



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 06:47 PM GMT

PDB ID : 1CGF
Title : CRYSTAL STRUCTURES OF RECOMBINANT 19-KDA HUMAN FIBROBLAST COLLAGENASE COMPLEXED TO ITSELF
Authors : Lovejoy, B.; Hassell, A.M.; Luther, M.A.; Weigl, D.; Jordan, S.R.
Deposited on : 1994-02-03
Resolution : 2.10 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
<http://wwpdb.org/validation/2016/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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

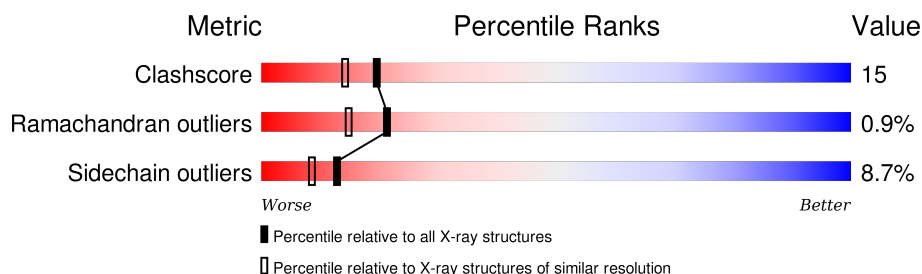
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)

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. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	162	 73% 22% 5%
1	B	162	 73% 22% 5%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3647 atoms, of which 908 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 FIBROBLAST COLLAGENASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	162	Total	C	H	N	O	S	0	0	0
			1547	797	273	226	249	2			
1	B	162	Total	C	H	N	O	S	0	0	0
			1547	797	273	226	249	2			

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

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

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	3	Total	Ca	0	0
			3	3		
3	A	3	Total	Ca	0	0
			3	3		

- Molecule 4 is water.

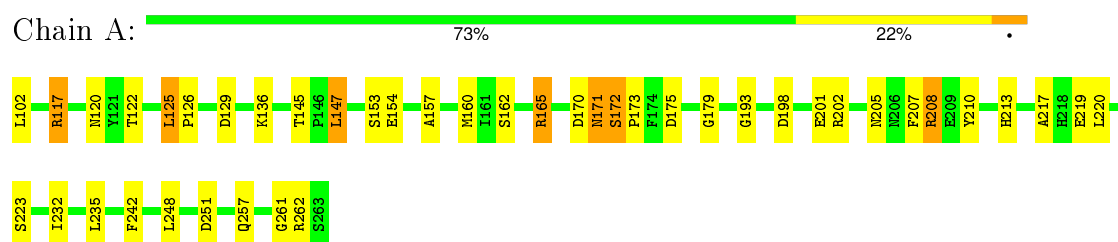
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	65	Total	H	O	0	0
			195	130	65		
4	B	116	Total	H	O	0	0
			348	232	116		

3 Residue-property plots

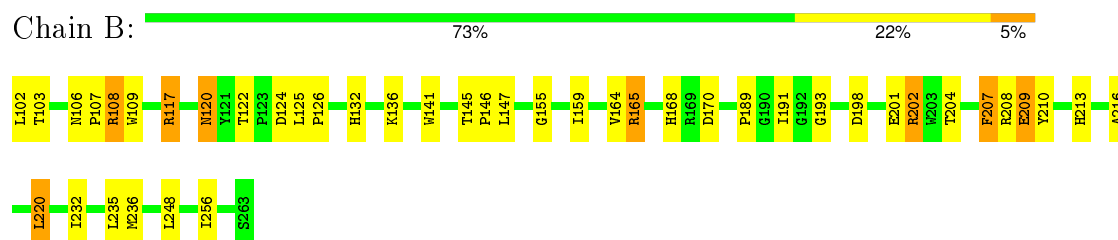
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

• Molecule 1: FIBROBLAST COLLAGENASE



• Molecule 1: FIBROBLAST COLLAGENASE



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	71.00 Å 50.50 Å 48.00 Å 90.00° 100.00° 90.00°	Depositor
Resolution (Å)	7.00 – 2.10	Depositor
% Data completeness (in resolution range)	(Not available) (7.00-2.10)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.197 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3647	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.51	0/1311	0.78	1/1785 (0.1%)
1	B	0.56	0/1311	0.78	2/1785 (0.1%)
All	All	0.54	0/2622	0.78	3/3570 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	125	LEU	CA-CB-CG	6.28	129.73	115.30
1	B	170	ASP	CB-CG-OD1	6.14	123.82	118.30
1	B	124	ASP	CB-CG-OD1	5.26	123.03	118.30

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	1274	273	1162	31	4
1	B	1274	273	1162	42	1
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	65	130	0	4	4
4	B	116	232	0	11	2
All	All	2739	908	2324	73	6

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 15.

