Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 11:11 pm BST

PDB ID	:	1LSG
Title	:	THREE-DIMENSIONAL STRUCTURE OF THE PLATELET INTEGRIN RECOGNITION SEGMENT OF THE FIBRINOGEN GAMMA CHAIN OBTAINED BY CARRIER PROTEIN-DRIVEN CRYSTALLIZATION
Authors	:	Patel, H.; Anderson, W.F.
Deposited on	:	1994-10-25
Resolution	:	2.40 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*
A user guide is available at
https://www.wwpdb.org/validation/2017/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:

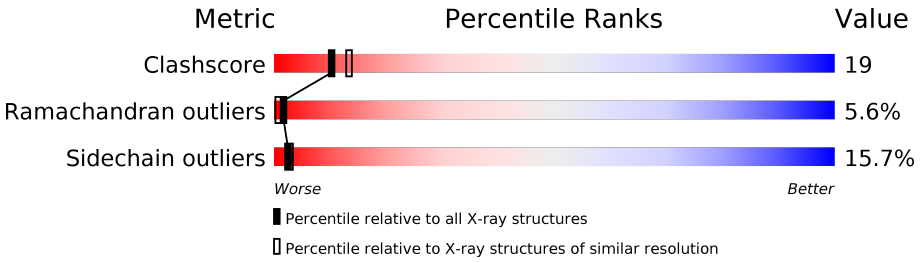
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.40 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	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)

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	A	144	50% 35% 10% 5%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1110 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 HEN EGG WHITE LYSOZYME.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	144	1110	678	216	205	11	0	0	0

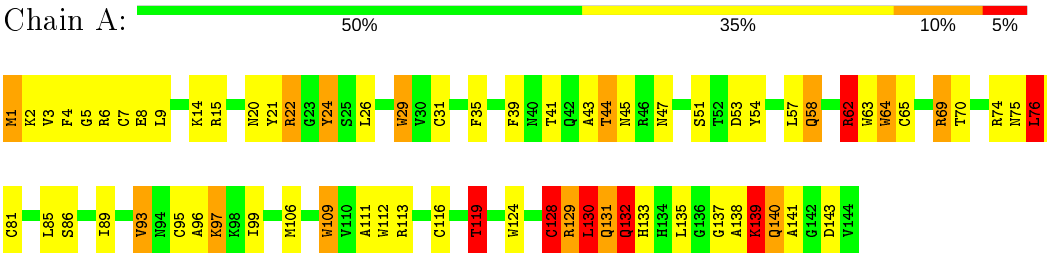
3 Residue-property plots (i)

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: HEN EGG WHITE LYSOZYME

Chain A:



4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	55.90Å 74.00Å 30.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.40	Depositor
% Data completeness (in resolution range)	(Not available) (15.00-2.40)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.202 , 0.328	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1110	wwPDB-VP
Average B, all atoms (Å^2)	15.0	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	A	1.21	1/1132 (0.1%)	2.42	66/1527 (4.3%)

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	A	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	112	TRP	CG-CD2	-5.90	1.33	1.43

