



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 11:04 PM GMT

PDB ID : 1WEJ
Title : IGG1 FAB FRAGMENT (OF E8 ANTIBODY) COMPLEXED WITH HORSE CYTOCHROME C AT 1.8 Å RESOLUTION
Authors : Mylvaganam, S.E.; Paterson, Y.; Getzoff, E.D.
Deposited on : 1998-03-26
Resolution : 1.80 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)
Xtrriage (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

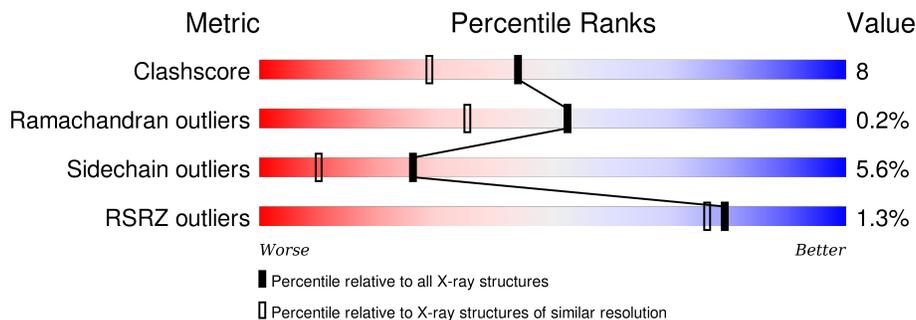
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	5383 (1.80-1.80)
Ramachandran outliers	100387	5320 (1.80-1.80)
Sidechain outliers	100360	5319 (1.80-1.80)
RSRZ outliers	91569	4547 (1.80-1.80)

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.

Mol	Chain	Length	Quality of chain
1	L	214	
2	H	223	
3	F	105	

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 4846 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 E8 ANTIBODY.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	L	214	1664	1038	282	337	7	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	85	SER	THR	CONFLICT	GB 2072141
L	89	GLN	HIS	CONFLICT	GB 2072141
L	106	ILE	VAL	CONFLICT	GB 2072141
L	118	PHE	LEU	CONFLICT	GB 2072141

- Molecule 2 is a protein called E8 ANTIBODY.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	H	223	1676	1056	272	340	8	0	0	0

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	3	GLN	LYS	CONFLICT	PIR S49220
H	5	GLN	LEU	CONFLICT	PIR S49220
H	6	GLN	GLU	CONFLICT	PIR S49220
H	14	PRO	SER	CONFLICT	PIR S49220
H	43	LYS	GLN	CONFLICT	PIR S49220
H	55	SER	ASN	CONFLICT	PIR S49220
H	57	ASN	GLU	CONFLICT	PIR S49220
H	58	THR	ILE	CONFLICT	PIR S49220
H	66	ASP	GLY	CONFLICT	PIR S49220
H	67	LYS	THR	CONFLICT	PIR S49220
H	76	SER	THR	CONFLICT	PIR S49220
H	?	-	VAL	DELETION	PIR S49220

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Chain	Residue	Modelled	Actual	Comment	Reference
H	?	-	ARG	DELETION	PIR S49220
H	97	ALA	ARG	CONFLICT	PIR S49220
H	100	ASP	GLY	CONFLICT	PIR S49220
H	101	TYR	SER	CONFLICT	PIR S49220
H	102	GLY	SER	CONFLICT	PIR S49220
H	103	ASN	GLN	CONFLICT	PIR S49220
H	104	PHE	GLU	CONFLICT	PIR S49220
H	105	ASP	PRO	CONFLICT	PIR S49220
H	119	GLU	LYS	CONFLICT	PIR S49220
H	132	THR	SER	CONFLICT	PIR S49220
H	135	LEU	GLN	CONFLICT	PIR S49220
H	136	LYS	THR	CONFLICT	PIR S49220
H	137	SER	ASN	CONFLICT	PIR S49220
H	182	THR	SER	CONFLICT	PIR S49220
H	195	GLN	GLU	CONFLICT	PIR S49220

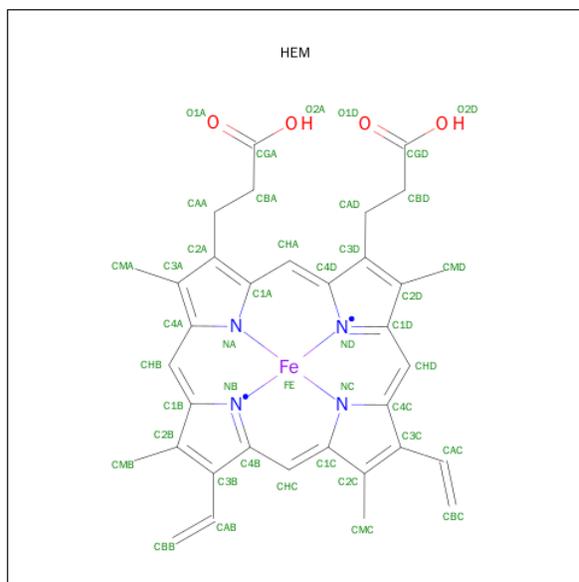
- Molecule 3 is a protein called CYTOCHROME C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	F	105	826	526	144	152	4	0	0	0

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
4	L	1	1	1	0	0

- Molecule 5 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: C₃₄H₃₂FeN₄O₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	F	1	42	34	4	4	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	F	118	Total	O	0	0
			118	118		
6	H	250	Total	O	0	0
			250	250		
6	L	269	Total	O	0	0
			269	269		

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 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.

