



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:32 AM GMT

PDB ID : 2DH3  
Title : Crystal Structure of human ED-4F2hc  
Authors : Fort, J.; Fita, I.; Palacin, M.  
Deposited on : 2006-03-21  
Resolution : 2.80 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.

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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

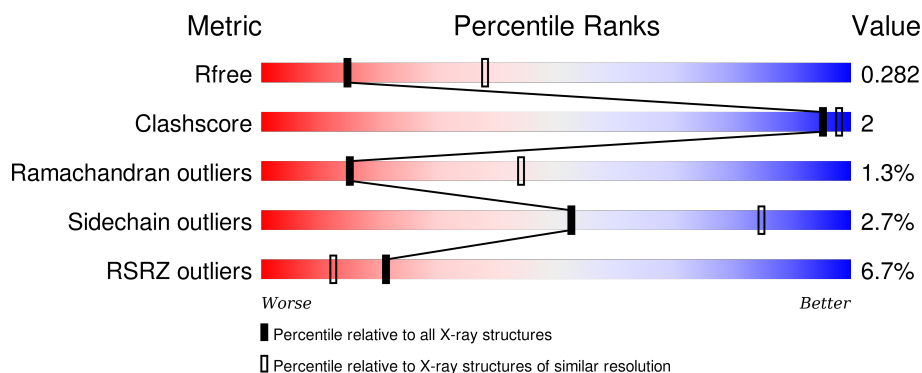
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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))
$R_{free}$	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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  $\geq 3$ , 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	A	424	<div> <div>4%</div> <div>90%</div> <div>7% ..</div> </div>
1	B	424	<div> <div>9%</div> <div>92%</div> <div>7% .</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6533 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 4F2 cell-surface antigen heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	416	Total	C	N	O	S	0	0	0
			3235	2056	552	622	5			
1	B	421	Total	C	N	O	S	0	0	0
			3269	2077	557	630	5			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	106	ASP	-	EXPRESSION TAG	UNP P08195
A	107	ARG	-	EXPRESSION TAG	UNP P08195
A	108	TRP	-	EXPRESSION TAG	UNP P08195
A	109	GLY	-	EXPRESSION TAG	UNP P08195
A	110	SER	-	EXPRESSION TAG	UNP P08195
B	106	ASP	-	EXPRESSION TAG	UNP P08195
B	107	ARG	-	EXPRESSION TAG	UNP P08195
B	108	TRP	-	EXPRESSION TAG	UNP P08195
B	109	GLY	-	EXPRESSION TAG	UNP P08195
B	110	SER	-	EXPRESSION TAG	UNP P08195

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

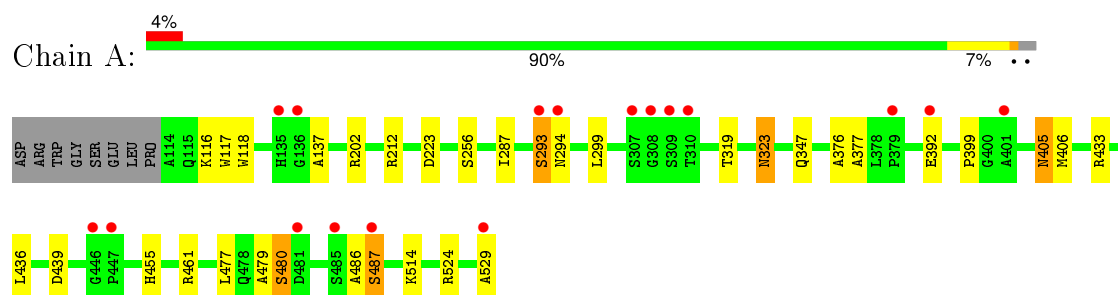
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	15	Total	O	0	0
			15	15		
3	B	13	Total	O	0	0
			13	13		

