



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2018 – 09:49 pm GMT

PDB ID : 3SHI
Title : Crystal structure of human MMP1 catalytic domain at 2.2 Å resolution
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Deposited on : 2011-06-16
Resolution : 2.20 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	trunk30967
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac	:	5.8.0158
CCP4	:	7.0 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk30967

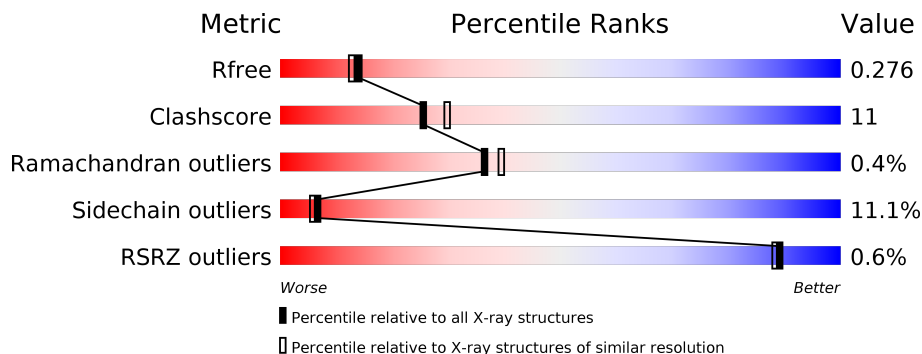
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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))
R_{free}	111664	4343 (2.20-2.20)
Clashscore	122126	5027 (2.20-2.20)
Ramachandran outliers	120053	4952 (2.20-2.20)
Sidechain outliers	120020	4953 (2.20-2.20)
RSRZ outliers	108989	4245 (2.20-2.20)

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.

Mol	Chain	Length	Quality of chain
1	A	156	 76% 18% 6% •
1	G	156	 % 71% 22% 6% •
1	M	156	 % 74% 19% 6%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4024 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 Interstitial collagenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	156	Total	C	N	O	S	0	0	0
			1236	774	218	242	2			
1	G	156	Total	C	N	O	S	0	0	0
			1236	774	218	242	2			
1	M	156	Total	C	N	O	S	0	0	0
			1236	774	218	242	2			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	2	Total	Zn	0	0
			2	2		
2	A	2	Total	Zn	0	0
			2	2		
2	M	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	G	3	Total	Ca	0	0
			3	3		
3	A	3	Total	Ca	0	0
			3	3		
3	M	3	Total	Ca	0	0
			3	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	128	Total	O	0	0
			128	128		

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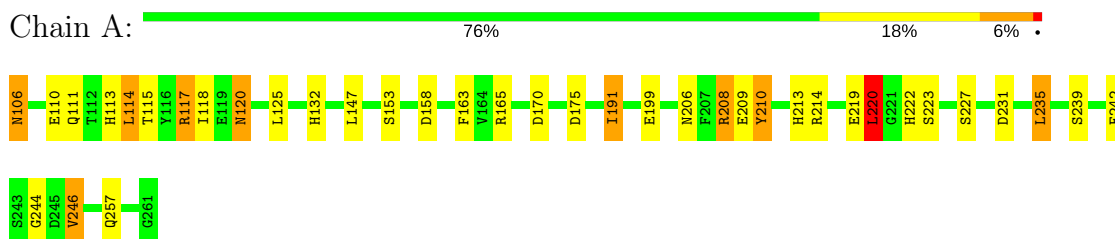
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	G	87	Total	O	0	0
			87	87		
4	M	86	Total	O	0	0
			86	86		

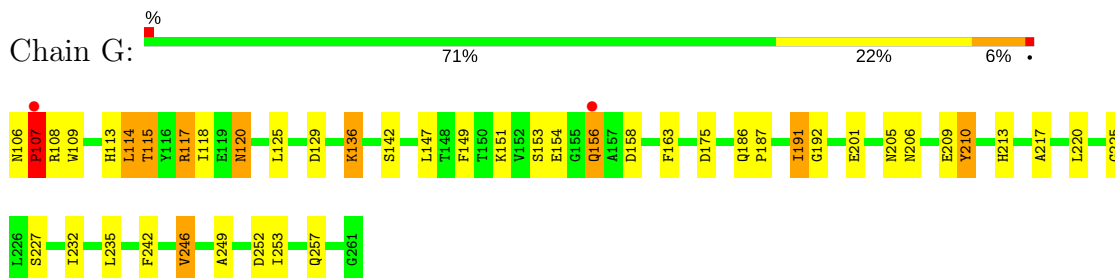
3 Residue-property plots [i](#)

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 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.

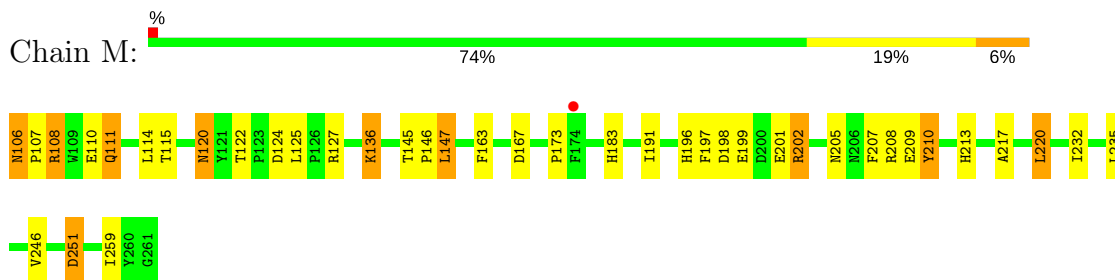
• Molecule 1: Interstitial collagenase



• Molecule 1: Interstitial collagenase



• Molecule 1: Interstitial collagenase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	147.69Å 54.53Å 94.91Å 90.00° 120.69° 90.00°	Depositor
Resolution (Å)	81.65 – 2.20 81.61 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.9 (81.65-2.20) 98.9 (81.61-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.48 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.6.0109	Depositor
R, R_{free}	0.209 , 0.278 0.209 , 0.276	Depositor DCC
R_{free} test set	2988 reflections (9.08%)	wwPDB-VP
Wilson B-factor (Å ²)	34.7	Xtriage
Anisotropy	0.332	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 38.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4024	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.36% of the height of the origin peak. No significant pseudotranslation is detected.*

