



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2018 – 08:23 pm GMT

PDB ID : 1MQK
Title : Crystal structure of the unliganded Fv-fragment of the anti-cytochrome C oxidase antibody 7E2
Authors : Essen, L.-O.; Harrenga, A.; Ostermeier, C.; Michel, H.
Deposited on : 2002-09-16
Resolution : 1.28 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/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)	:	1.13
EDS	:	trunk30967
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac	:	5.8.0158
CCP4	:	7.0 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk30967

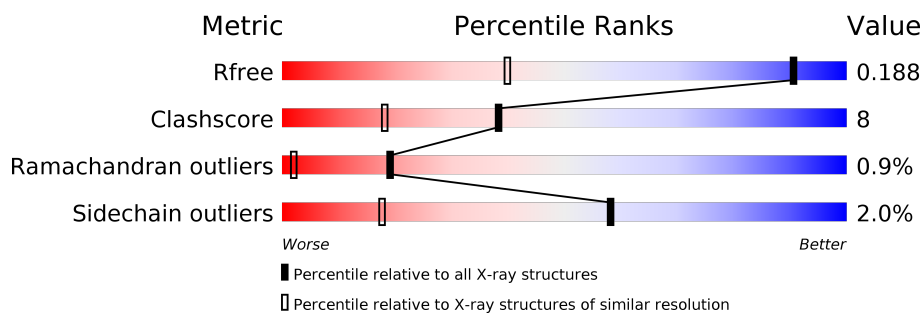
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.28 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}	111664	1552 (1.30-1.26)
Clashscore	122126	1620 (1.30-1.26)
Ramachandran outliers	120053	1562 (1.30-1.26)
Sidechain outliers	120020	1561 (1.30-1.26)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	L	120	
2	H	127	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2193 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 antibody 7E2 FV fragment, light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	109	Total	C	N	O	S	12	12	1
			862	548	137	174	3			

- Molecule 2 is a protein called antibody 7E2 FV fragment, heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	123	Total	C	N	O	S	33	14	0
			1013	635	171	198	9			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	L	150	Total	O	0	0
			150	150		
3	H	168	Total	O	0	0
			168	168		

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. 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. 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: antibody 7E2 FV fragment, light chain

Chain L: 



- Molecule 2: antibody 7E2 FV fragment, heavy chain

Chain H: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	51.44Å 56.05Å 99.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 1.28 22.46 – 1.28	Depositor EDS
% Data completeness (in resolution range)	(Not available) (8.00-1.28) 85.6 (22.46-1.28)	Depositor EDS
R_{merge}	0.40	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.98 (at 1.28Å)	Xtriage
Refinement program	SHELXL	Depositor
R, R_{free}	0.136 , 0.196 0.181 , 0.188	Depositor DCC
R_{free} test set	1921 reflections (2.99%)	wwPDB-VP
Wilson B-factor (Å ²)	12.5	Xtriage
Anisotropy	0.190	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.43 , 73.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2193	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.16% 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

5.1 Standard geometry

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	1.24	5/947 (0.5%)	1.28	5/1285 (0.4%)
2	H	1.08	1/1109 (0.1%)	1.17	3/1500 (0.2%)
All	All	1.16	6/2056 (0.3%)	1.22	8/2785 (0.3%)

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	2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	17	GLU	CD-OE2	-9.48	1.15	1.25
1	L	12	SER	CB-OG	-7.53	1.32	1.42
2	H	7	SER	CB-OG	-6.39	1.33	1.42
1	L	77[A]	SER	CB-OG	-5.60	1.34	1.42
1	L	77[B]	SER	CB-OG	-5.60	1.34	1.42
1	L	24	ARG	NE-CZ	-5.01	1.26	1.33