All (66) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	22	ARG	NE-CZ-NH1	13.97	127.29	120.30
1	A	62	ARG	NE-CZ-NH2	-11.13	114.73	120.30
1	A	29	TRP	CD1-CG-CD2	10.31	114.55	106.30
1	A	64	TRP	CD1-CG-CD2	10.23	114.48	106.30
1	A	63	TRP	CD1-CG-CD2	10.07	114.35	106.30
1	A	112	TRP	CD1-CG-CD2	9.96	114.27	106.30
1	A	140	GLN	N-CA-C	9.96	137.90	111.00
1	A	128	CYS	CA-CB-SG	9.80	131.64	114.00
1	A	69	ARG	NE-CZ-NH2	-9.74	115.43	120.30
1	A	24	TYR	CB-CG-CD1	-9.66	115.20	121.00
1	A	15	ARG	CA-CB-CG	9.43	134.15	113.40
1	A	62	ARG	NE-CZ-NH1	9.40	125.00	120.30
1	A	15	ARG	NE-CZ-NH1	9.08	124.84	120.30
1	A	138	ALA	N-CA-C	8.78	134.70	111.00
1	A	138	ALA	CA-C-N	-8.72	98.03	117.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	63	TRP	CE2-CD2-CG	-8.52	100.48	107.30
1	A	139	LYS	N-CA-C	8.34	133.53	111.00
1	A	64	TRP	CE2-CD2-CG	-8.31	100.66	107.30
1	A	29	TRP	CE2-CD2-CG	-8.25	100.70	107.30
1	A	130	LEU	CA-CB-CG	8.24	134.26	115.30
1	A	74	ARG	NE-CZ-NH1	7.85	124.23	120.30
1	A	1	MET	CA-CB-CG	7.84	126.63	113.30
1	A	109	TRP	CD1-CG-CD2	7.80	112.54	106.30
1	A	132	GLN	CA-CB-CG	7.64	130.21	113.40
1	A	76	LEU	CA-CB-CG	7.62	132.84	115.30
1	A	124	TRP	CD1-CG-CD2	7.27	112.12	106.30
1	A	77	CYS	CA-CB-SG	-7.14	101.14	114.00
1	A	44	THR	CA-CB-CG2	6.97	122.16	112.40
1	A	112	TRP	CG-CD1-NE1	-6.93	103.17	110.10
1	A	138	ALA	C-N-CA	6.89	138.93	121.70
1	A	112	TRP	CE2-CD2-CG	-6.79	101.86	107.30
1	A	109	TRP	CE2-CD2-CG	-6.77	101.89	107.30
1	A	124	TRP	CE2-CD2-CG	-6.61	102.01	107.30
1	A	3	VAL	N-CA-C	-6.54	93.36	111.00
1	A	140	GLN	CA-CB-CG	-6.51	99.08	113.40
1	A	119	THR	CA-CB-CG2	6.50	121.50	112.40
1	A	130	LEU	N-CA-C	-6.42	93.66	111.00
1	A	113	ARG	NE-CZ-NH1	6.32	123.46	120.30
1	A	64	TRP	CG-CD1-NE1	-6.06	104.04	110.10
1	A	109	TRP	CG-CD1-NE1	-6.05	104.05	110.10
1	A	63	TRP	CG-CD1-NE1	-6.00	104.10	110.10
1	A	26	LEU	CA-CB-CG	5.93	128.93	115.30
1	A	140	GLN	N-CA-CB	-5.84	100.08	110.60
1	A	138	ALA	O-C-N	5.79	131.97	122.70
1	A	129	ARG	CB-CG-CD	5.76	126.58	111.60
1	A	29	TRP	CG-CD1-NE1	-5.76	104.34	110.10
1	A	6	ARG	NE-CZ-NH1	5.73	123.17	120.30
1	A	44	THR	CA-CB-OG1	-5.63	97.18	109.00
1	A	22	ARG	NE-CZ-NH2	-5.56	117.52	120.30
1	A	63	TRP	CB-CG-CD1	-5.53	119.81	127.00
1	A	128	CYS	CA-C-N	-5.52	105.06	117.20
1	A	129	ARG	CA-CB-CG	-5.46	101.39	113.40
1	A	21	TYR	CB-CG-CD1	-5.45	117.73	121.00
1	A	139	LYS	O-C-N	-5.43	114.01	122.70
1	A	124	TRP	CG-CD2-CE3	5.39	138.75	133.90
1	A	26	LEU	CB-CA-C	-5.37	100.00	110.20
1	A	5	GLY	N-CA-C	-5.32	99.81	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	69	ARG	CB-CG-CD	-5.31	97.80	111.60
1	A	143	ASP	N-CA-CB	5.23	120.01	110.60
1	A	93	VAL	CA-CB-CG2	-5.21	103.09	110.90
1	A	74	ARG	NE-CZ-NH2	-5.20	117.70	120.30
1	A	139	LYS	CA-C-N	5.18	128.60	117.20
1	A	15	ARG	O-C-N	-5.15	114.46	122.70
1	A	1	MET	CG-SD-CE	5.12	108.40	100.20
1	A	143	ASP	CA-C-N	-5.09	106.01	117.20
1	A	138	ALA	N-CA-CB	-5.02	103.07	110.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	128	CYS	Peptide

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	1110	0	1070	38	0
All	All	1110	0	1070	38	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 19.

