W O R L D W I D E
wwPDB
PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report ⓘ

May 16, 2020 – 01:55 am BST

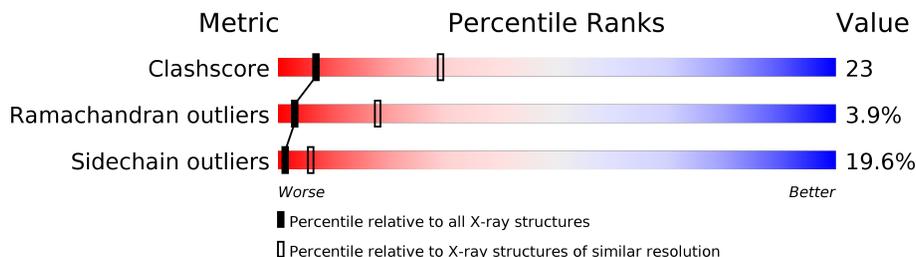|		
PDB ID	:	1HIN
Title	:	STRUCTURAL EVIDENCE FOR INDUCED FIT AS A MECHANISM FOR ANTIBODY-ANTIGEN RECOGNITION
Authors	:	Rini, J.M.; Wilson, I.A.
Deposited on	:	1992-07-08
Resolution	:	3.10 Å(reported)

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 3.10 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	Percentile Ranks	Value
Clashscore		23
Ramachandran outliers		3.9%
Sidechain outliers		19.6%

Worse   *Better*

■ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)

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 respectively. 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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	L	217	43% 43% 11% •
2	H	220	40% 44% 13% •
3	P	8	50% 13% 25% 13%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 3432 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 IGG2A-KAPPA 17/9 FAB (LIGHT CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	217	Total	C	N	O	S	0	0	0
			1680	1047	279	347	7			

- Molecule 2 is a protein called IGG2A-KAPPA 17/9 FAB (HEAVY CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	220	Total	C	N	O	S	0	0	0
			1664	1047	276	333	8			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	227	PRO	-	INSERTION	GB 533229

- Molecule 3 is a protein called INFLUENZA HEMAGGLUTININ HA1 (STRAIN X47) (RESIDUES 100-107).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	P	8	Total	C	N	O	0	0	0
			66	42	8	16			

- Molecule 4 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	L	11	Total	O	0	0
			11	11		
4	H	11	Total	O	0	0
			11	11		

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.
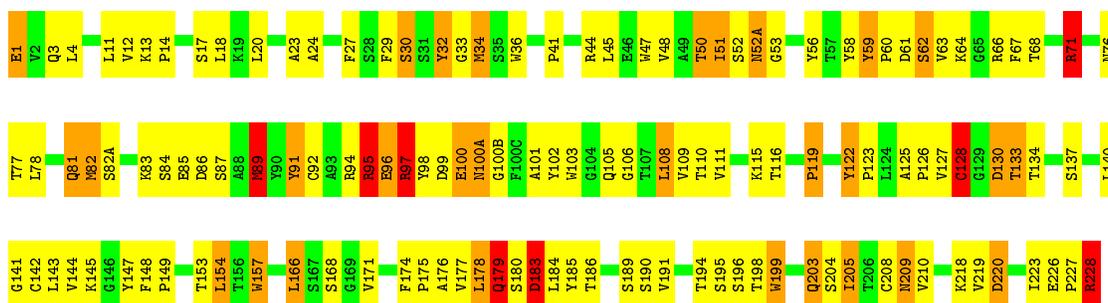
Note EDS was not executed.

