



Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 11:50 am BST

PDB ID : 5M3O
Title : HTRA2 A141S mutant structure
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Deposited on : 2016-10-15
Resolution : 1.70 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

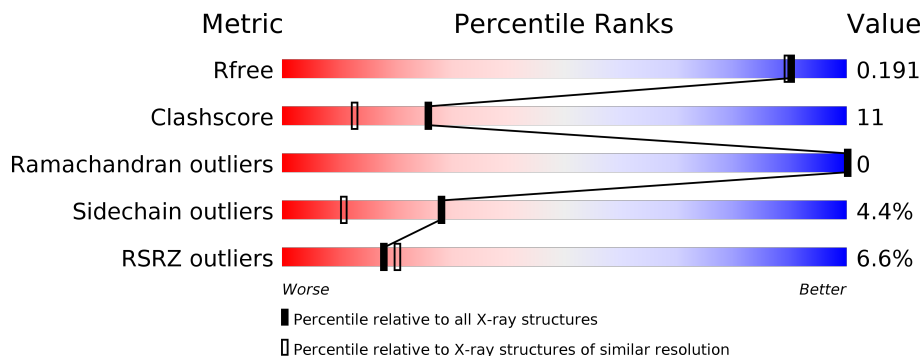
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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 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	334	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2300 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.

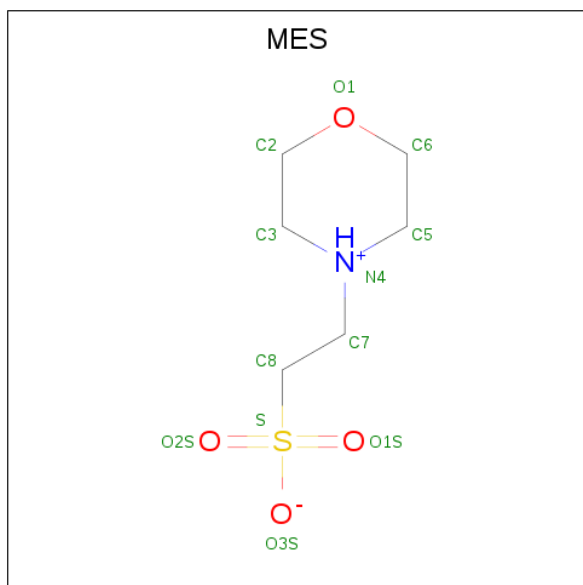
- Molecule 1 is a protein called Serine protease HTRA2, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	287	2170	1373	382	410	5	0	6	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	133	MET	-	initiating methionine	UNP O43464
A	141	SER	ALA	engineered mutation	UNP O43464
A	459	HIS	-	expression tag	UNP O43464
A	460	GLU	-	expression tag	UNP O43464
A	461	HIS	-	expression tag	UNP O43464
A	462	HIS	-	expression tag	UNP O43464
A	463	HIS	-	expression tag	UNP O43464
A	464	HIS	-	expression tag	UNP O43464
A	465	HIS	-	expression tag	UNP O43464
A	466	HIS	-	expression tag	UNP O43464

- Molecule 2 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C₆H₁₃NO₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	A	1	12	6	1	4	1	0	0

