



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 12, 2024 – 05:51 PM EDT

PDB ID : 1CGS
Title : LOCAL AND TRANSMITTED CONFORMATIONAL CHANGES ON COMPLEXATION OF AN ANTI-SWEETENER FAB
Authors : Guddat, L.W.; Shan, L.; Edmundson, A.B.
Deposited on : 1993-10-06
Resolution : 2.60 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

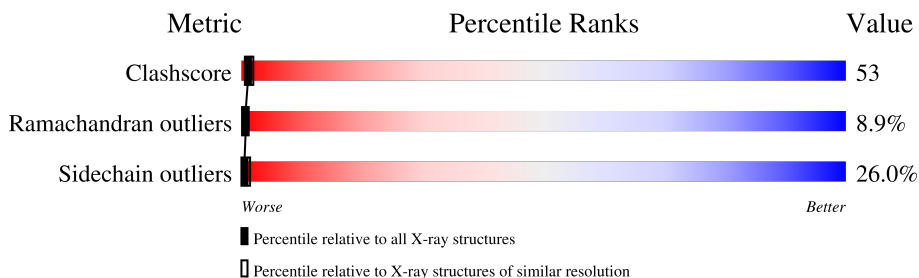
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)

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 of 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	L	219	 25% 52% 20% .
2	H	214	 32% 47% 18% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3412 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 IGG2B-KAPPA NC6.8 FAB (LIGHT CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	L	219	1696	1059	291	339	7	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	7	SER	THR	CONFLICT	PIR S16112
L	25	PRO	SER	CONFLICT	PIR S16112
L	39	HIS	TYR	CONFLICT	PIR S16112
L	51	LEU	PRO	CONFLICT	PIR S16112
L	75	ALA	ASP	CONFLICT	PIR S16112
L	94	SER	PHE	CONFLICT	PIR S16112
L	108	LYS	ARG	CONFLICT	PIR S16112
L	111	LEU	ILE	CONFLICT	PIR S16112

- Molecule 2 is a protein called IGG2B-KAPPA NC6.8 FAB (HEAVY CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	H	214	1608	1012	260	327	9	0	0	0

There are 17 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	5	LEU	VAL	CONFLICT	GB 1613777
H	19	GLN	LYS	CONFLICT	GB 1613777
H	31	GLU	SER	CONFLICT	GB 1613777
H	37	VAL	ILE	CONFLICT	GB 1613777
H	39	GLU	GLN	CONFLICT	GB 1613777
H	48	ILE	THR	CONFLICT	GB 1613777
H	57	ARG	THR	CONFLICT	GB 1613777
H	59	ASN	LYS	CONFLICT	GB 1613777

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Chain	Residue	Modelled	Actual	Comment	Reference
H	61	ARG	ASN	CONFLICT	GB 1613777
H	66	GLY	ASP	CONFLICT	GB 1613777
H	97	THR	ALA	CONFLICT	GB 1613777
H	?	-	SER	DELETION	GB 1613777
H	?	-	TYR	DELETION	GB 1613777
H	99	GLY	ARG	CONFLICT	GB 1613777
H	101	SER	ALA	CONFLICT	GB 1613777
H	102	SER	PRO	CONFLICT	GB 1613777
H	116	ALA	SER	CONFLICT	GB 1613777

- Molecule 3 is water.

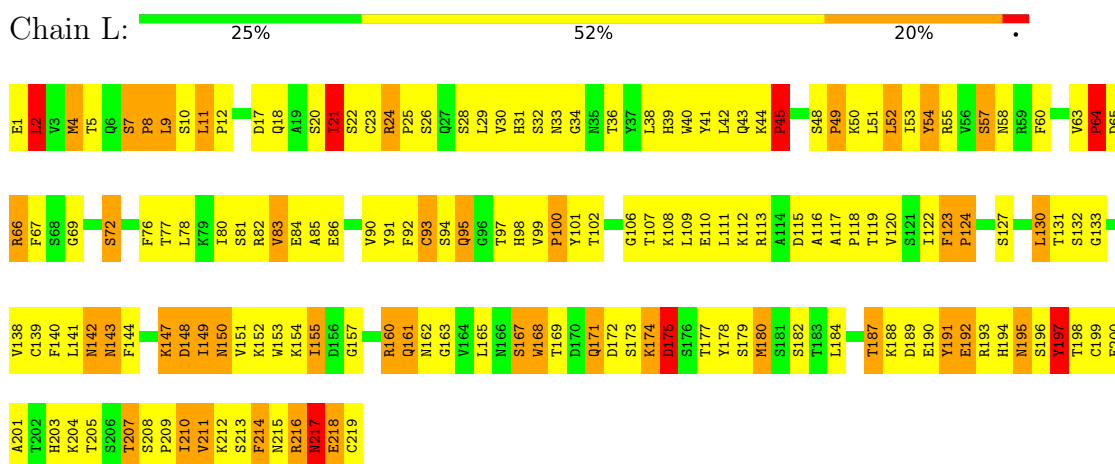
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	L	60	Total O 60 60	0	0
3	H	48	Total O 48 48	0	0