- Molecule 1: IGG2A-KAPPA 17/9 FAB (LIGHT CHAIN)
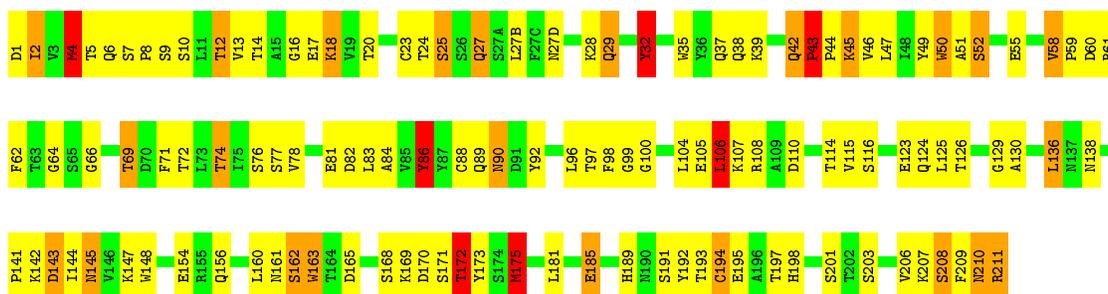
- Molecule 2: IGG2A-KAPPA 17/9 FAB (HEAVY CHAIN)

- Molecule 3: INFLUENZA HEMAGGLUTININ HA1 (STRAIN X47) (RESIDUES 100-107)

4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	63.50Å 73.40Å 62.70Å 90.00° 117.10° 90.00°	Depositor
Resolution (Å)	8.00 – 3.10	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-3.10)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.220 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3432	wwPDB-VP
Average B, all atoms (Å²)	11.0	wwPDB-VP

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	1.02	2/1718 (0.1%)	1.84	41/2334 (1.8%)
2	H	1.07	2/1705 (0.1%)	1.98	48/2322 (2.1%)
3	P	1.20	0/68	2.27	4/92 (4.3%)
All	All	1.05	4/3491 (0.1%)	1.92	93/4748 (2.0%)

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	L	0	2
2	H	0	1
All	All	0	3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	100	GLU	CD-OE2	-6.93	1.18	1.25
1	L	81	GLU	CB-CG	5.99	1.63	1.52
2	H	100	GLU	CD-OE1	-5.63	1.19	1.25
1	L	27	GLN	CA-CB	-5.05	1.42	1.53

The worst 5 of 93 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	L	211	ARG	NE-CZ-NH1	12.81	126.71	120.30
2	H	97	ARG	NE-CZ-NH1	12.48	126.54	120.30
3	P	101	ASP	CB-CG-OD1	-10.94	108.46	118.30
2	H	102	TYR	CB-CG-CD2	-9.89	115.06	121.00
2	H	157	TRP	CD1-CG-CD2	9.76	114.11	106.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	H	95	ARG	Sidechain
1	L	32	TYR	Sidechain
1	L	86	TYR	Sidechain

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	1680	0	1612	69	0
2	H	1664	0	1616	95	0
3	P	66	0	51	4	0
4	H	11	0	0	0	0
4	L	11	0	0	0	0
All	All	3432	0	3279	156	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 23.

The worst 5 of 156 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:11:LEU:HD13	2:H:110:THR:HG22	1.56	0.87
1:L:181:LEU:HD22	1:L:185:GLU:HG2	1.56	0.86
2:H:126:PRO:HG2	2:H:128:CYS:HA	1.60	0.84
2:H:166:LEU:HD13	2:H:191:VAL:HG21	1.61	0.83
1:L:83:LEU:HD11	1:L:106:LEU:HB3	1.58	0.83

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	215/217 (99%)	188 (87%)	22 (10%)	5 (2%)	6	28
2	H	218/220 (99%)	187 (86%)	19 (9%)	12 (6%)	2	11
3	P	6/8 (75%)	6 (100%)	0	0	100	100
All	All	439/445 (99%)	381 (87%)	41 (9%)	17 (4%)	3	18

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	29	GLN
2	H	149	PRO
2	H	180	SER
2	H	183	ASP
2	H	195	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	194/194 (100%)	155 (80%)	39 (20%)	1	5
2	H	187/187 (100%)	152 (81%)	35 (19%)	1	7
3	P	7/7 (100%)	5 (71%)	2 (29%)	0	1
All	All	388/388 (100%)	312 (80%)	76 (20%)	1	6

5 of 76 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	197	THR
2	H	41	PRO
2	H	209	ASN
1	L	203	SER
1	L	211	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
2	H	81	GLN
2	H	179	GLN
2	H	105	GLN
1	L	145	ASN
2	H	100(A)	ASN

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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.