



# wwPDB X-ray Structure Validation Summary Report

Feb 14, 2017 – 09:38 am GMT

PDB ID : 2C1O  
Title : ENAIIHIS FAB FRAGMENT IN THE FREE FORM  
Authors : Parkkinen, T.; Nevanen, T.K.; Koivula, A.; Rouvinen, J.  
Deposited on : 2005-09-19  
Resolution : 2.75 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  
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

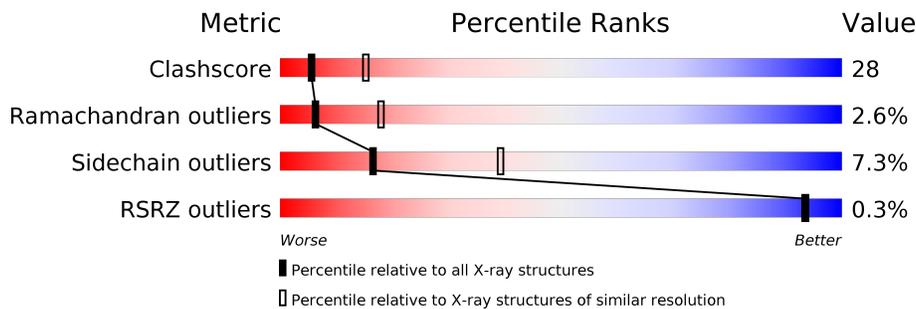
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.75 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	112137	4174 (2.80-2.72)
Ramachandran outliers	110173	4103 (2.80-2.72)
Sidechain outliers	110143	4106 (2.80-2.72)
RSRZ outliers	101464	3697 (2.80-2.72)

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	254	 52% 30% 15%
1	L	254	 43% 39% 15%
2	B	218	 56% 40%
2	H	218	 50% 41% 9%

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6848 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 IGK-C PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	217	1680	1052	283	339	6	0	0	0
1	L	217	1680	1052	283	339	6	0	0	0

- Molecule 2 is a protein called IGH-4 PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	218	1645	1034	277	327	7	0	0	1
2	H	218	1651	1037	277	329	8	0	0	0

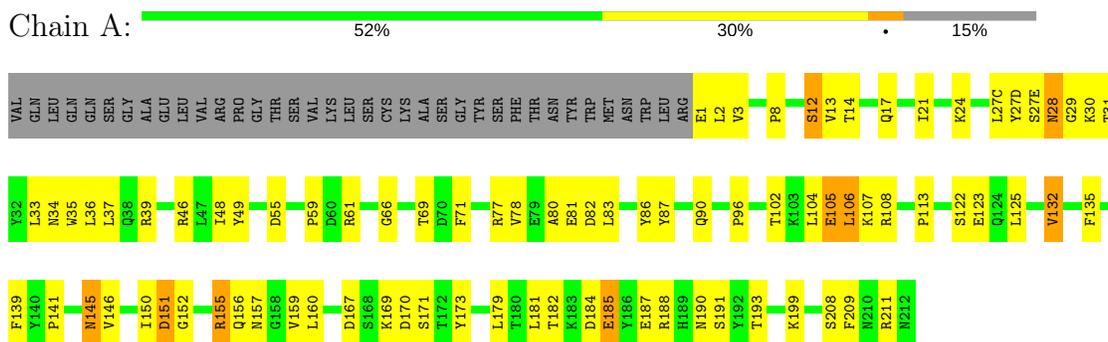
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	63	Total 63	O 63	0	0
3	B	40	Total 40	O 40	0	0
3	H	47	Total 47	O 47	0	0
3	L	42	Total 42	O 42	0	0

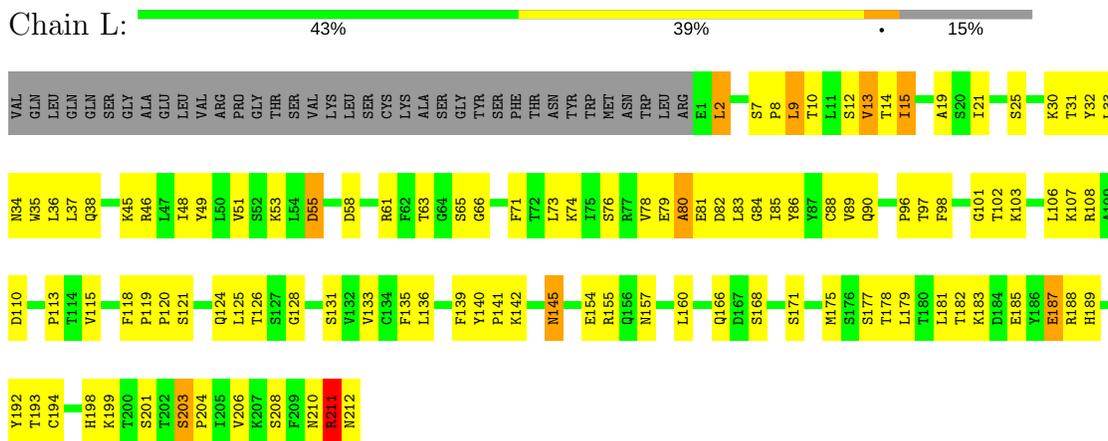
### 3 Residue-property plots

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.