All (73) 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:B:132:HIS:HE1	4:B:383:HOH:O	1.62	0.82
1:B:207:PHE:HB2	4:B:400:HOH:O	1.80	0.80
1:B:236:MET:SD	4:B:357:HOH:O	2.39	0.79
1:A:136:LYS:HE3	1:A:213:HIS:CE1	2.18	0.79
1:B:132:HIS:CE1	4:B:383:HOH:O	2.35	0.76
1:B:235:LEU:HD22	1:B:248:LEU:HD23	1.69	0.75
1:A:208:ARG:HB2	1:A:208:ARG:HH11	1.56	0.71
1:A:217:ALA:HB1	1:A:235:LEU:HD21	1.72	0.71
1:A:120:ASN:ND2	1:A:162:SER:HB2	2.09	0.68
1:B:204:THR:HG21	1:B:208:ARG:HB3	1.82	0.62
1:A:153:SER:O	1:A:154:GLU:HG3	1.99	0.61
1:B:202:ARG:CD	1:B:208:ARG:HH22	2.12	0.61
1:B:207:PHE:N	1:B:207:PHE:CD1	2.70	0.60
1:A:157:ALA:HB3	1:A:160:MET:SD	2.43	0.59
1:B:198:ASP:HB3	1:B:201:GLU:HG2	1.84	0.59
1:B:208:ARG:HD2	4:B:318:HOH:O	2.03	0.58
1:B:207:PHE:N	1:B:207:PHE:HD1	2.02	0.58
1:A:120:ASN:HD21	1:A:162:SER:HB2	1.69	0.57
1:B:202:ARG:CG	1:B:208:ARG:HH22	2.18	0.56
1:A:202:ARG:NH2	1:A:208:ARG:HG2	2.19	0.56
1:B:208:ARG:HG2	4:B:374:HOH:O	2.05	0.55
1:B:159:ILE:HG23	1:B:193:GLY:O	2.06	0.55
1:A:165:ARG:HG2	1:A:165:ARG:HH11	1.72	0.55
1:A:198:ASP:HB3	1:A:201:GLU:HG2	1.89	0.55
1:A:235:LEU:HD22	1:A:248:LEU:HD23	1.89	0.55
1:B:136:LYS:HG2	1:B:213:HIS:CE1	2.43	0.54
1:B:202:ARG:HB3	1:B:208:ARG:NH2	2.22	0.54
1:A:207:PHE:HA	1:A:242:PHE:HE2	1.72	0.54
1:B:202:ARG:CD	1:B:208:ARG:NH2	2.72	0.52
1:B:209:GLU:HB3	4:B:388:HOH:O	2.09	0.52
1:B:232:ILE:HG13	1:B:232:ILE:O	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:145:THR:HB	1:B:146:PRO:HD2	1.91	0.52
1:A:207:PHE:HD1	4:A:363:HOH:O	1.94	0.51
1:A:208:ARG:NH1	1:A:208:ARG:HB2	2.22	0.50
1:B:189:PRO:HB3	4:B:416:HOH:O	2.11	0.50
1:B:108:ARG:NH1	1:B:109:TRP:O	2.45	0.50
1:B:120:ASN:HD22	1:B:120:ASN:N	2.09	0.49
1:A:173:PRO:HB3	4:A:349:HOH:O	2.11	0.49
1:B:216:ALA:O	1:B:220:LEU:HD22	2.12	0.49
1:B:202:ARG:NE	1:B:208:ARG:HH22	2.10	0.49
1:A:125:LEU:HG	1:A:129:ASP:HB2	1.94	0.49
1:A:205:ASN:HA	4:A:321:HOH:O	2.12	0.48
1:A:117:ARG:NE	4:A:359:HOH:O	2.40	0.48
1:B:235:LEU:CD2	1:B:248:LEU:HD23	2.41	0.48
1:A:232:ILE:O	1:A:232:ILE:HG13	2.14	0.47
1:B:236:MET:SD	4:B:396:HOH:O	2.61	0.47
1:B:208:ARG:HD2	1:B:209:GLU:H	1.80	0.47
1:B:106:ASN:HB2	1:B:107:PRO:HD2	1.96	0.47
1:B:117:ARG:NH1	4:B:375:HOH:O	2.48	0.46
1:A:217:ALA:CB	1:A:235:LEU:HD21	2.43	0.46
1:A:172:SER:N	1:A:173:PRO:HD3	2.31	0.46
1:A:145:THR:OG1	1:A:147:LEU:HD22	2.16	0.45
1:B:102:LEU:HD23	1:B:103:THR:N	2.31	0.45
1:B:165:ARG:HH11	1:B:165:ARG:HG2	1.80	0.44
1:B:202:ARG:NE	1:B:208:ARG:NH2	2.65	0.44
1:B:202:ARG:HE	1:B:208:ARG:NH2	2.16	0.44
1:A:145:THR:OG1	1:A:147:LEU:HB2	2.18	0.44
1:A:171:ASN:C	1:A:173:PRO:HD3	2.38	0.44
1:B:164:VAL:HG21	1:B:168:HIS:CD2	2.54	0.43
1:B:141:TRP:CH2	1:B:236:MET:HE3	2.54	0.43
1:A:136:LYS:O	1:A:213:HIS:HE1	2.02	0.42
1:B:202:ARG:HE	1:B:208:ARG:CZ	2.33	0.42
1:A:175:ASP:OD2	1:A:179:GLY:HA3	2.20	0.42
1:A:193:GLY:O	1:A:223:SER:HB3	2.19	0.42
1:B:202:ARG:HE	1:B:208:ARG:NH1	2.18	0.41
1:A:257:GLN:HG2	1:A:261:GLY:O	2.19	0.41
1:A:219:GLU:OE1	1:A:219:GLU:HA	2.20	0.41
1:B:102:LEU:C	1:B:102:LEU:HD23	2.41	0.41
1:B:210:TYR:N	1:B:210:TYR:CD1	2.85	0.41
1:B:145:THR:HG21	1:B:256:ILE:HG13	2.02	0.41
1:A:165:ARG:HG2	1:A:165:ARG:NH1	2.34	0.40
1:A:126:PRO:HD2	1:A:129:ASP:OD2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:191:ILE:HG13	4:B:373:HOH:O	2.22	0.40

