



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 31, 2023 – 06:09 AM EDT

PDB ID : 1TFX
Title : COMPLEX OF THE SECOND KUNITZ DOMAIN OF TISSUE FACTOR
PATHWAY INHIBITOR WITH PORCINE TRYPSIN
Authors : Stubbs, M.T.; Huber, R.
Deposited on : 1997-01-21
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 : 4.02b-467
Xtrriage (Phenix) : 1.13
EDS : 2.34
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) : 2.34

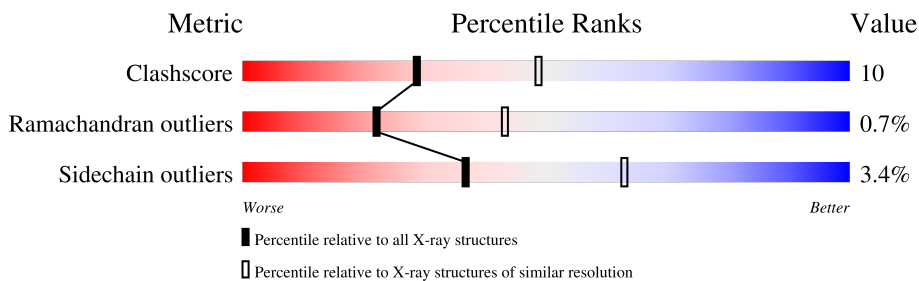
1 Overall quality at a glance

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))
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	223	
1	B	223	
2	C	58	
2	D	58	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4383 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 TRYPSIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	223	Total 1642	C 1020	N 287	O 321	S 14	0	0	0
1	B	223	Total 1642	C 1020	N 287	O 321	S 14	0	0	0

- Molecule 2 is a protein called TISSUE FACTOR PATHWAY INHIBITOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	58	Total 477	C 297	N 79	O 94	S 7	13	0	0
2	D	58	Total 477	C 297	N 79	O 94	S 7	13	0	0

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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


- Molecule 4 is water.

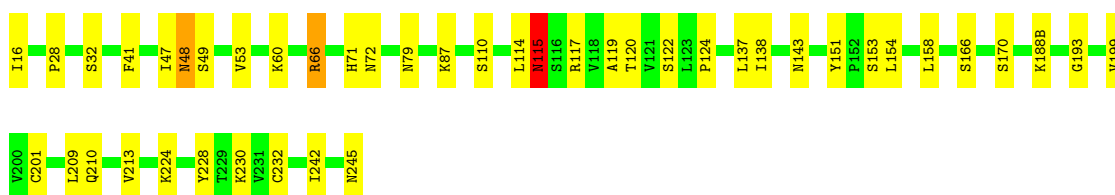
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	67	Total O 67 67	0	0
4	B	55	Total O 55 55	0	0
4	C	11	Total O 11 11	0	0
4	D	10	Total O 10 10	0	0

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. 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. 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.

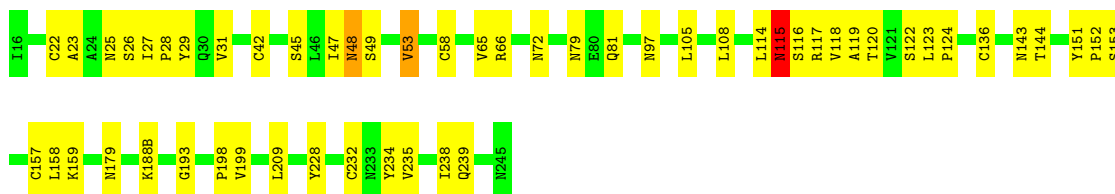
- Molecule 1: TRYPSIN

Chain A:  80% 18%




- Molecule 1: TRYPSIN

Chain B:  76% 23%



- Molecule 2: TISSUE FACTOR PATHWAY INHIBITOR

Chain C:  88% 10%



- Molecule 2: TISSUE FACTOR PATHWAY INHIBITOR

Chain D:  74% 24%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	41.90Å 96.20Å 137.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.00 – 2.60 19.06 – 1.94	Depositor EDS
% Data completeness (in resolution range)	84.5 (6.00-2.60) 58.8 (19.06-1.94)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.26 (at 1.94Å)	Xtrriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.162 , (Not available) 0.158 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	15.2	Xtrriage
Anisotropy	0.264	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 85.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4383	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.76% 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	0.39	0/1674	0.67	0/2273
1	B	0.43	0/1674	0.67	0/2273
2	C	0.49	0/487	0.68	0/650
2	D	0.49	0/487	0.72	0/650
All	All	0.43	0/4322	0.68	0/5846

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	1642	0	1595	26	0
1	B	1642	0	1607	33	0
2	C	477	0	432	5	0
2	D	477	0	438	13	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	67	0	0	1	0
4	B	55	0	0	2	0
4	C	11	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	10	0	0	0	0
All	All	4383	0	4072	74	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 10.