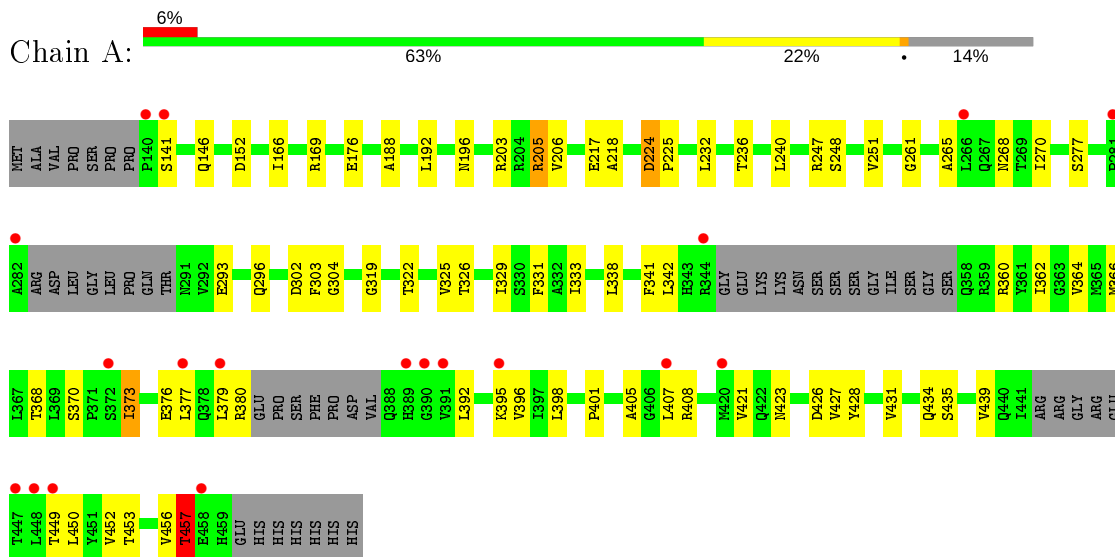
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	118	Total	O	0	0
			118	118		

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: Serine protease HTRA2, mitochondrial



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	84.29Å 84.29Å 127.98Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	31.70 – 1.70 31.70 – 1.70	Depositor EDS
% Data completeness (in resolution range)	100.0 (31.70-1.70) 99.9 (31.70-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.76 (at 1.70Å)	Xtrriage
Refinement program	PHENIX (1.10_2155: ???)	Depositor
R, R_{free}	0.168 , 0.200 0.171 , 0.191	Depositor DCC
R_{free} test set	1883 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	25.3	Xtrriage
Anisotropy	0.061	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 43.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtrriage
Estimated twinning fraction	0.268 for h,-h-k,-l	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	2300	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.07% 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: MES

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	0.52	0/2220	0.68	2/3027 (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	A	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	457	THR	O-C-N	-9.76	107.09	122.70
1	A	457	THR	CA-C-N	5.53	129.37	117.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	457	THR	Mainchain

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	2170	0	2172	46	0
2	A	12	0	13	1	0
3	A	118	0	0	2	0
All	All	2300	0	2185	46	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 11.

