 8, 17, 30	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	138	THR	5.0
2	H	134	CYS	3.2
2	H	1	GLU	2.9
2	H	161	ASN	2.8
2	H	198	THR	2.6
2	H	192	SER	2.5
2	H	27	SER	2.2
3	P	1	LEU	2.2
2	H	167	SER	2.2
2	H	133	GLY	2.0

### 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.