



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 10:20 AM UTC

PDB ID : 6Z0E / pdb_00006z0e
Title : HtrA1 inactive protease domain S328A with CARASIL mutation R274Q
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Deposited on : 2020-05-08
Resolution : 2.60 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

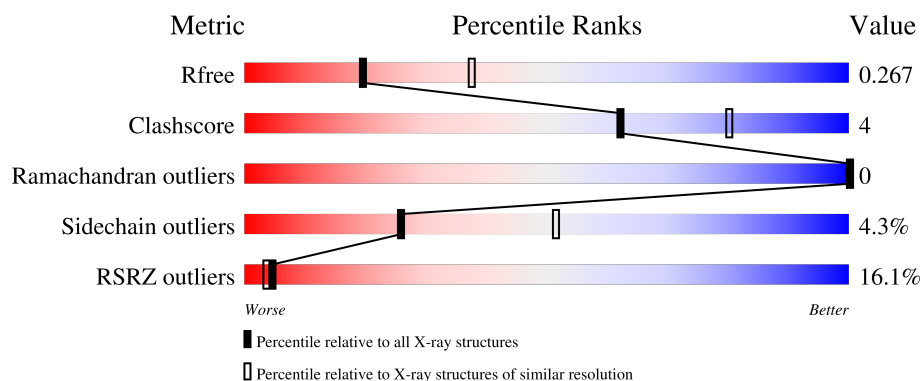
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	236	13% 72% 10% 17%
1	B	236	14% 68% 11% 20%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2961 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 Serine protease HTRA1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	196	Total	C	N	O	0	0	0
			1497	957	254	286			
1	B	188	Total	C	N	O	0	0	0
			1429	912	242	275			

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	140	MET	-	initiating methionine	UNP Q92743
A	141	GLY	-	expression tag	UNP Q92743
A	142	SER	-	expression tag	UNP Q92743
A	143	SER	-	expression tag	UNP Q92743
A	144	HIS	-	expression tag	UNP Q92743
A	145	HIS	-	expression tag	UNP Q92743
A	146	HIS	-	expression tag	UNP Q92743
A	147	HIS	-	expression tag	UNP Q92743
A	148	HIS	-	expression tag	UNP Q92743
A	149	HIS	-	expression tag	UNP Q92743
A	150	SER	-	expression tag	UNP Q92743
A	151	SER	-	expression tag	UNP Q92743
A	152	GLY	-	expression tag	UNP Q92743
A	153	LEU	-	expression tag	UNP Q92743
A	154	VAL	-	expression tag	UNP Q92743
A	155	PRO	-	expression tag	UNP Q92743
A	156	ARG	-	expression tag	UNP Q92743
A	157	GLY	-	expression tag	UNP Q92743
A	158	SER	-	expression tag	UNP Q92743
A	159	HIS	-	expression tag	UNP Q92743
A	160	MET	-	expression tag	UNP Q92743
A	274	GLN	ARG	engineered mutation	UNP Q92743
A	328	ALA	SER	engineered mutation	UNP Q92743
B	140	MET	-	initiating methionine	UNP Q92743
B	141	GLY	-	expression tag	UNP Q92743

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Chain	Residue	Modelled	Actual	Comment	Reference
B	142	SER	-	expression tag	UNP Q92743
B	143	SER	-	expression tag	UNP Q92743
B	144	HIS	-	expression tag	UNP Q92743
B	145	HIS	-	expression tag	UNP Q92743
B	146	HIS	-	expression tag	UNP Q92743
B	147	HIS	-	expression tag	UNP Q92743
B	148	HIS	-	expression tag	UNP Q92743
B	149	HIS	-	expression tag	UNP Q92743
B	150	SER	-	expression tag	UNP Q92743
B	151	SER	-	expression tag	UNP Q92743
B	152	GLY	-	expression tag	UNP Q92743
B	153	LEU	-	expression tag	UNP Q92743
B	154	VAL	-	expression tag	UNP Q92743
B	155	PRO	-	expression tag	UNP Q92743
B	156	ARG	-	expression tag	UNP Q92743
B	157	GLY	-	expression tag	UNP Q92743
B	158	SER	-	expression tag	UNP Q92743
B	159	HIS	-	expression tag	UNP Q92743
B	160	MET	-	expression tag	UNP Q92743
B	274	GLN	ARG	engineered mutation	UNP Q92743
B	328	ALA	SER	engineered mutation	UNP Q92743

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Ca 1 1	0	0
2	B	1	Total Ca 1 1	0	0

