



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 07:03 AM UTC

PDB ID : 2F9R / pdb_00002f9r
Title : Crystal structure of the inactive state of the Smase I, a sphingomyelinase D from *Loxosceles laeta* venom
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Deposited on : 2005-12-06
Resolution : 1.85 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 : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

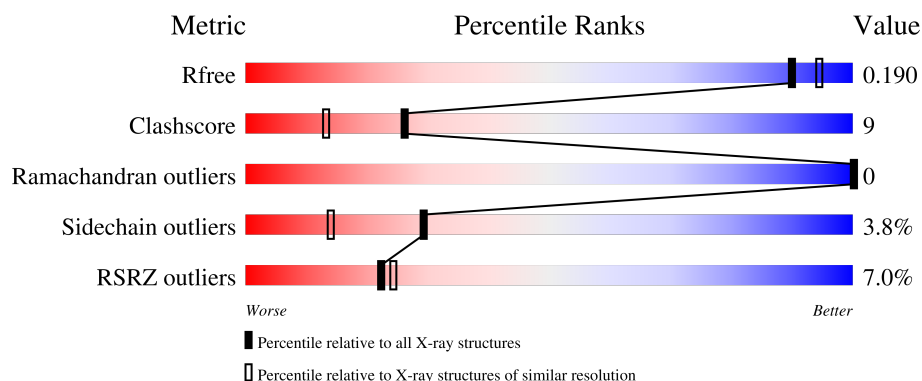
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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}	180053	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (1.86-1.86)

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	285	4% 82% 18%
1	B	285	6% 82% 16% .
1	C	285	10% 78% 20% .
1	D	285	8% 81% 17% .

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9891 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.

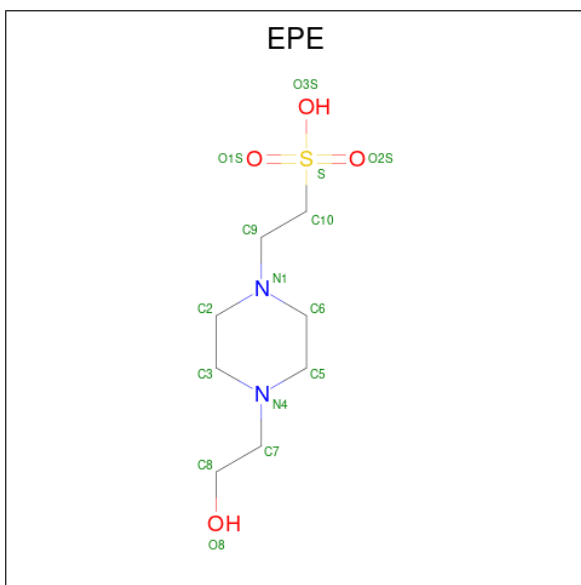
- Molecule 1 is a protein called Sphingomyelinase D 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	285	Total	C	N	O	S	0	12	0
			2346	1511	391	438	6			
1	B	285	Total	C	N	O	S	0	8	0
			2318	1488	386	438	6			
1	C	285	Total	C	N	O	S	0	11	0
			2339	1506	388	439	6			
1	D	285	Total	C	N	O	S	0	10	0
			2329	1497	389	437	6			

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		
2	B	1	Total	Mg	0	0
			1	1		
2	C	1	Total	Mg	0	0
			1	1		
2	D	1	Total	Mg	0	0
			1	1		

- Molecule 3 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: C₈H₁₈N₂O₄S).



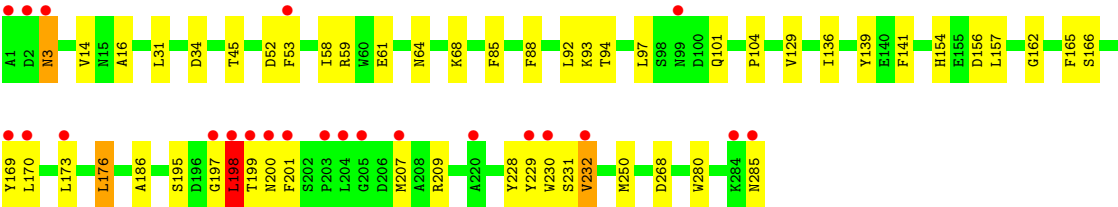
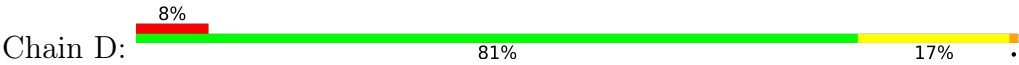
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
3	C	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
3	D	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	180	Total	O	0	2
			182	182		
4	B	162	Total	O	0	0
			162	162		
4	C	72	Total	O	0	0
			72	72		
4	D	93	Total	O	0	1
			94	94		

- Molecule 1: Sphingomyelinase D 1





4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	140.59Å 140.59Å 113.61Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 1.85 20.00 – 1.85	Depositor EDS
% Data completeness (in resolution range)	83.5 (20.00-1.85) 83.4 (20.00-1.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.72 (at 1.85Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.187 , 0.234 0.189 , 0.190	Depositor DCC
R_{free} test set	4507 reflections (4.16%)	wwPDB-VP
Wilson B-factor (Å ²)	19.5	Xtriage
Anisotropy	0.425	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 42.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.066 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9891	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.74% 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: MG, EPE

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	0.70	0/2439	0.89	1/3312 (0.0%)
1	B	0.71	0/2398	0.86	0/3260
1	C	0.63	2/2429 (0.1%)	0.85	4/3298 (0.1%)
1	D	0.63	1/2415 (0.0%)	0.92	2/3283 (0.1%)
All	All	0.67	3/9681 (0.0%)	0.88	7/13153 (0.1%)