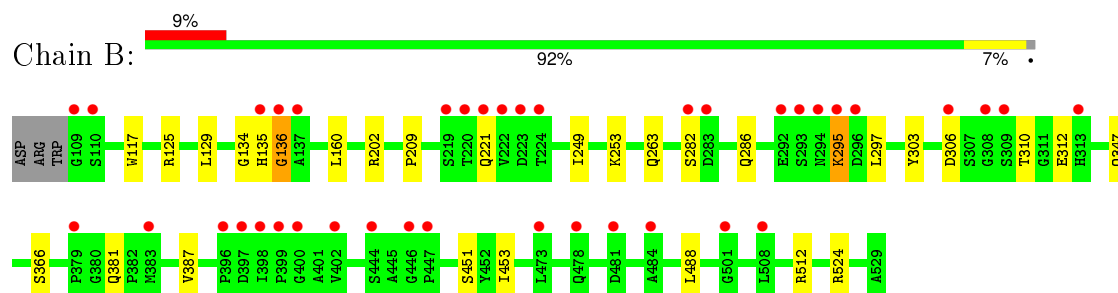
### 3 Residue-property plots [i](#)

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: 4F2 cell-surface antigen heavy chain



- Molecule 1: 4F2 cell-surface antigen heavy chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	69.50Å 101.79Å 121.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 2.80 29.65 – 2.80	Depositor EDS
% Data completeness (in resolution range)	94.6 (25.00-2.80) 94.6 (29.65-2.80)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.50 (at 2.80Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.217 , 0.275 0.221 , 0.282	Depositor DCC
$R_{free}$ test set	1066 reflections (5.42%)	DCC
Wilson B-factor (Å <sup>2</sup> )	48.6	Xtriage
Anisotropy	0.392	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 55.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 20740 reflections (0.005%)	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	6533	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.49% 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

### 5.1 Standard geometry

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

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	A	0.34	0/3307	0.59	1/4484 (0.0%)
1	B	0.34	0/3342	0.51	0/4532
All	All	0.34	0/6649	0.55	1/9016 (0.0%)

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
1	B	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	529	ALA	CA-C-O	20.44	163.02	120.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	295	LYS	Peptide

### 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	A	3235	0	3194	12	0
1	B	3269	0	3226	9	0
2	A	1	0	0	0	0
3	A	15	0	0	0	0
3	B	13	0	0	0	0
All	All	6533	0	6420	21	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 2.

All (21) 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:A:376:ALA:O	1:A:377:ALA:HB3	2.04	0.57
1:A:287:ILE:HG23	1:A:299:LEU:HD23	1.89	0.55
1:B:129:LEU:HD21	1:B:160:LEU:HD11	1.88	0.55
1:A:319:THR:O	1:A:323:ASN:HB2	2.10	0.52
1:B:282:SER:O	1:B:286:GLN:NE2	2.42	0.51
1:B:286:GLN:HE21	1:B:303:TYR:HD2	1.59	0.50
1:A:433:ARG:HA	1:A:436:LEU:HD12	1.94	0.50
1:B:453:ILE:HD11	1:B:488:LEU:HD11	1.98	0.45
1:A:486:ALA:O	1:A:487:SER:C	2.55	0.45
1:A:439:ASP:HB3	1:A:455:HIS:O	2.16	0.45
1:B:263:GLN:HE21	1:B:295:LYS:HB3	1.82	0.45
1:A:405:ASN:HD22	1:A:406:MET:N	2.16	0.43
1:A:376:ALA:O	1:A:377:ALA:CB	2.65	0.43
1:A:479:ALA:O	1:A:480:SER:C	2.57	0.43
1:A:117:TRP:CD2	1:A:202:ARG:HG3	2.54	0.42
1:B:125:ARG:HB2	1:B:366:SER:HA	2.00	0.42
1:A:256:SER:HB2	1:A:293:SER:HB2	2.02	0.42
1:A:116:LYS:HD3	1:A:118:TRP:CZ2	2.55	0.41
1:B:381:GLN:HE22	1:B:387:VAL:HG23	1.85	0.41
1:B:117:TRP:CD2	1:B:202:ARG:HG3	2.56	0.41
1:B:134:GLY:O	1:B:136:GLY:N	2.54	0.40

