



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:27 AM UTC

PDB ID : 5R3X / pdb_00005r3x
Title : PanDDA analysis group deposition – Auto-refined data of Endothiapepsin for ground state model 57, DMSO-Free
Authors : Wollenhaupt, J.; Metz, A.; Barthel, T.; Lima, G.M.A.; Heine, A.; Mueller, U.; Klebe, G.; Weiss, M.S.
Deposited on : 2020-02-13
Resolution : 1.17 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	:	4-5-2 with Phenix2.0
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

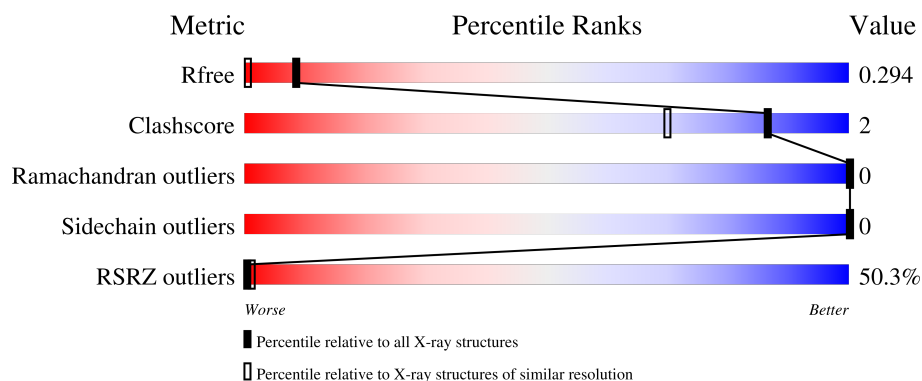
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.17 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	1256 (1.18-1.14)
Clashscore	190562	1272 (1.18-1.14)
Ramachandran outliers	187476	1246 (1.18-1.14)
Sidechain outliers	187428	1246 (1.18-1.14)
RSRZ outliers	180081	1255 (1.18-1.14)

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	419	40% 77% 21%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4937 atoms, of which 2341 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 Endothiapepsin.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	330	Total	C	H	N	O	S	0	25	0
			4803	1566	2341	367	527	2			

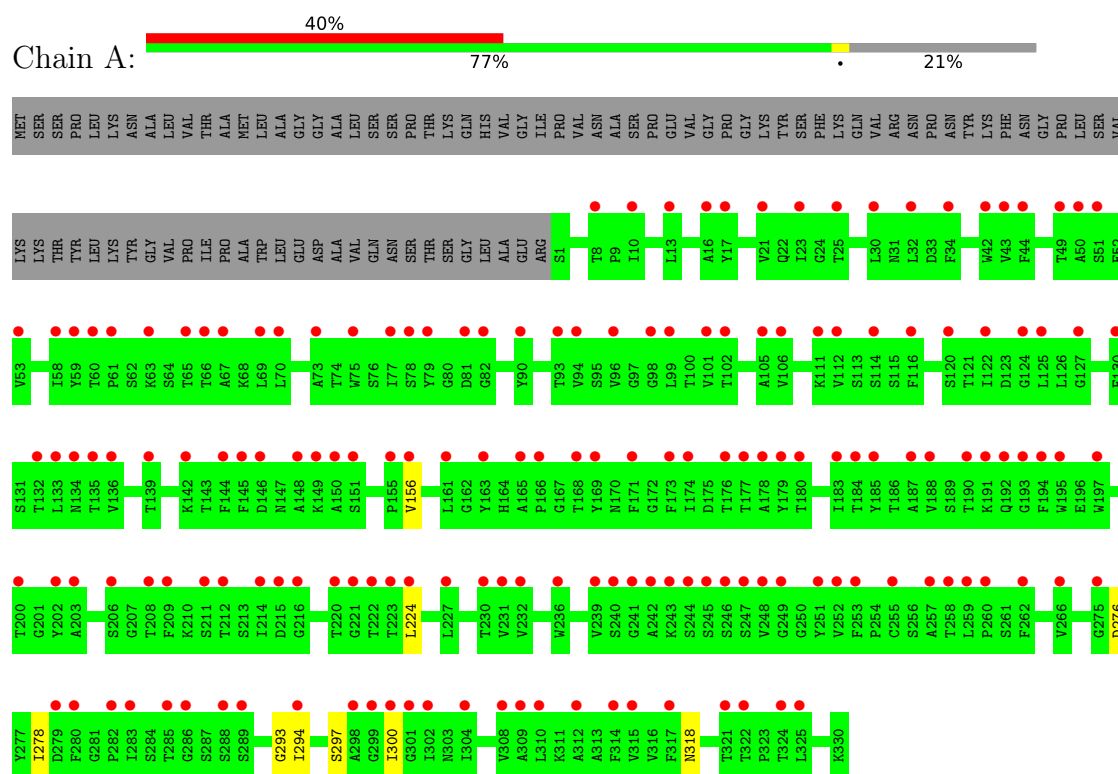
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	134	Total	O	0	0
			134	134		