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	B	0	1
1	C	0	2
All	All	0	3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	202	SER	C-N	11.64	1.61	1.33
1	C	203	PRO	N-CD	-6.46	1.38	1.47
1	D	52	ASP	C-N	-5.65	1.26	1.33

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	197	GLY	N-CA-C	18.81	140.25	114.85
1	C	202	SER	O-C-N	11.12	134.10	121.32
1	A	200	ASN	N-CA-CB	-10.80	93.05	111.96
1	D	198	LEU	N-CA-C	-8.07	101.23	112.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	201	PHE	CB-CA-C	6.16	118.74	109.13

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	44	TYR	Peptide
1	C	199	THR	Peptide
1	C	201	PHE	Mainchain

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	2346	0	2299	57	0
1	B	2318	0	2250	39	0
1	C	2339	0	2282	56	0
1	D	2329	0	2272	42	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	B	15	0	17	0	0
3	C	15	0	17	0	0
3	D	15	0	17	2	0
4	A	182	0	0	10	0
4	B	162	0	0	9	0
4	C	72	0	0	1	0
4	D	94	0	0	1	0
All	All	9891	0	9154	174	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 9.

The worst 5 of 174 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:C:201:PHE:CG	1:D:58:ILE:HD11	1.76	1.19
1:C:230[B]:TRP:HB3	1:C:250[B]:MET:HB3	1.25	1.09
1:C:201:PHE:CB	1:D:58:ILE:HD11	1.86	1.04
1:C:230[B]:TRP:HB3	1:C:250[B]:MET:CB	2.06	0.84
1:A:269:LYS:HE3	4:A:724:HOH:O	1.77	0.84

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	295/285 (104%)	290 (98%)	5 (2%)	0	100	100
1	B	291/285 (102%)	284 (98%)	7 (2%)	0	100	100
1	C	294/285 (103%)	285 (97%)	9 (3%)	0	100	100
1	D	293/285 (103%)	284 (97%)	9 (3%)	0	100	100
All	All	1173/1140 (103%)	1143 (97%)	30 (3%)	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	252/240 (105%)	246 (98%)	6 (2%)	43	28
1	B	248/240 (103%)	236 (95%)	12 (5%)	23	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	251/240 (105%)	241 (96%)	10 (4%)	28	13
1	D	250/240 (104%)	239 (96%)	11 (4%)	25	10
All	All	1001/960 (104%)	962 (96%)	39 (4%)	29	13

5 of 39 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	3	ASN
1	D	207	MET
1	D	156	ASP
1	D	198	LEU
1	D	232	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	99	ASN
1	D	123	ASN
1	C	116	ASN
1	D	154	HIS
1	C	154	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 4 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	$\# Z > 2$
3	EPE	B	701	-	15,15,15	0.61	0	19,20,20	1.51	2 (10%)
3	EPE	D	704	-	15,15,15	0.51	0	19,20,20	2.22	6 (31%)
3	EPE	C	703	-	15,15,15	0.57	0	19,20,20	1.76	3 (15%)

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
3	EPE	B	701	-	-	1/9/19/19	0/1/1/1
3	EPE	D	704	-	-	7/9/19/19	0/1/1/1
3	EPE	C	703	-	-	2/9/19/19	0/1/1/1

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	704	EPE	C5-N4-C3	6.26	122.34	108.84
3	C	703	EPE	C5-N4-C3	5.00	119.60	108.84
3	B	701	EPE	C5-N4-C3	4.06	117.58	108.84
3	D	704	EPE	O2S-S-C10	3.79	112.45	106.73
3	D	704	EPE	C2-C3-N4	2.99	116.69	110.65

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	701	EPE	C8-C7-N4-C3
3	D	704	EPE	C10-C9-N1-C6
3	D	704	EPE	C9-C10-S-O2S
3	D	704	EPE	C8-C7-N4-C3
3	C	703	EPE	N4-C7-C8-O8

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	704	EPE	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	202:SER	C	203:PRO	N	1.61

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	285/285 (100%)	-0.07	12 (4%)	40	44	8, 18, 27, 39	22 (7%)
1	B	285/285 (100%)	-0.04	16 (5%)	30	33	8, 18, 29, 46	19 (6%)
1	C	285/285 (100%)	0.71	29 (10%)	12	12	8, 28, 40, 46	37 (12%)
1	D	285/285 (100%)	0.35	23 (8%)	18	19	10, 24, 37, 42	31 (10%)
All	All	1140/1140 (100%)	0.24	80 (7%)	22	24	8, 21, 37, 46	109 (9%)

The worst 5 of 80 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	201	PHE	10.2
1	A	198	LEU	8.8
1	A	203	PRO	8.8
1	A	201	PHE	7.9
1	D	1	ALA	7.9

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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
2	MG	C	603	1/1	0.96	0.11	25,25,25,25	1
3	EPE	D	704	15/15	0.96	0.08	22,25,27,30	0
3	EPE	C	703	15/15	0.97	0.08	23,28,30,32	0
2	MG	D	604	1/1	0.98	0.06	19,19,19,19	1
3	EPE	B	701	15/15	0.98	0.05	15,17,19,19	0
2	MG	B	602	1/1	0.99	0.03	19,19,19,19	0
2	MG	A	601	1/1	0.99	0.09	18,18,18,18	1

6.5 Other polymers [i](#)

There are no such residues in this entry.