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	A	414/424 (98%)	379 (92%)	29 (7%)	6 (1%)	14	42
1	B	419/424 (99%)	395 (94%)	19 (4%)	5 (1%)	16	47
All	All	833/848 (98%)	774 (93%)	48 (6%)	11 (1%)	15	44

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	223	ASP
1	A	487	SER
1	A	480	SER
1	A	293	SER
1	B	221	GLN
1	A	137	ALA
1	B	135	HIS
1	B	306	ASP
1	B	209	PRO
1	B	136	GLY
1	A	399	PRO

### 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	A	350/357 (98%)	340 (97%)	10 (3%)	50	83
1	B	354/357 (99%)	345 (98%)	9 (2%)	55	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	704/714 (99%)	685 (97%)	19 (3%)	52 85

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	212	ARG
1	A	294	ASN
1	A	323	ASN
1	A	347	GLN
1	A	392	GLU
1	A	405	ASN
1	A	461	ARG
1	A	477	LEU
1	A	514	LYS
1	A	524	ARG
1	B	249	ILE
1	B	253	LYS
1	B	297	LEU
1	B	310	THR
1	B	312	GLU
1	B	347	GLN
1	B	451	SER
1	B	512	ARG
1	B	524	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	167	GLN
1	A	194	GLN
1	A	251	ASN
1	A	285	GLN
1	A	294	ASN
1	A	320	GLN
1	A	347	GLN
1	A	405	ASN
1	A	428	GLN
1	B	130	GLN
1	B	194	GLN
1	B	221	GLN
1	B	263	GLN

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Mol	Chain	Res	Type
1	B	320	GLN
1	B	323	ASN
1	B	347	GLN
1	B	459	ASN

### 5.3.3 RNA ⓘ

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 ⓘ

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

### 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

### 6.1 Protein, DNA and RNA chains

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	A	416/424 (98%)	0.15	17 (4%) 41 29	42, 50, 60, 64	0
1	B	421/424 (99%)	0.38	39 (9%) 11 5	44, 50, 60, 67	0
All	All	837/848 (98%)	0.27	56 (6%) 21 12	42, 50, 60, 67	0

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	219	SER	5.5
1	B	135	HIS	5.4
1	A	307	SER	5.2
1	B	484	ALA	5.0
1	B	220	THR	4.9
1	B	399	PRO	4.8
1	B	223	ASP	4.5
1	B	447	PRO	3.8
1	B	397	ASP	3.8
1	B	444	SER	3.8
1	A	481	ASP	3.8
1	B	282	SER	3.7
1	A	309	SER	3.7
1	A	529	ALA	3.5
1	A	293	SER	3.5
1	B	222	VAL	3.5
1	B	137	ALA	3.4
1	A	308	GLY	3.2
1	B	224	THR	3.1
1	B	501	GLY	3.1
1	B	309	SER	3.1
1	A	446	GLY	3.0
1	B	295	LYS	2.9
1	B	296	ASP	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	313	HIS	2.9
1	B	478	GLN	2.8
1	A	294	ASN	2.8
1	B	221	GLN	2.8
1	A	485	SER	2.8
1	B	136	GLY	2.7
1	A	136	GLY	2.7
1	B	383	MET	2.6
1	A	379	PRO	2.5
1	A	310	THR	2.5
1	A	401	ALA	2.5
1	B	109	GLY	2.4
1	B	293	SER	2.4
1	B	400	GLY	2.4
1	B	402	VAL	2.4
1	B	379	PRO	2.3
1	B	446	GLY	2.3
1	A	447	PRO	2.3
1	B	473	LEU	2.3
1	A	135	HIS	2.3
1	B	283	ASP	2.2
1	A	392	GLU	2.2
1	B	294	ASN	2.2
1	B	481	ASP	2.2
1	B	110	SER	2.1
1	B	398	ILE	2.1
1	B	292	GLU	2.1
1	B	508	LEU	2.1
1	B	306	ASP	2.1
1	B	308	GLY	2.1
1	A	487	SER	2.0
1	B	396	PRO	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](#)

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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
2	ZN	A	601	1/1	0.99	0.09	-1.90	46,46,46,46	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.