All (46) 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:360:ARG:HH22	1:A:435:SER:HA	1.60	0.66
1:A:370:SER:OG	1:A:373:ILE:HG12	1.98	0.63
1:A:325:VAL:HG12	1:A:377:LEU:HD13	1.85	0.58
1:A:188:ALA:HB3	1:A:192:LEU:HB3	1.84	0.58
1:A:166:ILE:HD13	1:A:203:ARG:HG3	1.85	0.57
1:A:302:ASP:OD1	1:A:304:GLY:N	2.37	0.57
1:A:405:ALA:O	1:A:450:LEU:HD22	2.03	0.57
1:A:368:THR:HG23	1:A:423:ASN:HA	1.86	0.57
1:A:225:PRO:HB2	1:A:428:TYR:CZ	2.39	0.57
1:A:331:PHE:HZ	1:A:373:ILE:HD12	1.68	0.56
1:A:236:THR:HG21	1:A:240:LEU:HD21	1.86	0.56
1:A:224[A]:ASP:HB2	1:A:341:PHE:CE1	2.41	0.55
1:A:423:ASN:O	1:A:426:ASP:HB2	2.06	0.55
1:A:338:LEU:O	1:A:342:LEU:HG	2.07	0.54
1:A:396:VAL:HG21	1:A:407:LEU:O	2.08	0.54
1:A:360:ARG:NH2	1:A:435:SER:HA	2.23	0.53
1:A:152:ASP:OD2	2:A:501:MES:H52	2.08	0.53
1:A:362:ILE:HG13	1:A:364:VAL:HG22	1.91	0.52
1:A:225:PRO:HB2	1:A:428:TYR:CE2	2.46	0.51
1:A:439:VAL:O	1:A:449:THR:HA	2.12	0.50
1:A:362:ILE:HD13	1:A:431:VAL:HG21	1.94	0.49
1:A:366:MET:HA	1:A:392:LEU:O	2.14	0.48
1:A:319:GLY:HA2	1:A:333:ILE:O	2.12	0.48
1:A:277:SER:HB3	1:A:296[A]:GLN:HG3	1.96	0.47
1:A:141:SER:O	1:A:146:GLN:NE2	2.48	0.46
1:A:303:PHE:CE1	1:A:395:LYS:HD2	2.51	0.46
1:A:261:GLY:H	1:A:270:ILE:HD13	1.81	0.46
1:A:331:PHE:CZ	1:A:373:ILE:HD12	2.50	0.45
1:A:360:ARG:NH2	1:A:434:GLN:O	2.49	0.45
1:A:326:THR:CG2	1:A:329:ILE:HD12	2.48	0.43
1:A:405:ALA:CB	1:A:452:VAL:HG22	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:205:ARG:HD3	1:A:217[A]:GLU:OE1	2.18	0.43
1:A:450:LEU:HA	1:A:450:LEU:HD23	1.74	0.43
1:A:398:LEU:HD12	3:A:679:HOH:O	2.18	0.43
1:A:401:PRO:HB3	1:A:453:THR:O	2.18	0.43
1:A:265:ALA:O	1:A:268:ASN:HB3	2.19	0.42
1:A:421:VAL:HG11	1:A:427:VAL:HG23	2.01	0.42
1:A:248:SER:HA	1:A:251:VAL:HG23	2.02	0.42
1:A:247:ARG:NH2	3:A:607:HOH:O	2.43	0.42
1:A:206:VAL:HG23	1:A:218:ALA:HB3	2.02	0.41
1:A:196[A]:ASN:OD1	1:A:322:THR:HG22	2.21	0.41
1:A:376:GLU:O	1:A:380:ARG:HD2	2.21	0.41
1:A:166:ILE:HD13	1:A:203:ARG:CG	2.51	0.41
1:A:196[A]:ASN:HD21	1:A:322:THR:HA	1.87	0.40
1:A:379:LEU:HD23	1:A:380:ARG:NH1	2.36	0.40
1:A:376:GLU:HA	1:A:380:ARG:NH1	2.37	0.40

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	283/334 (85%)	273 (96%)	10 (4%)	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	233/280 (83%)	222 (95%)	11 (5%)	26 10

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	169	ARG
1	A	176	GLU
1	A	205	ARG
1	A	224[A]	ASP
1	A	224[B]	ASP
1	A	232	LEU
1	A	293	GLU
1	A	373	ILE
1	A	408	ARG
1	A	456	VAL
1	A	457	THR

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

Mol	Chain	Res	Type
1	A	146	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 [i](#)

1 ligand 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	MES	A	501	-	12,12,12	1.80	1 (8%)	14,16,16	1.55	3 (21%)

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	MES	A	501	-	-	1/6/14/14	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	MES	C8-S	-5.79	1.69	1.77

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	MES	C6-C5-N4	2.65	114.12	110.10
2	A	501	MES	O3S-S-C8	2.31	109.50	105.77
2	A	501	MES	O1-C6-C5	2.29	116.84	111.80

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	MES	C8-C7-N4-C5

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	MES	1	0

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 [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	287/334 (85%)	0.29	19 (6%) 18 20	13, 33, 65, 96	1 (0%)

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	140	PRO	4.2
1	A	282	ALA	4.0
1	A	448	LEU	3.7
1	A	281	PRO	3.3
1	A	377	LEU	3.3
1	A	447	THR	2.9
1	A	372	SER	2.8
1	A	344	ARG	2.8
1	A	395	LYS	2.6
1	A	458	GLU	2.6
1	A	407	LEU	2.5
1	A	391	VAL	2.5
1	A	390	GLY	2.2
1	A	449	THR	2.2
1	A	141	SER	2.1
1	A	420	MET	2.1
1	A	389	HIS	2.1
1	A	266	LEU	2.1
1	A	379	LEU	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 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
2	MES	A	501	12/12	0.96	0.10	17,21,22,23	0

6.5 Other polymers [i](#)

There are no such residues in this entry.