



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 22, 2025 – 12:08 PM EDT

PDB ID : 6M8W
Title : PSEUDOMONAS SERINE-CARBOXYL PROTEINASE (SEDOLISIN)
COMPLEXED WITH THE INHIBITOR AIAF
Authors : Wlodawer, A.; Li, M.; Gustchina, A.; Dauter, Z.; Uchida, K.; Oyama, H.;
Goldfarb, N.E.; Dunn, B.M.; Oda, K.
Deposited on : 2018-08-22
Resolution : 1.10 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

<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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.21
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.41.4

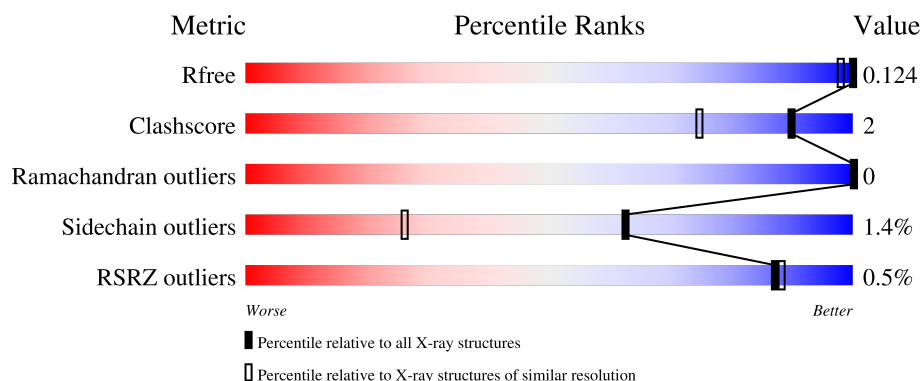
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.10 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))
R_{free}	164625	1365 (1.12-1.08)
Clashscore	180529	1561 (1.12-1.08)
Ramachandran outliers	177936	1524 (1.12-1.08)
Sidechain outliers	177891	1520 (1.12-1.08)
RSRZ outliers	164620	1365 (1.12-1.08)

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 $\leq 5\%$. 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	369	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 1%, green 98%);"></div> <div style="display: flex; justify-content: space-between; width: 90%; margin: 0 auto;"> % 93% 7% </div> </div>
2	B	4	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 75%, yellow 25%);"></div> <div style="display: flex; justify-content: space-between; width: 90%; margin: 0 auto;"> 75% 25% </div> </div>

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 5674 atoms, of which 2418 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 SEDOLISIN.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	369	Total	C	H	N	O	S	0	20	0
			5166	1714	2402	462	585	3			

- Molecule 2 is a protein called AIAF PEPTIDE INHIBITOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	4	Total	C	H	N	O	0	0	0
			43	20	16	3	4			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Ca	0	0
			1	1		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Cl 1 1	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	438	Total O 438 438	0	0
6	B	7	Total O 7 7	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 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: SEDOLISIN

Chain A: 



- Molecule 2: AIAF PEPTIDE INHIBITOR

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 62	Depositor
Cell constants a, b, c, α , β , γ	97.29Å 97.29Å 83.46Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 1.10 30.00 – 1.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (30.00-1.10) 90.7 (30.00-1.10)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.36 (at 1.10Å)	Xtriage
Refinement program	SHELXL 2018/3	Depositor
R, R_{free}	0.132 , 0.150 0.107 , 0.124	Depositor DCC
R_{free} test set	9065 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	8.9	Xtriage
Anisotropy	0.005	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.44 , 60.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.033 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.99	EDS
Total number of atoms	5674	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.67% 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: PHL, CL, CA, ACE, GOL

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	0.78	0/2907	1.22	23/3969 (0.6%)
2	B	0.53	0/13	0.84	0/17
All	All	0.78	0/2920	1.22	23/3986 (0.6%)

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

There are no bond length outliers.

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	366[A]	ARG	NE-CZ-NH1	-17.05	111.78	120.30
1	A	366[B]	ARG	NE-CZ-NH1	-17.05	111.78	120.30
1	A	80[A]	GLU	OE1-CD-OE2	10.94	136.42	123.30
1	A	80[B]	GLU	OE1-CD-OE2	10.94	136.42	123.30
1	A	366[A]	ARG	NE-CZ-NH2	9.07	124.84	120.30
1	A	366[B]	ARG	NE-CZ-NH2	9.07	124.84	120.30
1	A	256	ARG	CD-NE-CZ	8.35	135.28	123.60
1	A	80[A]	GLU	CG-CD-OE2	-7.47	103.36	118.30
1	A	80[B]	GLU	CG-CD-OE2	-7.47	103.36	118.30
1	A	2	ALA	C-N-CA	-7.38	106.81	122.30
1	A	179	ARG	NE-CZ-NH2	-7.32	116.64	120.30
1	A	366[A]	ARG	CD-NE-CZ	6.89	133.24	123.60
1	A	366[B]	ARG	CD-NE-CZ	6.89	133.24	123.60
1	A	148	GLN	CB-CG-CD	6.84	129.38	111.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	256	ARG	NE-CZ-NH1	-6.49	117.06	120.30
1	A	336	TYR	CB-CG-CD2	-6.37	117.18	121.00
1	A	82	ASP	CB-CG-OD2	-5.73	113.14	118.30
1	A	160	GLN	CG-CD-OE1	-5.66	110.27	121.60
1	A	225	ASP	CB-CG-OD1	5.62	123.36	118.30
1	A	179	ARG	NE-CZ-NH1	5.44	123.02	120.30
1	A	151	ASP	CB-CG-OD2	-5.38	113.46	118.30
1	A	126[A]	VAL	CA-CB-CG2	5.19	118.69	110.90
1	A	126[B]	VAL	CA-CB-CG2	5.19	118.69	110.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	152	ARG	Sidechain