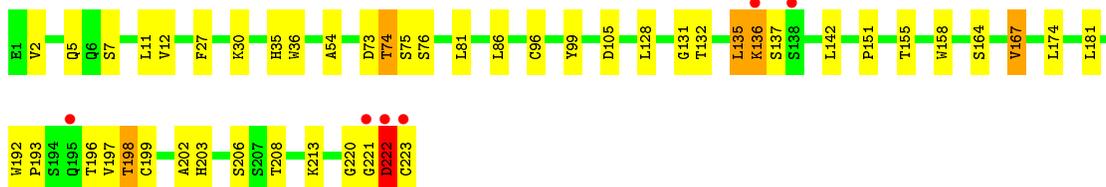
- Molecule 1: E8 ANTIBODY

Chain L:  87% 12%



- Molecule 2: E8 ANTIBODY

Chain H:  3% 78% 19%



- Molecule 3: CYTOCHROME C

Chain F:  85% 13%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	79.58Å 72.54Å 94.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 1.80 9.97 – 1.80	Depositor EDS
% Data completeness (in resolution range)	94.1 (10.00-1.80) 94.2 (9.97-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	X-PLOR 3.8	Depositor
R, R_{free}	0.200 , 0.256 0.210 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	18.6	Xtriage
Anisotropy	0.260	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 65.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ¹	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 47995 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4846	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.57% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Theoretical 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, ZN, ACE

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	0.46	0/1705	0.66	0/2315
2	H	0.49	0/1719	0.75	0/2352
3	F	0.43	0/840	0.63	0/1120
All	All	0.46	0/4264	0.69	0/5787

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	1664	0	1581	15	0
2	H	1676	0	1623	40	0
3	F	826	0	848	11	0
4	L	1	0	0	0	0
5	F	42	0	30	2	0
6	F	118	0	0	1	0
6	H	250	0	0	2	0
6	L	269	0	0	2	0
All	All	4846	0	4082	66	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.

The worst 5 of 66 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:193:PRO:HG2	2:H:223:CYS:HA	1.46	0.96
3:F:26:HIS:HD2	3:F:31:ASN:H	1.29	0.79
2:H:30:LYS:HG3	2:H:74:THR:HG21	1.63	0.79
2:H:131:GLY:O	2:H:135:LEU:HD12	1.87	0.75
2:H:151:PRO:O	2:H:203:HIS:HE1	1.74	0.70

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	212/214 (99%)	208 (98%)	4 (2%)	0	100	100
2	H	221/223 (99%)	209 (95%)	11 (5%)	1 (0%)	34	17
3	F	103/105 (98%)	100 (97%)	3 (3%)	0	100	100
All	All	536/542 (99%)	517 (96%)	18 (3%)	1 (0%)	52	35

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	222	ASP

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	188/188 (100%)	180 (96%)	8 (4%)	35	17
2	H	190/190 (100%)	177 (93%)	13 (7%)	20	6
3	F	86/86 (100%)	81 (94%)	5 (6%)	25	9
All	All	464/464 (100%)	438 (94%)	26 (6%)	26	10

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	75	SER
2	H	136	LYS
3	F	57	ILE
2	H	128	LEU
2	H	135	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	L	198	HIS
1	L	212	ASN
2	H	203	HIS
1	L	156	GLN
2	H	168	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](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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
5	HEM	F	105	3	29,46,50	5.70	20 (68%)	23,68,82	4.55	16 (69%)

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
5	HEM	F	105	3	-	0/21/30/54	0/0/4/8

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	F	105	HEM	C3C-C2C	-12.86	1.39	1.55
5	F	105	HEM	CHB-C1B	-12.24	1.39	1.53
5	F	105	HEM	CHD-C4C	-9.42	1.38	1.53
5	F	105	HEM	C3D-C2D	-9.25	1.36	1.55
5	F	105	HEM	CHD-C1D	-8.53	1.39	1.53

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	105	HEM	CBD-CAD-C3D	-6.46	105.96	115.73
5	F	105	HEM	CHB-C4A-C3A	-4.05	123.58	130.41
5	F	105	HEM	CBA-CAA-C2A	-3.75	105.82	112.53
5	F	105	HEM	C3B-CAB-CBB	-3.38	119.27	124.46
5	F	105	HEM	CHA-C1A-C2A	-3.02	125.30	130.41

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
5	F	105	HEM	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 [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, 95th 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 ²)	Q<0.9
1	L	214/214 (100%)	-0.30	1 (0%) 91 90	10, 18, 30, 52	0
2	H	223/223 (100%)	-0.12	6 (2%) 58 53	11, 18, 37, 66	0
3	F	104/105 (99%)	-0.11	0 100 100	14, 22, 35, 40	0
All	All	541/542 (99%)	-0.19	7 (1%) 79 76	10, 19, 35, 66	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	214	CYS	6.0
2	H	222	ASP	5.2
2	H	221	GLY	4.6
2	H	223	CYS	4.1
2	H	136	LYS	2.7

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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors

of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
5	HEM	F	105	42/43	0.91	0.09	-0.33	11,15,18,18	0
4	ZN	L	215	1/1	0.73	0.56	-	38,38,38,38	0

6.5 Other polymers [i](#)

There are no such residues in this entry.