



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 23, 2024 – 04:38 AM EDT

PDB ID : 5BRR
Title : Michaelis complex of tPA-S195A:PAI-1
Authors : Gong, L.
Deposited on : 2015-06-01
Resolution : 3.16 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	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
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)	:	2.37.1

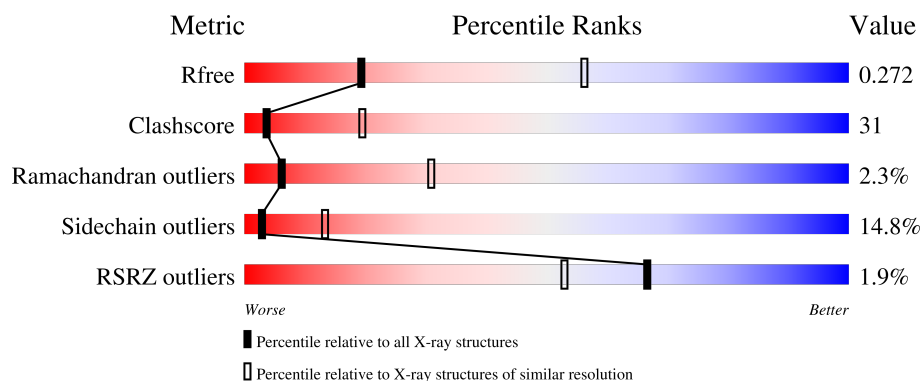
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.16 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	1665 (3.20-3.12)
Clashscore	141614	1804 (3.20-3.12)
Ramachandran outliers	138981	1770 (3.20-3.12)
Sidechain outliers	138945	1769 (3.20-3.12)
RSRZ outliers	127900	1616 (3.20-3.12)

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	I	379	<div> <div>2%</div> <div>50% 37% 10% ..</div> </div>
2	E	252	<div> <div>%</div> <div>66% 27% 7%</div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4988 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 Plasminogen activator inhibitor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	I	372	Total	C	N	O	S	0	0	0
			2952	1893	504	540	15			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	150	HIS	ASN	engineered mutation	UNP P05121
I	154	THR	LYS	engineered mutation	UNP P05121
I	319	LEU	GLN	engineered mutation	UNP P05121
I	354	ILE	MET	engineered mutation	UNP P05121

- Molecule 2 is a protein called Tissue-type plasminogen activator.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	251	Total	C	N	O	S	0	0	0
			1966	1234	351	368	13			

There are 3 discrepancies between the modelled and reference sequences:

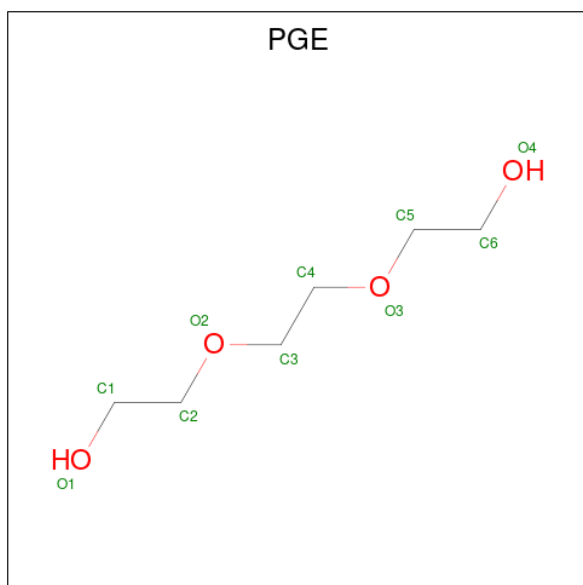
Chain	Residue	Modelled	Actual	Comment	Reference
E	122	ALA	CYS	engineered mutation	UNP P00750
E	173	GLN	ASN	engineered mutation	UNP P00750
E	195	ALA	SER	engineered mutation	UNP P00750