All (6) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:136:LYS:HZ1	4:A:357:HOH:H1[2_848]	1.07	0.53
1:A:136:LYS:HZ1	4:A:357:HOH:O[2_848]	1.07	0.53
1:A:136:LYS:HZ1	4:A:368:HOH:H1[2_848]	1.28	0.32
1:A:136:LYS:NZ	4:A:357:HOH:O[2_848]	1.89	0.31
4:B:318:HOH:H1	4:B:421:HOH:O[2_748]	1.42	0.18
1:B:146:PRO:O	4:B:352:HOH:H1[2_757]	1.50	0.10

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	160/162 (99%)	152 (95%)	6 (4%)	2 (1%)	15	9
1	B	160/162 (99%)	151 (94%)	8 (5%)	1 (1%)	30	24
All	All	320/324 (99%)	303 (95%)	14 (4%)	3 (1%)	21	15

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	155	GLY
1	A	210	TYR
1	A	170	ASP

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	132/134 (98%)	121 (92%)	11 (8%)	14	9
1	B	132/134 (98%)	120 (91%)	12 (9%)	12	7
All	All	264/268 (98%)	241 (91%)	23 (9%)	13	8

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	102	LEU
1	A	117	ARG
1	A	122	THR
1	A	147	LEU
1	A	165	ARG
1	A	171	ASN
1	A	172	SER
1	A	208	ARG
1	A	220	LEU
1	A	251	ASP
1	A	262	ARG
1	B	108	ARG
1	B	117	ARG
1	B	120	ASN
1	B	122	THR
1	B	125	LEU
1	B	126	PRO
1	B	147	LEU
1	B	165	ARG
1	B	202	ARG
1	B	207	PHE
1	B	209	GLU
1	B	220	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	120	ASN
1	A	171	ASN
1	A	257	GLN
1	B	106	ASN
1	B	120	ASN
1	B	132	HIS
1	B	186	GLN
1	B	250	GLN
1	B	257	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](#)

Of 10 ligands modelled in this entry, 10 are 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 [i](#)

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.