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 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: Endothiapepsin



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	45.18Å 73.14Å 52.57Å 90.00° 109.14° 90.00°	Depositor
Resolution (Å)	42.68 – 1.17 42.68 – 1.17	Depositor EDS
% Data completeness (in resolution range)	98.7 (42.68-1.17) 98.7 (42.68-1.17)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.94 (at 1.16Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.245 , 0.288 0.263 , 0.294	Depositor DCC
R_{free} test set	2088 reflections (1.90%)	wwPDB-VP
Wilson B-factor (Å ²)	18.9	Xtriage
Anisotropy	0.161	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.44 , 34.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.54$, $\langle L^2 \rangle = 0.38$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4937	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.94% 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 [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	0.39	0/2594	0.60	0/3553

There are no bond length outliers.

There are no bond angle outliers.

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	2462	2341	2300	10	0
2	A	134	0	0	0	0
All	All	2596	2341	2300	10	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 (10) 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:278:ILE:HG23	1:A:294:ILE:HD13	1.76	0.67
1:A:293:GLY:C	1:A:294:ILE:HD12	2.29	0.58
1:A:278:ILE:CG2	1:A:294:ILE:HD13	2.34	0.57
1:A:276[B]:ASP:OD1	1:A:276[B]:ASP:N	2.38	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:224:LEU:HD22	1:A:293:GLY:HA2	1.99	0.44
1:A:278:ILE:HG12	1:A:294:ILE:HD11	1.99	0.44
1:A:278:ILE:HG12	1:A:294:ILE:CD1	2.46	0.44
1:A:294:ILE:HD12	1:A:294:ILE:N	2.34	0.43
1:A:156:VAL:HG12	1:A:318:ASN:HA	2.00	0.43
1:A:297:SER:HA	1:A:300[A]:ILE:HD12	2.02	0.42

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	353/419 (84%)	349 (99%)	4 (1%)	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	273/336 (81%)	273 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	GLN
1	A	31	ASN
1	A	140	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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	330/419 (78%)	2.09	166 (50%) 0 1	9, 21, 30, 40	19 (5%)