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	E	1	Total	C	O	0	0
			6	3	3		
3	E	1	Total	C	O	0	0
			6	3	3		
3	E	1	Total	C	O	0	0
			6	3	3		
3	E	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	E	1	Total	C	O	0	0
			10	6	4		

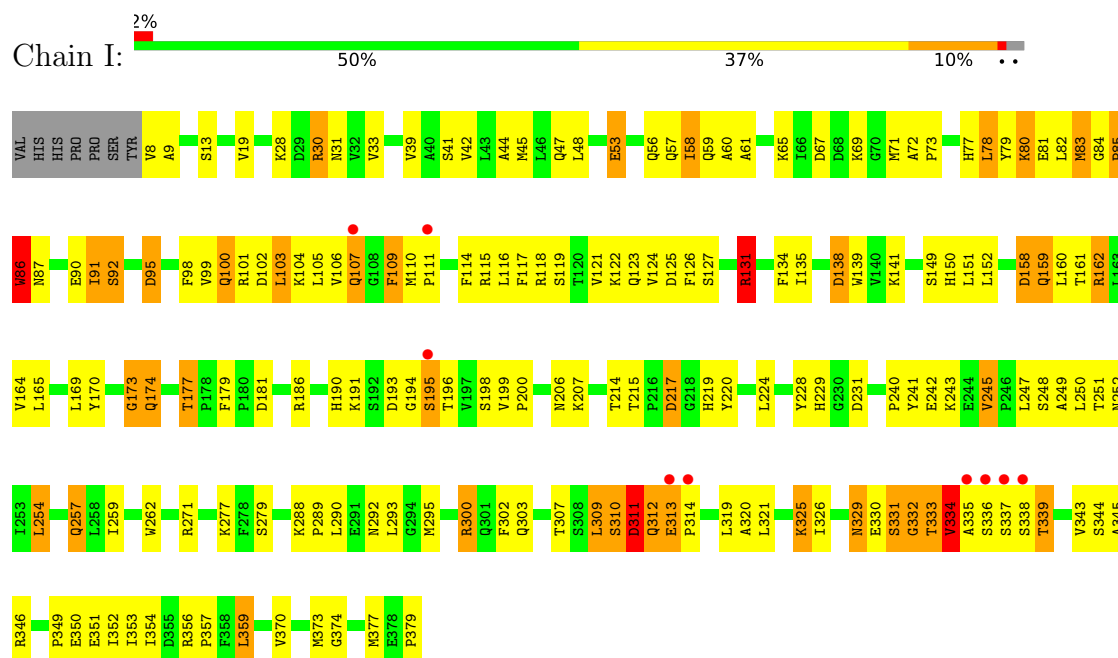
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	I	17	Total	O	0	0
			17	17		
5	E	19	Total	O	0	0
			19	19		

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: Plasminogen activator inhibitor 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	49.74Å 73.94Å 201.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.43 – 3.16 35.43 – 3.16	Depositor EDS
% Data completeness (in resolution range)	99.8 (35.43-3.16) 99.9 (35.43-3.16)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.87 (at 3.18Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.203 , 0.276 0.205 , 0.272	Depositor DCC
R_{free} test set	662 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	53.4	Xtriage
Anisotropy	0.036	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 46.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4988	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.29% 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: GOL, PGE

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	I	0.67	0/3022	0.76	0/4099
2	E	0.84	2/2014 (0.1%)	0.85	1/2732 (0.0%)
All	All	0.74	2/5036 (0.0%)	0.80	1/6831 (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	I	0	2
2	E	0	1
All	All	0	3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	169(A)	SER	C-N	8.02	1.52	1.34
2	E	169	THR	C-O	-7.27	1.09	1.23

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	60(D)	PRO	C-N-CD	5.83	140.65	128.40

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	E	217	LEU	Peptide
1	I	131	ARG	Peptide
1	I	252	ASN	Peptide

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	I	2952	0	2953	241	5
2	E	1966	0	1899	75	0
3	E	24	0	32	5	0
4	E	10	0	14	3	0
5	E	19	0	0	4	0
5	I	17	0	0	25	0
All	All	4988	0	4898	310	5

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 31.

