



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 09:48 PM UTC

PDB ID : 9I9A / pdb_00009i9a
Title : COLLAGEN-LIKE (PRO-PRO-GLY)10 AT 0.86 GPa HYDROSTATIC PRESSURE
Authors : Prange, T.; Girard, E.; Colloc'h, N.; Dhaussy, A.C.
Deposited on : 2025-02-06
Resolution : 1.70 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	:	4-5-2 with Phenix2.0
Mogul	:	NOT EXECUTED
Xtriage (Phenix)	:	2.0
EDS	:	NOT EXECUTED
Buster-report	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

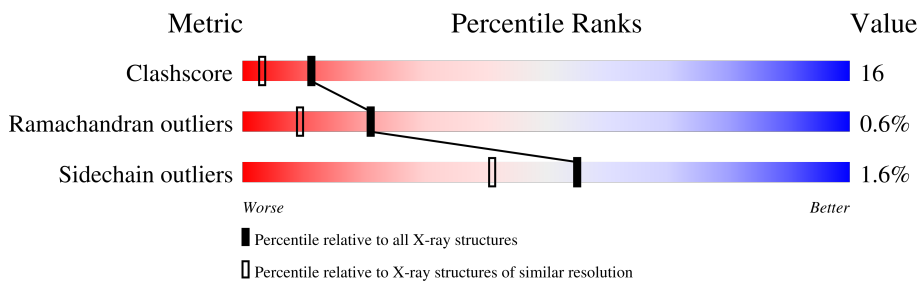
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)

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	A	33	
1	B	33	
1	D	33	
2	C	30	
2	E	30	
2	F	30	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 1446 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 TRIPLE-HELIX#1 (A,B,C).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	33	Total	C	N	O	0	6	0
			199	132	33	34			
1	B	33	Total	C	N	O	0	6	0
			199	132	33	34			
1	D	33	Total	C	N	O	0	6	0
			199	132	33	34			

- Molecule 2 is a protein called TRIPLE-HELIX#2 (D,E,F).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	30	Total	C	N	O	0	0	0
			181	120	30	31			
2	E	30	Total	C	N	O	0	0	0
			181	120	30	31			
2	F	30	Total	C	N	O	0	0	0
			181	120	30	31			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	49	Total	O	0	0
			49	49		
3	B	51	Total	O	0	1
			51	51		
3	C	57	Total	O	0	5
			57	57		
3	D	50	Total	O	0	0
			50	50		
3	E	49	Total	O	0	0
			49	49		
3	F	50	Total	O	0	0
			50	50		

3 Residue-property plots [i](#)

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: TRIPLE-HELIX#1 (A,B,C)

Chain A:  70% 30%




- Molecule 1: TRIPLE-HELIX#1 (A,B,C)

Chain B:  76% 21% .




- Molecule 1: TRIPLE-HELIX#1 (A,B,C)

Chain D:  88% 6% 6%



- Molecule 2: TRIPLE-HELIX#2 (D,E,F)

Chain C:  80% 20%



- Molecule 2: TRIPLE-HELIX#2 (D,E,F)

Chain E:  93% 7%



- Molecule 2: TRIPLE-HELIX#2 (D,E,F)

Chain F:

87%

13%



4 Data and refinement statistics

EDS was 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	26.20Å 25.75Å 180.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.76 – 1.70	Depositor
% Data completeness (in resolution range)	84.7 (24.76-1.70)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.09 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.8.0425	Depositor
R, R_{free}	0.200 , 0.256	Depositor
Wilson B-factor (Å ²)	8.0	Xtriage
Anisotropy	0.449	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.105 for k,h,-l	Xtriage
Total number of atoms	1446	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 65.89 % 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 6.5950e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical 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	0.82	0/220	0.92	1/315 (0.3%)
1	B	0.83	0/220	1.03	0/315
1	D	0.83	0/220	0.90	0/315
2	C	0.82	0/200	0.86	0/286
2	E	0.84	0/200	0.92	0/286
2	F	0.91	0/200	1.01	0/286
All	All	0.84	0/1260	0.94	1/1803 (0.1%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1[A]	PRO	CA-N-CD	-5.44	104.38	112.00

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	199	0	189	11	0
1	B	199	0	189	17	0
1	D	199	0	189	8	0
2	C	181	0	172	8	0
2	E	181	0	172	3	0
2	F	181	0	172	6	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	49	0	0	0	0
3	B	51	0	0	5	0
3	C	57	0	0	2	0
3	D	50	0	0	1	0
3	E	49	0	0	0	0
3	F	50	0	0	0	0
All	All	1446	0	1083	36	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 16.

The worst 5 of 36 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:1[A]:PRO:HB2	1:B:2[A]:PRO:HD2	1.51	0.92
1:A:32[B]:PRO:HB3	3:C:302[B]:HOH:O	1.73	0.87
1:B:32[B]:PRO:HD2	3:B:130:HOH:O	1.83	0.78
1:B:32[B]:PRO:HD3	3:B:131:HOH:O	1.85	0.76
1:A:32[B]:PRO:O	1:A:33[B]:GLY:O	2.05	0.74

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	31/33 (94%)	30 (97%)	1 (3%)	0	100	100
1	B	31/33 (94%)	29 (94%)	2 (6%)	0	100	100
1	D	31/33 (94%)	30 (97%)	0	1 (3%)	3	0
2	C	28/30 (93%)	28 (100%)	0	0	100	100
2	E	28/30 (93%)	28 (100%)	0	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	F	28/30 (93%)	28 (100%)	0	0	100	100
All	All	177/189 (94%)	173 (98%)	3 (2%)	1 (1%)	21	9

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	2[A]	PRO

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	22/22 (100%)	22 (100%)	0	100	100
1	B	22/22 (100%)	21 (96%)	1 (4%)	24	9
1	D	22/22 (100%)	21 (96%)	1 (4%)	24	9
2	C	20/20 (100%)	20 (100%)	0	100	100
2	E	20/20 (100%)	20 (100%)	0	100	100
2	F	20/20 (100%)	20 (100%)	0	100	100
All	All	126/126 (100%)	124 (98%)	2 (2%)	55	41

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	1[A]	PRO
1	D	1[A]	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

Mogul was not executed - this section is therefore empty.

5.5 Carbohydrates [i](#)

Mogul was not executed - this section is therefore empty.

5.6 Ligand geometry [i](#)

Mogul was not executed - this section is therefore empty.

5.7 Other polymers [i](#)

Mogul was not executed - this section is therefore empty.

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.