5.2 Too-close contacts

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	2764	2402	2557	9	0
2	B	27	16	29	0	0
3	A	1	0	0	0	0
4	A	12	0	15	2	0
4	B	6	0	8	0	0
5	A	1	0	0	0	0
6	A	438	0	0	2	0
6	B	7	0	0	0	0
All	All	3256	2418	2609	9	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 2.

All (9) 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:280[A]:LEU:HD21	4:A:402:GOL:O3	2.02	0.58
1:A:9[B]:ASN:ND2	4:A:402:GOL:H2	2.20	0.57
1:A:191:TRP:CD2	1:A:192:PRO:HA	2.43	0.54
1:A:287:SER:HB3	6:A:504:HOH:O	2.17	0.44
1:A:366[A]:ARG:NE	6:A:507:HOH:O	2.49	0.44
1:A:60[A]:GLN:NE2	1:A:98:GLN:HE22	2.17	0.42
1:A:41:THR:HA	1:A:82:ASP:OD1	2.20	0.42
1:A:9[B]:ASN:OD1	1:A:10:PRO:HD2	2.21	0.41

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	387/369 (105%)	380 (98%)	7 (2%)	0	100	100
2	B	2/4 (50%)	2 (100%)	0	0	100	100
All	All	389/373 (104%)	382 (98%)	7 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	300/280 (107%)	296 (99%)	4 (1%)	65	28

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	1/1 (100%)	1 (100%)	0	100	100
All	All	301/281 (107%)	297 (99%)	4 (1%)	62	28

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	257	ARG
1	A	291	PRO
1	A	323	PRO
1	A	370	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	111	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	PHL	B	384	1,2	11,11,11	1.66	2 (18%)	11,13,13	0.61	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PHL	B	384	1,2	-	3/6/6/6	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	384	PHL	C-CA	4.66	1.60	1.52
2	B	384	PHL	CD2-CG	2.42	1.43	1.38

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	384	PHL	CA-CB-CG-CD1
2	B	384	PHL	CA-CB-CG-CD2
2	B	384	PHL	O-C-CA-N

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	GOL	B	401	-	5,5,5	1.77	1 (20%)	5,5,5	1.71	1 (20%)
4	GOL	A	403	-	5,5,5	2.94	2 (40%)	5,5,5	0.98	1 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	GOL	A	402	-	5,5,5	1.18	1 (20%)	5,5,5	0.93	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	B	401	-	-	0/4/4/4	-
4	GOL	A	403	-	-	0/4/4/4	-
4	GOL	A	402	-	-	0/4/4/4	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	403	GOL	C1-C2	5.11	1.71	1.51
4	B	401	GOL	O1-C1	3.49	1.57	1.42
4	A	403	GOL	C3-C2	3.35	1.64	1.51
4	A	402	GOL	O3-C3	2.14	1.51	1.42

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	401	GOL	C3-C2-C1	-3.19	100.11	111.80
4	A	403	GOL	C3-C2-C1	-2.14	103.94	111.80

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	402	GOL	2	0

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	369/369 (100%)	-0.74	2 (0%) 87 88	7, 12, 25, 47	20 (5%)
2	B	2/4 (50%)	-0.94	0 100 100	14, 14, 14, 15	0
All	All	371/373 (99%)	-0.74	2 (0%) 87 88	7, 12, 25, 47	20 (5%)

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	ALA	8.2
1	A	67	SER	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
2	PHL	B	384	11/11	0.99	0.04	8,8,9,9	0

6.3 Carbohydrates [i](#)

There are no monosaccharides 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
4	GOL	A	403	6/6	0.95	0.09	20,25,27,45	0
4	GOL	A	402	6/6	0.98	0.07	10,15,17,20	0
5	CL	A	404	1/1	0.98	0.05	20,20,20,20	1
4	GOL	B	401	6/6	0.99	0.05	14,17,20,23	0
3	CA	A	401	1/1	1.00	0.02	9,9,9,9	0

6.5 Other polymers [i](#)

There are no such residues in this entry.