The worst 5 of 310 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:I:320:ALA:C	1:I:321:LEU:HD23	1.40	1.36
1:I:190:HIS:HB2	1:I:243:LYS:NZ	1.40	1.32
1:I:102:ASP:O	1:I:103:LEU:HD23	1.18	1.32
1:I:320:ALA:O	1:I:321:LEU:HD23	1.38	1.21
2:E:116:SER:HB2	5:E:411:HOH:O	1.39	1.18

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:115:ARG:NH1	1:I:303:GLN:OE1[4_455]	1.52	0.68
1:I:115:ARG:CG	1:I:302:PHE:CZ[4_455]	1.71	0.49
1:I:115:ARG:CD	1:I:302:PHE:CD2[4_455]	1.92	0.28
1:I:80:LYS:NZ	1:I:313:GLU:OE2[4_455]	1.97	0.23

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:118:ARG:NH1	1:I:313:GLU:CG[4_455]	2.06	0.14

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	I	370/379 (98%)	313 (85%)	44 (12%)	13 (4%)	3	21
2	E	249/252 (99%)	226 (91%)	22 (9%)	1 (0%)	34	68
All	All	619/631 (98%)	539 (87%)	66 (11%)	14 (2%)	6	31

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	I	86	TRP
1	I	174	GLN
1	I	195	SER
1	I	331	SER
1	I	334	VAL

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	I	326/333 (98%)	275 (84%)	51 (16%)	2	11
2	E	213/214 (100%)	184 (86%)	29 (14%)	3	16

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	539/547 (98%)	459 (85%)	80 (15%)	3 13

5 of 80 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	39	ARG
2	E	148	SER
2	E	86	GLU
2	E	111	CYS
2	E	204	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	63	HIS
2	E	113	GLN
1	I	150	HIS
1	I	174	GLN
1	I	265	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

5 ligands are 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
3	GOL	E	303	-	5,5,5	0.33	0	5,5,5	0.29	0
4	PGE	E	305	-	9,9,9	0.48	0	8,8,8	0.38	0
3	GOL	E	304	-	5,5,5	0.28	0	5,5,5	0.28	0
3	GOL	E	302	-	5,5,5	0.40	0	5,5,5	0.60	0
3	GOL	E	301	-	5,5,5	0.17	0	5,5,5	0.49	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
3	GOL	E	303	-	-	4/4/4/4	-
4	PGE	E	305	-	-	5/7/7/7	-
3	GOL	E	304	-	-	2/4/4/4	-
3	GOL	E	302	-	-	2/4/4/4	-
3	GOL	E	301	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	302	GOL	O1-C1-C2-O2
3	E	302	GOL	O1-C1-C2-C3
3	E	303	GOL	C1-C2-C3-O3
3	E	303	GOL	O2-C2-C3-O3
3	E	304	GOL	C1-C2-C3-O3

There are no ring outliers.

3 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	305	PGE	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	304	GOL	2	0
3	E	301	GOL	3	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	I	372/379 (98%)	-0.16	9 (2%) 59 43	27, 53, 90, 118	0
2	E	251/252 (99%)	-0.37	3 (1%) 79 68	19, 33, 57, 114	0
All	All	623/631 (98%)	-0.25	12 (1%) 66 53	19, 44, 84, 118	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	186(E)	PRO	4.7
1	I	336	SER	4.1
1	I	337	SER	3.2
1	I	335	ALA	3.1
2	E	186(D)	GLY	2.7

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 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(\AA^2)	Q<0.9
3	GOL	E	304	6/6	0.86	0.30	59,66,67,76	0
4	PGE	E	305	10/10	0.86	0.30	34,48,55,55	0
3	GOL	E	303	6/6	0.93	0.29	41,49,50,51	0
3	GOL	E	302	6/6	0.94	0.25	42,45,46,50	0
3	GOL	E	301	6/6	0.97	0.17	46,48,50,51	0

6.5 Other polymers [i](#)

There are no such residues in this entry.