All (74) 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:B:47:ILE:HD13	1:B:53:VAL:HG22	1.44	0.99
1:B:42:CYS:SG	1:B:58:CYS:SG	2.52	0.79
1:B:47:ILE:HD13	1:B:53:VAL:CG2	2.16	0.75
2:D:5:CYS:HG	2:D:55:CYS:HG	0.96	0.74
2:D:30:CYS:SG	2:D:51:CYS:SG	2.55	0.71
1:B:47:ILE:CD1	1:B:53:VAL:HG22	2.22	0.69
1:A:158:LEU:HD11	1:A:188(B):LYS:HB3	1.78	0.65
1:B:144:THR:HG23	1:B:152:PRO:HD3	1.80	0.63
1:B:235:VAL:O	1:B:239:GLN:HG3	1.99	0.62
2:D:5:CYS:SG	2:D:55:CYS:SG	2.71	0.62
1:A:41:PHE:CZ	1:A:60:LYS:HD2	2.35	0.61
1:B:26:SER:O	1:B:28:PRO:HD3	2.01	0.61
1:A:143:ASN:HB2	1:A:151:TYR:CZ	2.37	0.59
1:B:232:CYS:O	1:B:235:VAL:HG23	2.02	0.59
1:A:71:HIS:CE1	1:A:154:LEU:HD22	2.38	0.58
1:A:114:LEU:O	1:A:115:ASN:HB2	2.05	0.57
1:A:193:GLY:HA2	2:C:17:TYR:HB2	1.87	0.57
2:D:4:PHE:HA	2:D:7:LEU:HG	1.87	0.57
2:D:5:CYS:HG	2:D:55:CYS:CB	2.18	0.56
1:A:230:LYS:HE2	1:A:232:CYS:SG	2.47	0.54
1:A:124:PRO:HG3	1:A:209:LEU:O	2.08	0.54
1:A:138:ILE:HD12	1:A:158:LEU:HD23	1.89	0.53
1:B:193:GLY:HA2	2:D:17:TYR:HB2	1.89	0.52
1:B:23:ALA:O	1:B:26:SER:HB2	2.11	0.51
1:B:115:ASN:HD22	1:B:116:SER:N	2.08	0.51
2:D:48:LEU:HD11	2:D:52:LYS:HE3	1.91	0.51
2:D:25:ASN:ND2	2:D:25:ASN:H	2.09	0.51
2:D:24:ASN:OD1	2:D:26:GLN:HB2	2.11	0.51
1:A:28:PRO:HB2	1:A:119:ALA:HB3	1.92	0.51
2:C:25:ASN:ND2	2:C:25:ASN:H	2.09	0.50
1:B:158:LEU:HD11	1:B:188(B):LYS:HB3	1.94	0.49
2:C:7:LEU:HB3	2:C:41:ASN:HD22	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:45:SER:OG	1:B:198:PRO:HG3	2.13	0.49
1:B:72:ASN:HA	1:B:153:SER:O	2.13	0.48
1:B:49:SER:HB3	1:B:114:LEU:HD11	1.96	0.48
1:B:115:ASN:HD22	1:B:116:SER:H	1.61	0.48
1:A:72:ASN:HA	1:A:153:SER:O	2.15	0.47
1:B:79:ASN:HB2	4:B:6005:HOH:O	2.13	0.47
1:A:47:ILE:HD13	1:A:53:VAL:HG23	1.96	0.47
1:A:79:ASN:ND2	1:A:117:ARG:NH1	2.64	0.46
1:A:137:LEU:HD12	1:A:158:LEU:O	2.15	0.46
2:D:25:ASN:H	2:D:25:ASN:HD22	1.61	0.46
1:B:151:TYR:HB3	4:B:408:HOH:O	2.16	0.46
1:B:105:LEU:HD11	1:B:238:ILE:HG23	1.97	0.46
1:A:48:ASN:HA	1:A:120:THR:HG21	1.98	0.46
1:B:65:VAL:HG21	1:B:108:LEU:HD21	1.98	0.46
2:D:30:CYS:SG	2:D:56:GLU:HG3	2.56	0.46
1:B:97:ASN:HA	2:D:39:LEU:HD21	1.98	0.45
1:A:199:VAL:HG21	1:A:228:TYR:CD2	2.52	0.45
1:B:48:ASN:HA	1:B:120:THR:HG21	1.99	0.44
1:B:199:VAL:HG21	1:B:228:TYR:CD2	2.52	0.44
1:A:47:ILE:HD11	1:A:242:ILE:HD11	1.98	0.44