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	24	ARG	CD-NE-CZ	10.69	138.57	123.60
2	H	32	TYR	CB-CG-CD2	-9.45	115.33	121.00
2	H	32	TYR	CB-CG-CD1	6.96	125.17	121.00
1	L	62	PHE	CB-CG-CD1	6.56	125.39	120.80
1	L	2	ILE	CA-CB-CG1	5.67	121.78	111.00
2	H	90	ASP	CB-CG-OD1	5.29	123.06	118.30
1	L	24	ARG	NE-CZ-NH2	5.20	122.90	120.30
1	L	92	TYR	CB-CG-CD1	5.05	124.03	121.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	H	121	ARG	Sidechain
2	H	44	ARG	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	862	0	851	23	0
2	H	1013	0	974	7	0
3	H	168	0	0	2	0
3	L	150	0	0	7	0
All	All	2193	0	1825	30	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 8.

All (30) 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:L:21[B]:ILE:CD1	3:L:122:HOH:O	2.10	0.98
1:L:21[A]:ILE:HG22	3:L:122:HOH:O	1.60	0.98
1:L:21[A]:ILE:CG2	3:L:122:HOH:O	2.12	0.95
1:L:21[B]:ILE:HG13	3:L:122:HOH:O	1.67	0.92
1:L:6:GLN:HG2	1:L:23[B]:CYS:SG	2.09	0.91
1:L:6:GLN:CG	1:L:23[B]:CYS:SG	2.66	0.84
1:L:21[B]:ILE:HD11	3:L:122:HOH:O	1.77	0.81
1:L:21[B]:ILE:CG1	3:L:122:HOH:O	2.21	0.69
1:L:24:ARG:NH1	1:L:70:GLN:OE1	2.27	0.68
1:L:2:ILE:O	1:L:98[A]:THR:HG21	1.97	0.65
1:L:24:ARG:NH1	1:L:70:GLN:HG3	2.12	0.64
2:H:110[B]:GLN:HG3	3:H:239:HOH:O	1.98	0.63
1:L:98[A]:THR:HG22	3:L:245:HOH:O	2.01	0.61
2:H:122:HIS:CD2	2:H:122:HIS:O	2.55	0.59
1:L:24:ARG:HH11	1:L:70:GLN:HG3	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:53[B]:ASN:OD1	2:H:54:GLY:N	2.40	0.55
1:L:6:GLN:HG3	1:L:23[B]:CYS:SG	2.46	0.52
2:H:122:HIS:O	2:H:122:HIS:CG	2.62	0.52
1:L:21[B]:ILE:HD12	1:L:103:THR:CB	2.40	0.52
2:H:19:LYS:NZ	2:H:80:TYR:CD1	2.84	0.46
2:H:12[A]:VAL:HG21	2:H:86:LEU:HD13	1.98	0.46
1:L:1:ASP:OD1	1:L:1:ASP:O	2.34	0.46
1:L:2:ILE:HD12	1:L:27:GLU:HG2	2.00	0.44
1:L:104[B]:LYS:HE2	1:L:106:GLU:OE2	2.18	0.44
1:L:24:ARG:HH12	1:L:70:GLN:CD	2.22	0.43
1:L:24:ARG:HH11	1:L:24:ARG:CG	2.31	0.42
1:L:56[B]:GLU:HG2	3:H:156:HOH:O	2.20	0.42
1:L:24:ARG:NH1	1:L:70:GLN:CG	2.82	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	120/120 (100%)	116 (97%)	4 (3%)	0	100	100
2	H	134/127 (106%)	130 (97%)	2 (2%)	2 (2%)	11	1
All	All	254/247 (103%)	246 (97%)	6 (2%)	2 (1%)	19	3

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	102	TYR
2	H	122	HIS

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	105/104 (101%)	103 (98%)	2 (2%)	60	20
2	H	119/107 (111%)	117 (98%)	2 (2%)	63	25
All	All	224/211 (106%)	220 (98%)	4 (2%)	58	23

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	3	GLU
1	L	108	LYS
2	H	44	ARG
2	H	122	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
2	H	122	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

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.