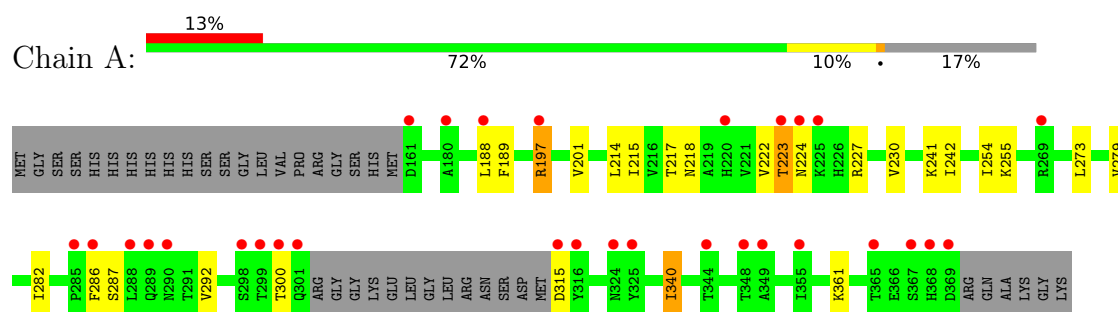
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	20	Total O 20 20	0	0
3	B	13	Total O 13 13	0	0

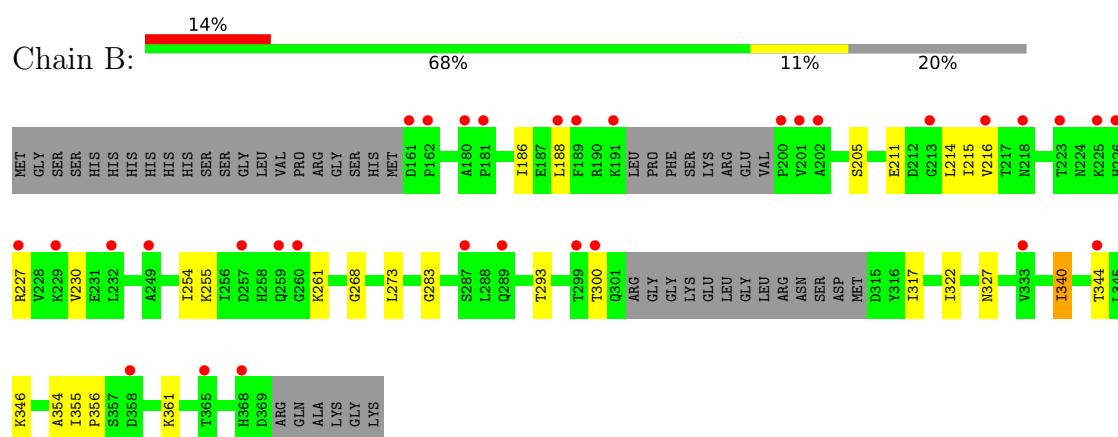
3 Residue-property plots [i](#)

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: Serine protease HTRA1



• Molecule 1: Serine protease HTRA1



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	109.86Å 109.86Å 114.40Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.02 – 2.60 49.02 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.02-2.60) 100.0 (49.02-2.60)	Depositor EDS
R_{merge}	0.33	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.04 (at 2.61Å)	Xtriage
Refinement program	PHENIX 1.18rc2_3794	Depositor
R, R_{free}	0.238 , 0.265 0.240 , 0.267	Depositor DCC
R_{free} test set	791 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	54.9	Xtriage
Anisotropy	0.037	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 33.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.026 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	2961	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.71% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.29	0/1522	0.59	0/2064
1	B	0.31	0/1451	0.66	1/1966 (0.1%)
All	All	0.30	0/2973	0.62	1/4030 (0.0%)

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 (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	227	ARG	NE-CZ-NH2	5.58	124.23	119.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	223	THR	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	1497	0	1536	11	0
1	B	1429	0	1463	13	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	20	0	0	0	0
3	B	13	0	0	1	0
All	All	2961	0	2999	24	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 4.