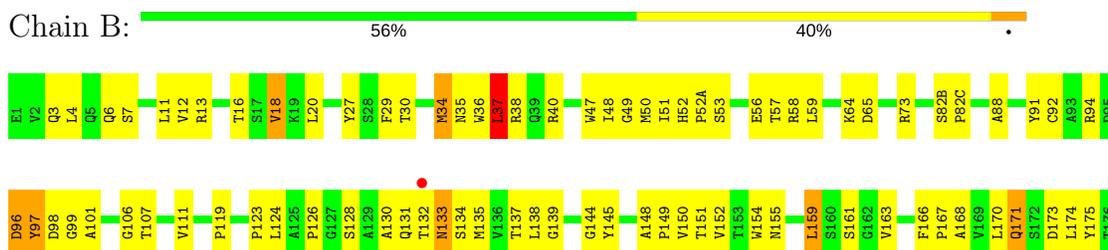
#### • Molecule 1: IGK-C PROTEIN



#### • Molecule 1: IGK-C PROTEIN



#### • Molecule 2: IGH-4 PROTEIN





● Molecule 2: IGH-4 PROTEIN



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	71.81Å 88.68Å 141.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 2.75 75.13 – 2.70	Depositor EDS
% Data completeness (in resolution range)	95.9 (25.00-2.75) 91.8 (75.13-2.70)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.76 (at 2.69Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.218 , 0.301 0.226 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	39.7	Xtrriage
Anisotropy	0.463	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 47.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	6848	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	37.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 33.68 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to  $7.6984e-04$ . The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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	A	0.42	0/1717	0.69	0/2329
1	L	0.40	0/1717	0.65	0/2329
2	B	0.42	0/1688	0.71	1/2311 (0.0%)
2	H	0.40	0/1694	0.66	0/2317
All	All	0.41	0/6816	0.68	1/9286 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	37	LEU	CA-CB-CG	5.03	126.86	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	A	1680	0	1642	79	0
1	L	1680	0	1642	107	0
2	B	1645	0	1599	81	0
2	H	1651	0	1604	113	0
3	A	63	0	0	2	0
3	B	40	0	0	1	0
3	H	47	0	0	2	0
3	L	42	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	6848	0	6487	373	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 28.

The worst 5 of 373 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:155:ASN:HD22	2:H:159:LEU:HD22	1.18	1.08
1:A:21:ILE:HD12	1:A:102:THR:HG21	1.39	1.01
2:B:30:THR:HA	2:B:52(A):PRO:HG2	1.45	0.99
1:A:151:ASP:HA	1:A:191:SER:HB3	1.50	0.94
1:L:21:ILE:HD12	1:L:102:THR:HG21	1.51	0.93

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	A	215/254 (85%)	196 (91%)	17 (8%)	2 (1%)	20	49
1	L	215/254 (85%)	187 (87%)	22 (10%)	6 (3%)	6	16
2	B	216/218 (99%)	189 (88%)	22 (10%)	5 (2%)	7	21
2	H	216/218 (99%)	185 (86%)	22 (10%)	9 (4%)	3	9
All	All	862/944 (91%)	757 (88%)	83 (10%)	22 (3%)	6	18

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	128	SER
2	B	133	ASN

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Mol	Chain	Res	Type
2	H	41	PRO
2	H	129	ALA
2	H	213	ARG

### 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	A	194/226 (86%)	185 (95%)	9 (5%)	31	62
1	L	194/226 (86%)	182 (94%)	12 (6%)	21	49
2	B	187/188 (100%)	171 (91%)	16 (9%)	12	31
2	H	188/188 (100%)	169 (90%)	19 (10%)	9	23
All	All	763/828 (92%)	707 (93%)	56 (7%)	16	39

5 of 56 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	3	GLN
2	H	41	PRO
1	L	168	SER
2	H	11	LEU
2	H	23	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
2	H	6	GLN
2	H	31	ASN
1	L	145	ASN
2	H	3	GLN
1	L	156	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	A	217/254 (85%)	-0.27	0 <a href="#">100</a> <a href="#">100</a>	13, 33, 54, 68	0
1	L	217/254 (85%)	-0.09	0 <a href="#">100</a> <a href="#">100</a>	16, 40, 61, 66	0
2	B	218/218 (100%)	-0.31	1 (0%) <a href="#">90</a> <a href="#">89</a>	15, 33, 58, 99	0
2	H	218/218 (100%)	-0.08	2 (0%) <a href="#">84</a> <a href="#">82</a>	16, 38, 66, 94	0
All	All	870/944 (92%)	-0.19	3 (0%) <a href="#">93</a> <a href="#">93</a>	13, 35, 61, 99	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	131	GLN	2.9
2	B	132	THR	2.4
2	H	132	THR	2.3

### 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.