1:B:81:GLN:NE2	1:B:118:VAL:HG21	2.33	0.44
1:B:124:PRO:HD3	1:B:209:LEU:O	2.18	0.44
1:B:27:ILE:HG23	1:B:29:TYR:CZ	2.52	0.43
1:A:79:ASN:ND2	1:A:117:ARG:HH11	2.16	0.43
1:B:136:CYS:O	1:B:159:LYS:HA	2.18	0.43
2:C:32:ARG:NH2	4:C:411:HOH:O	2.51	0.43
2:C:33:PHE:HB2	4:C:424:HOH:O	2.18	0.43
1:A:47:ILE:HD13	1:A:53:VAL:CG2	2.49	0.43
2:D:4:PHE:O	2:D:43:ASN:HB2	2.19	0.43
1:B:28:PRO:HB2	1:B:119:ALA:HB3	2.00	0.42
1:B:179:ASN:HB3	1:B:234:TYR:OH	2.19	0.42
1:B:143:ASN:HB2	1:B:151:TYR:CZ	2.55	0.42
1:A:87:LYS:HE3	1:A:245:ASN:O	2.19	0.42
1:B:22:CYS:HG	1:B:157:CYS:HG	0.66	0.42
1:A:143:ASN:HB2	1:A:151:TYR:OH	2.20	0.41
1:A:210:GLN:NE2	4:A:2063:HOH:O	2.52	0.41
1:A:224:LYS:HA	1:A:224:LYS:HD3	1.92	0.41
1:A:32:SER:HB3	1:A:66:ARG:HB2	2.02	0.41
1:A:213:VAL:HG22	1:A:228:TYR:HE2	1.86	0.41
1:B:25:ASN:ND2	1:B:117:ARG:HB3	2.37	0.40
1:A:16:ILE:HG21	1:A:158:LEU:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:123:LEU:HD23	1:B:123:LEU:HA	1.96	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	221/223 (99%)	206 (93%)	13 (6%)	2 (1%)	17	35
1	B	221/223 (99%)	202 (91%)	18 (8%)	1 (0%)	29	52
2	C	56/58 (97%)	51 (91%)	4 (7%)	1 (2%)	8	16
2	D	56/58 (97%)	51 (91%)	5 (9%)	0	100	100
All	All	554/562 (99%)	510 (92%)	40 (7%)	4 (1%)	22	43

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	57	ASP
1	A	115	ASN
1	A	49	SER
1	B	115	ASN

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	183/183 (100%)	175 (96%)	8 (4%)	28	53
1	B	183/183 (100%)	177 (97%)	6 (3%)	38	64
2	C	52/52 (100%)	51 (98%)	1 (2%)	57	79
2	D	52/52 (100%)	51 (98%)	1 (2%)	57	79
All	All	470/470 (100%)	454 (97%)	16 (3%)	37	63

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	ASN
1	A	66	ARG
1	A	110	SER
1	A	115	ASN
1	A	122	SER
1	A	166	SER
1	A	170	SER
1	A	201	CYS
1	B	31	VAL
1	B	48	ASN
1	B	53	VAL
1	B	66	ARG
1	B	115	ASN
1	B	122	SER
2	C	25	ASN
2	D	25	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	71	HIS
1	A	79	ASN
1	A	101	ASN
1	A	210	GLN
1	A	245	ASN
1	B	30	GLN
1	B	48	ASN
1	B	79	ASN
1	B	101	ASN
1	B	115	ASN

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Mol	Chain	Res	Type
1	B	175	GLN
1	B	210	GLN
2	C	25	ASN
2	D	25	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](#)

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.