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 ⓘ

5.1 Standard geometry ⓘ

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	1.07	4/1273 (0.3%)	1.15	13/1733 (0.8%)
1	G	0.99	0/1273	1.00	6/1733 (0.3%)
1	M	0.90	1/1273 (0.1%)	0.95	5/1733 (0.3%)
All	All	0.99	5/3819 (0.1%)	1.04	24/5199 (0.5%)

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	G	1	0
1	M	0	1
All	All	1	1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	239	SER	CB-OG	-6.22	1.34	1.42
1	A	199	GLU	CB-CG	5.67	1.62	1.52
1	A	110	GLU	CG-CD	5.35	1.59	1.51
1	M	110	GLU	CG-CD	5.21	1.59	1.51
1	A	210	TYR	CE2-CZ	5.08	1.45	1.38

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	208	ARG	NE-CZ-NH2	11.65	126.12	120.30
1	A	208	ARG	NE-CZ-NH1	-8.65	115.97	120.30
1	A	214	ARG	NE-CZ-NH2	-8.12	116.24	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	210	TYR	N-CA-C	7.38	130.91	111.00
1	A	208	ARG	CG-CD-NE	7.32	127.18	111.80

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	G	210	TYR	CA

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	M	209	GLU	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	1236	0	1128	21	0
1	G	1236	0	1128	30	0
1	M	1236	0	1128	31	0
2	A	2	0	0	0	0
2	G	2	0	0	0	0
2	M	2	0	0	0	0
3	A	3	0	0	0	0
3	G	3	0	0	0	0
3	M	3	0	0	0	0
4	A	128	0	0	4	0
4	G	87	0	0	6	1
4	M	86	0	0	7	1
All	All	4024	0	3384	81	1

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 11.

The worst 5 of 81 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:M:108:ARG:HG2	1:M:259:ILE:HG23	1.53	0.89
1:G:253:ILE:O	1:G:257:GLN:HG3	1.73	0.89
1:G:156:GLN:HA	4:G:263:HOH:O	1.76	0.86
1:G:120:ASN:HD21	1:G:163:PHE:H	1.23	0.86
1:M:111:GLN:HG2	4:M:293:HOH:O	1.77	0.85

All (1) 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)
4:G:291:HOH:O	4:M:31:HOH:O[3_546]	2.17	0.03

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	154/156 (99%)	149 (97%)	5 (3%)	0	100	100
1	G	154/156 (99%)	145 (94%)	8 (5%)	1 (1%)	27	28
1	M	154/156 (99%)	147 (96%)	6 (4%)	1 (1%)	27	28
All	All	462/468 (99%)	441 (96%)	19 (4%)	2 (0%)	36	39

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	107	PRO
1	M	210	TYR

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	129/129 (100%)	117 (91%)	12 (9%)	10	9
1	G	129/129 (100%)	111 (86%)	18 (14%)	4	3
1	M	129/129 (100%)	116 (90%)	13 (10%)	8	7
All	All	387/387 (100%)	344 (89%)	43 (11%)	7	6

5 of 43 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	147	LEU
1	G	201	GLU
1	M	191	ILE
1	G	153	SER
1	G	154	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	139	GLN
1	G	171	ASN
1	M	120	ASN
1	G	120	ASN
1	G	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

Of 15 ligands modelled in this entry, 15 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

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](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	156/156 (100%)	-0.33	0 100 100	19, 28, 51, 87	0
1	G	156/156 (100%)	-0.28	2 (1%) 77 75	25, 38, 61, 89	0
1	M	156/156 (100%)	-0.09	1 (0%) 89 88	24, 41, 67, 92	0
All	All	468/468 (100%)	-0.24	3 (0%) 89 88	19, 36, 65, 92	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	156	GLN	4.3
1	G	107	PRO	2.8
1	M	174	PHE	2.1

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	CA	M	303	1/1	0.90	0.10	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	CA	M	305	1/1	0.95	0.12	38,38,38,38	0
3	CA	M	304	1/1	0.97	0.11	41,41,41,41	0
2	ZN	M	302	1/1	0.97	0.10	53,53,53,53	0
2	ZN	M	301	1/1	0.98	0.14	45,45,45,45	0
2	ZN	G	301	1/1	0.98	0.17	40,40,40,40	0
2	ZN	A	301	1/1	0.98	0.19	26,26,26,26	0
3	CA	G	305	1/1	0.98	0.10	32,32,32,32	0
3	CA	G	303	1/1	0.98	0.10	32,32,32,32	0
3	CA	A	305	1/1	0.99	0.14	32,32,32,32	0
3	CA	G	304	1/1	0.99	0.13	31,31,31,31	0
2	ZN	G	302	1/1	0.99	0.13	32,32,32,32	0
3	CA	A	304	1/1	1.00	0.13	25,25,25,25	0
2	ZN	A	302	1/1	1.00	0.14	25,25,25,25	0
3	CA	A	303	1/1	1.00	0.15	24,24,24,24	0

6.5 Other polymers [i](#)

There are no such residues in this entry.