3 Residue-property plots

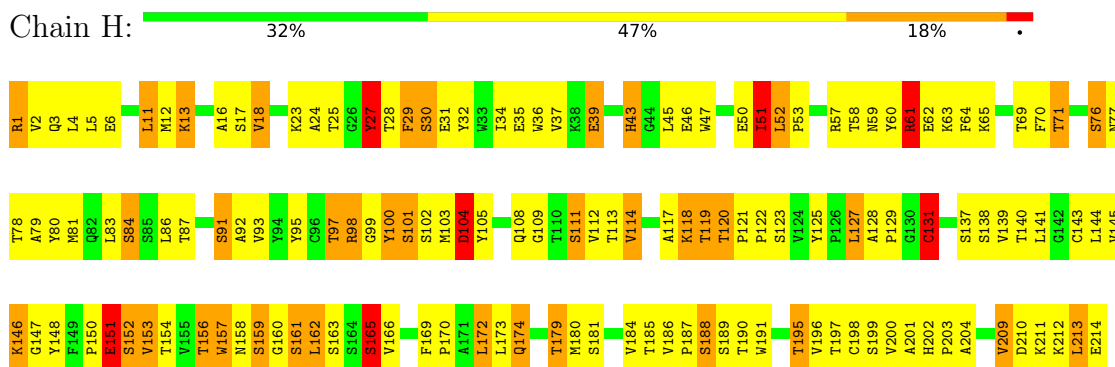
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: IGG2B-KAPPA NC6.8 FAB (LIGHT CHAIN)



- Molecule 2: IGG2B-KAPPA NC6.8 FAB (HEAVY CHAIN)



4 Data and refinement statistics

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	139.90Å 51.40Å 96.20Å 90.00° 132.80° 90.00°	Depositor
Resolution (Å)	10.00 – 2.60	Depositor
% Data completeness (in resolution range)	(Not available) (10.00-2.60)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.218 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	3412	wwPDB-VP
Average B, all atoms (Å ²)	10.0	wwPDB-VP

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	L	0.83	0/1736	1.12	5/2355 (0.2%)
2	H	0.87	0/1650	1.20	9/2251 (0.4%)
All	All	0.85	0/3386	1.16	14/4606 (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
1	L	0	2

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	162	LEU	CA-CB-CG	8.76	135.46	115.30
2	H	5	LEU	CA-CB-CG	8.37	134.56	115.30
1	L	163	GLY	N-CA-C	-6.65	96.46	113.10
1	L	52	LEU	CA-CB-CG	-6.13	101.20	115.30
1	L	217	ASN	N-CA-C	5.78	126.61	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	L	191	TYR	Sidechain
1	L	197	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	1696	0	1637	205	0
2	H	1608	0	1550	168	0
3	H	48	0	0	6	0
3	L	60	0	0	16	0
All	All	3412	0	3187	347	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 53.

The worst 5 of 347 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:54:TYR:CE1	1:L:58:ASN:HB3	1.80	1.17
2:H:160:GLY:HA3	2:H:196:VAL:HG22	1.33	1.06
1:L:149:ILE:HD13	1:L:203:HIS:HB2	1.37	1.05
1:L:117:ALA:HB2	1:L:205:THR:HG21	1.44	0.98
1:L:120:VAL:HG12	1:L:141:LEU:HG	1.41	0.98

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	217/219 (99%)	152 (70%)	43 (20%)	22 (10%)	0 0
2	H	212/214 (99%)	164 (77%)	32 (15%)	16 (8%)	1 1

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	429/433 (99%)	316 (74%)	75 (18%)	38 (9%)	1 0

5 of 38 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	2	LEU
1	L	7	SER
1	L	8	PRO
1	L	49	PRO
1	L	85	ALA

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	195/195 (100%)	144 (74%)	51 (26%)	0 1
2	H	182/182 (100%)	135 (74%)	47 (26%)	0 1
All	All	377/377 (100%)	279 (74%)	98 (26%)	0 1

5 of 98 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	29	PHE
2	H	98	ARG
2	H	34	ILE
2	H	61	ARG
2	H	111	SER

Sometimes 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	43	HIS
2	H	158	ASN
1	L	150	ASN

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Mol	Chain	Res	Type
1	L	162	ASN
1	L	171	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 monosaccharides 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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.