All (24) 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:273:LEU:HD11	1:A:340:ILE:HD13	1.88	0.55
1:A:282:ILE:HG13	1:A:292:VAL:HG22	1.92	0.51
1:B:215:ILE:HD13	1:B:230:VAL:HG11	1.92	0.51
1:B:215:ILE:HB	1:B:254:ILE:HG13	1.93	0.50
1:B:273:LEU:HD11	1:B:340:ILE:HD13	1.94	0.49
1:B:317:ILE:HB	1:B:354:ALA:HB3	1.94	0.49
1:A:189:PHE:HB2	1:A:227:ARG:HB3	1.94	0.49
1:B:268:GLY:O	1:B:361:LYS:NZ	2.44	0.48
1:A:315:ASP:OD2	1:A:315:ASP:N	2.49	0.46
1:A:217:THR:OG1	1:A:218:ASN:N	2.50	0.45
1:B:283:GLY:HA3	1:B:327:ASN:HA	1.99	0.44
1:A:242:ILE:HA	1:A:254:ILE:HG22	1.98	0.44
1:B:344:THR:HG22	1:B:346:LYS:H	1.83	0.44
1:B:293:THR:HG21	1:B:322:ILE:HB	1.99	0.43
1:A:215:ILE:HD13	1:A:230:VAL:HG11	2.00	0.43
1:B:214:LEU:HD23	1:B:255:LYS:HB2	2.02	0.42
1:B:186:ILE:HG12	1:B:230:VAL:HG22	2.01	0.41
1:B:211:GLU:HB2	1:B:261:LYS:HD2	2.02	0.41
1:A:197:ARG:HE	1:A:197:ARG:HB2	1.67	0.41
1:A:223:THR:OG1	1:A:224:ASN:N	2.53	0.41
1:A:286:PHE:HB3	1:A:287:SER:H	1.71	0.41
1:B:346:LYS:NZ	3:B:504:HOH:O	2.54	0.41
1:A:214:LEU:HD23	1:A:255:LYS:HB2	2.02	0.40
1:B:355:ILE:HA	1:B:356:PRO:HD3	1.91	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	192/236 (81%)	184 (96%)	8 (4%)	0	100	100
1	B	182/236 (77%)	173 (95%)	9 (5%)	0	100	100
All	All	374/472 (79%)	357 (96%)	17 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	167/199 (84%)	158 (95%)	9 (5%)	20	42
1	B	159/199 (80%)	154 (97%)	5 (3%)	35	63
All	All	326/398 (82%)	312 (96%)	14 (4%)	26	51

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	188	LEU
1	A	197	ARG
1	A	201	VAL
1	A	222	VAL
1	A	241	LYS
1	A	279	VAL
1	A	300	THR
1	A	340	ILE

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Mol	Chain	Res	Type
1	A	361	LYS
1	B	188	LEU
1	B	205	SER
1	B	216	VAL
1	B	300	THR
1	B	340	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	290	ASN
1	A	301	GLN
1	B	224	ASN
1	B	290	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 2 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 [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	196/236 (83%)	0.97	30 (15%) 5 4	29, 51, 86, 107	0
1	B	188/236 (79%)	1.21	32 (17%) 4 3	37, 61, 94, 108	0
All	All	384/472 (81%)	1.09	62 (16%) 4 3	29, 57, 90, 108	0

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	300	THR	5.9
1	A	368	HIS	5.0
1	A	288	LEU	4.5
1	B	180	ALA	4.0
1	A	223	THR	3.9
1	A	300	THR	3.9
1	B	200	PRO	3.9
1	B	191	LYS	3.8
1	A	299	THR	3.7
1	B	226	HIS	3.6
1	A	365	THR	3.4
1	B	202	ALA	3.4
1	B	225	LYS	3.3
1	A	367	SER	3.2
1	A	369	ASP	3.1
1	A	285	PRO	3.0
1	A	225	LYS	3.0
1	B	299	THR	3.0
1	A	290	ASN	3.0
1	B	223	THR	2.9
1	A	301	GLN	2.6
1	A	289	GLN	2.6
1	B	188	LEU	2.5
1	A	344	THR	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	269	ARG	2.5
1	A	286	PHE	2.5
1	B	162	PRO	2.5
1	A	298	SER	2.4
1	B	287	SER	2.4
1	A	315	ASP	2.4
1	A	355	ILE	2.4
1	B	232	LEU	2.4
1	A	197	ARG	2.3
1	B	201	VAL	2.3
1	A	220	HIS	2.3
1	A	161	ASP	2.3
1	A	224	ASN	2.3
1	B	368	HIS	2.3
1	B	227	ARG	2.3
1	B	257	ASP	2.3
1	B	259	GLN	2.3
1	B	289	GLN	2.3
1	A	316	TYR	2.2
1	B	161	ASP	2.2
1	B	249	ALA	2.2
1	B	333	VAL	2.2
1	A	180	ALA	2.2
1	A	349	ALA	2.2
1	A	348	THR	2.2
1	B	216	VAL	2.1
1	B	344	THR	2.1
1	B	365	THR	2.1
1	B	181	PRO	2.1
1	A	188	LEU	2.1
1	A	325	TYR	2.1
1	B	213	GLY	2.1
1	B	358	ASP	2.1
1	B	229	LYS	2.1
1	A	324	ASN	2.1
1	B	189	PHE	2.1
1	B	260	GLY	2.0
1	B	218	ASN	2.0

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

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	CA	B	401	1/1	0.82	0.13	48,48,48,48	1
2	CA	A	401	1/1	0.96	0.05	42,42,42,42	1

6.5 Other polymers [i](#)

There are no such residues in this entry.