All (166) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	300[A]	ILE	6.6
1	A	150[A]	ALA	6.2
1	A	299[A]	GLY	5.6
1	A	321	THR	5.3
1	A	208	THR	5.1
1	A	294	ILE	4.9
1	A	302	ILE	4.3
1	A	209	PHE	4.2
1	A	190	THR	4.0
1	A	248	VAL	3.9
1	A	322	THR	3.9
1	A	53	VAL	3.8
1	A	77	ILE	3.7
1	A	96	VAL	3.5
1	A	255	CYS	3.5
1	A	42	TRP	3.4
1	A	258	THR	3.4
1	A	151	SER	3.4
1	A	112	VAL	3.4
1	A	188	VAL	3.4
1	A	197	TRP	3.4
1	A	289[A]	SER	3.4
1	A	285	THR	3.4
1	A	240[A]	SER	3.4
1	A	78	SER	3.3
1	A	246[A]	SER	3.3
1	A	69	LEU	3.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	180	THR	3.2
1	A	249	GLY	3.2
1	A	252	VAL	3.2
1	A	82	GLY	3.1
1	A	215[A]	ASP	3.1
1	A	195	TRP	3.1
1	A	149[A]	LYS	3.1
1	A	288	SER	3.1
1	A	191	LYS	3.0
1	A	101	VAL	3.0
1	A	257	ALA	3.0
1	A	30	LEU	3.0
1	A	325[A]	LEU	3.0
1	A	247	SER	3.0
1	A	231	VAL	3.0
1	A	49	THR	3.0
1	A	122	ILE	3.0
1	A	230	THR	3.0
1	A	192	GLN	2.9
1	A	50	ALA	2.9
1	A	165	ALA	2.9
1	A	309	ALA	2.9
1	A	75	TRP	2.9
1	A	25	THR	2.9
1	A	61	PRO	2.9
1	A	156	VAL	2.9
1	A	8	THR	2.9
1	A	132	THR	2.9
1	A	155	PRO	2.8
1	A	106	VAL	2.8
1	A	114	SER	2.8
1	A	79	TYR	2.8
1	A	90	TYR	2.8
1	A	221	GLY	2.8
1	A	44	PHE	2.8
1	A	280	PHE	2.8
1	A	314	PHE	2.8
1	A	308	VAL	2.8
1	A	23	ILE	2.8
1	A	223	THR	2.7
1	A	144	PHE	2.7
1	A	58	ILE	2.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	222	THR	2.7
1	A	283	ILE	2.7
1	A	133	LEU	2.6
1	A	177	THR	2.6
1	A	184	THR	2.6
1	A	312	ALA	2.6
1	A	98	GLY	2.6
1	A	124	GLY	2.6
1	A	116	PHE	2.6
1	A	232	VAL	2.6
1	A	70	LEU	2.5
1	A	145	PHE	2.5
1	A	178	ALA	2.5
1	A	301[A]	GLY	2.5
1	A	81	ASP	2.5
1	A	148	ALA	2.5
1	A	194	PHE	2.5
1	A	253	PHE	2.5
1	A	10	ILE	2.5
1	A	214	ILE	2.5
1	A	185	TYR	2.5
1	A	105	ALA	2.5
1	A	65	THR	2.4
1	A	200	THR	2.4
1	A	304	ILE	2.4
1	A	21	VAL	2.4
1	A	236	TRP	2.4
1	A	241	GLY	2.4
1	A	286	GLY	2.4
1	A	262	PHE	2.4
1	A	60	THR	2.4
1	A	176	THR	2.4
1	A	127	GLY	2.4
1	A	142	LYS	2.4
1	A	183[A]	ILE	2.4
1	A	136	VAL	2.4
1	A	315	VAL	2.4
1	A	120	SER	2.4
1	A	227	LEU	2.4
1	A	310	LEU	2.4
1	A	163	TYR	2.4
1	A	202	TYR	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	203	ALA	2.4
1	A	242	ALA	2.4
1	A	239	VAL	2.4
1	A	67	ALA	2.3
1	A	59	TYR	2.3
1	A	244	SER	2.3
1	A	134	ASN	2.3
1	A	13	LEU	2.3
1	A	73	ALA	2.3
1	A	282	PRO	2.3
1	A	99	LEU	2.3
1	A	125	LEU	2.3
1	A	212	THR	2.3
1	A	146	ASP	2.3
1	A	130	PHE	2.3
1	A	32	LEU	2.3
1	A	259	LEU	2.3
1	A	66	THR	2.3
1	A	93	THR	2.3
1	A	220	THR	2.3
1	A	173	PHE	2.2
1	A	245	SER	2.2
1	A	174[A]	ILE	2.2
1	A	111	LYS	2.2
1	A	16	ALA	2.2
1	A	135	THR	2.2
1	A	94	VAL	2.2
1	A	161	LEU	2.2
1	A	193	GLY	2.2
1	A	216	GLY	2.2
1	A	179	TYR	2.2
1	A	251	TYR	2.2
1	A	166	PRO	2.1
1	A	34	PHE	2.1
1	A	102	THR	2.1
1	A	139	THR	2.1
1	A	298[A]	ALA	2.1
1	A	324	THR	2.1
1	A	63	LYS	2.1
1	A	43	VAL	2.1
1	A	266	VAL	2.1
1	A	169	TYR	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	168	THR	2.1
1	A	171	PHE	2.0
1	A	51	SER	2.0
1	A	224	LEU	2.0
1	A	243	LYS	2.0
1	A	260	PRO	2.0
1	A	17	TYR	2.0
1	A	279	ASP	2.0
1	A	187	ALA	2.0
1	A	206[A]	SER	2.0
1	A	211	SER	2.0
1	A	317	PHE	2.0
1	A	275	GLY	2.0

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.