All (38) 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:31:CYS:SG	1:A:116:CYS:SG	2.56	0.87
1:A:31:CYS:HG	1:A:116:CYS:HG	0.79	0.78
1:A:53:ASP:HB3	1:A:58:GLN:HG3	1.74	0.69
1:A:99:ILE:HD12	1:A:109:TRP:CZ2	2.29	0.68
1:A:75:ASN:ND2	1:A:78:ASN:HA	2.11	0.64
1:A:93:VAL:O	1:A:97:LYS:HG2	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:9:LEU:HD22	1:A:39:PHE:CD1	2.37	0.60
1:A:140:GLN:HA	1:A:140:GLN:HE21	1.71	0.55
1:A:31:CYS:CB	1:A:116:CYS:HG	2.20	0.54
1:A:4:PHE:HB2	1:A:39:PHE:HB3	1.90	0.54
1:A:140:GLN:HA	1:A:140:GLN:NE2	2.21	0.53
1:A:75:ASN:HD21	1:A:78:ASN:HA	1.72	0.53
1:A:2:LYS:HE2	1:A:4:PHE:CZ	2.44	0.53
1:A:106:MET:HG2	1:A:109:TRP:CZ3	2.44	0.53
1:A:64:TRP:CZ3	1:A:76:LEU:HD12	2.44	0.53
1:A:62:ARG:HA	1:A:70:THR:HG21	1.91	0.52
1:A:116:CYS:O	1:A:119:THR:HB	2.11	0.51
1:A:132:GLN:O	1:A:133:HIS:ND1	2.45	0.50
1:A:2:LYS:HG2	1:A:4:PHE:CE1	2.48	0.49
1:A:24:TYR:HB2	1:A:29:TRP:HE1	1.79	0.48
1:A:31:CYS:SG	1:A:116:CYS:CB	3.01	0.48
1:A:96:ALA:HA	1:A:99:ILE:HG13	1.98	0.46
1:A:8:GLU:HA	1:A:130:LEU:HD22	1.98	0.46
1:A:64:TRP:HZ3	1:A:76:LEU:HD12	1.81	0.46
1:A:35:PHE:HB3	1:A:111:ALA:HB1	1.98	0.45
1:A:139:LYS:HD2	1:A:140:GLN:HG2	1.98	0.45
1:A:106:MET:HG2	1:A:109:TRP:CE3	2.54	0.43
1:A:97:LYS:HE2	1:A:97:LYS:HB3	1.76	0.43
1:A:43:ALA:HB3	1:A:58:GLN:HE22	1.84	0.43
1:A:95:CYS:O	1:A:99:ILE:HG13	2.18	0.42
1:A:64:TRP:CZ2	1:A:99:ILE:HG23	2.54	0.42
1:A:128:CYS:H	1:A:137:GLY:HA3	1.84	0.42
1:A:65:CYS:HB2	1:A:81:CYS:HA	2.02	0.42
1:A:7:CYS:HB2	1:A:131:GLN:OE1	2.20	0.41
1:A:132:GLN:OE1	1:A:133:HIS:N	2.54	0.41
1:A:54:TYR:CD2	1:A:85:LEU:HD11	2.56	0.40
1:A:45:ASN:HB2	1:A:53:ASP:HB2	2.03	0.40
1:A:99:ILE:HD12	1:A:109:TRP:HZ2	1.82	0.40

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	142/144 (99%)	109 (77%)	25 (18%)	8 (6%)	2 1

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	22	ARG
1	A	139	LYS
1	A	20	ASN
1	A	141	ALA
1	A	97	LYS
1	A	131	GLN
1	A	135	LEU
1	A	41	THR

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	115/115 (100%)	97 (84%)	18 (16%)	2 3

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	14	LYS
1	A	44	THR
1	A	47	ASN
1	A	51	SER
1	A	57	LEU
1	A	58	GLN
1	A	62	ARG
1	A	69	ARG

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Mol	Chain	Res	Type
1	A	76	LEU
1	A	80	PRO
1	A	86	SER
1	A	89	ILE
1	A	119	THR
1	A	129	ARG
1	A	130	LEU
1	A	132	GLN
1	A	139	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	42	GLN
1	A	45	ASN
1	A	58	GLN
1	A	140	GLN

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

There are no ligands in this entry.

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

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.