



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 09:37 AM UTC

PDB ID : 1QTY / pdb_00001qty
Title : VASCULAR ENDOTHELIAL GROWTH FACTOR IN COMPLEX WITH
DOMAIN 2 OF THE FLT-1 RECEPTOR
Authors : Wiesmann, C.; de Vos, A.M.
Deposited on : 1999-06-29
Resolution : 2.70 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 : 4-5-2 with Phenix2.0
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

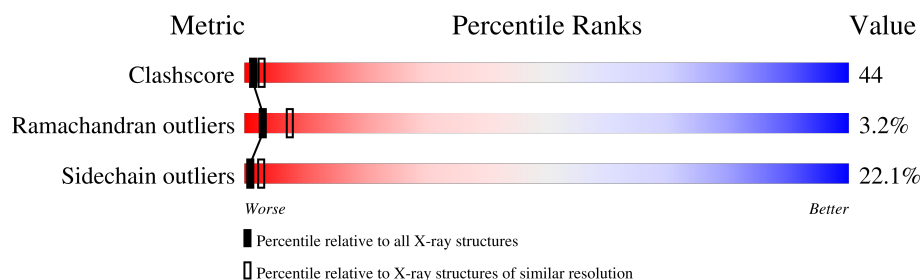
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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))
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)

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 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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	R	102	36% 42% 14% • 7%
1	S	102	41% 42% 11% 6%
1	V	102	43% 37% 11% • 7%
1	W	102	34% 47% 12% 7%
2	T	101	32% 47% 15% 7%
2	U	101	33% 43% 17% • 7%
2	X	101	32% 43% 18% • 7%
2	Y	101	33% 45% 14% • 7%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6121 atoms, of which 0 are hydrogens and 0 are deuteriums.

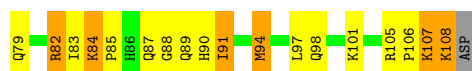
In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called VASCULAR ENDOTHELIAL GROWTH FACTOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	V	95	Total	C	N	O	S	0	0	0
			770	483	129	145	13			
1	W	95	Total	C	N	O	S	0	0	0
			770	483	129	145	13			
1	R	95	Total	C	N	O	S	0	0	0
			770	483	129	145	13			
1	S	96	Total	C	N	O	S	0	0	0
			779	489	131	146	13			

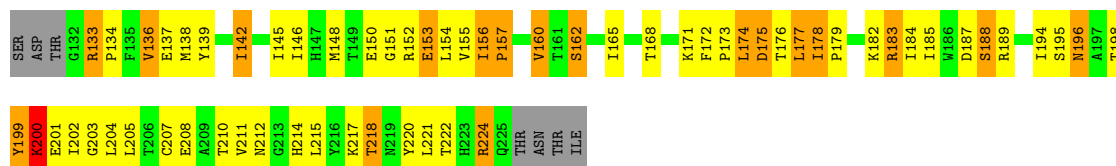
- Molecule 2 is a protein called FMS-LIKE TYROSINE KINASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	X	94	Total	C	N	O	S	0	0	0
			758	487	130	137	4			
2	Y	94	Total	C	N	O	S	0	0	0
			758	487	130	137	4			
2	T	94	Total	C	N	O	S	0	0	0
			758	487	130	137	4			
2	U	94	Total	C	N	O	S	0	0	0
			758	487	130	137	4			



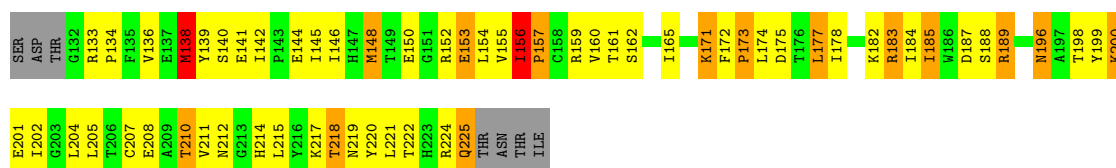
• Molecule 2: FMS-LIKE TYROSINE KINASE 1

Chain X: 32% 43% 18% 7%



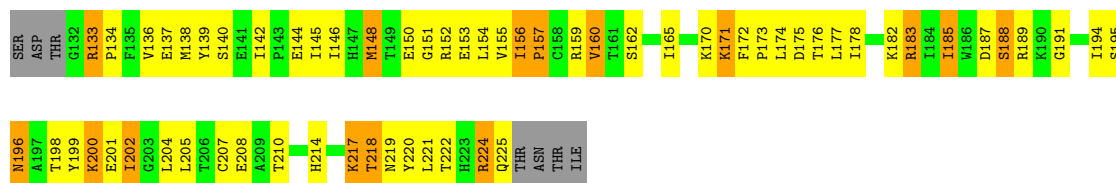
• Molecule 2: FMS-LIKE TYROSINE KINASE 1

Chain Y: 33% 45% 14% 7%



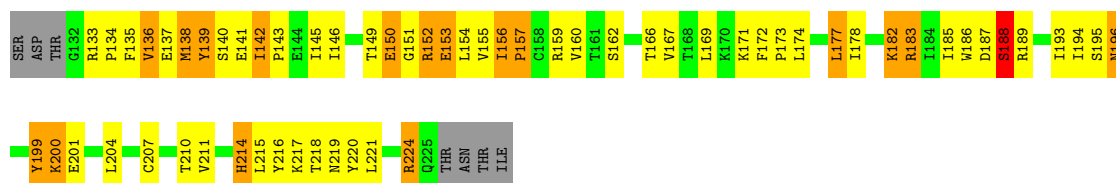
• Molecule 2: FMS-LIKE TYROSINE KINASE 1

Chain T: 32% 47% 15% 7%



• Molecule 2: FMS-LIKE TYROSINE KINASE 1

Chain U: 33% 43% 17% 7%



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	124.31Å 67.01Å 120.84Å 90.00° 118.15° 90.00°	Depositor
Resolution (Å)	20.00 – 2.70	Depositor
% Data completeness (in resolution range)	92.6 (20.00-2.70)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.233 , 0.284	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6121	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

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	R	0.67	0/788	1.02	5/1062 (0.5%)
1	S	0.66	0/797	0.99	1/1073 (0.1%)
1	V	0.71	0/788	1.04	2/1062 (0.2%)
1	W	0.70	0/788	1.00	2/1062 (0.2%)
2	T	0.70	0/775	1.20	6/1051 (0.6%)
2	U	0.77	0/775	1.19	7/1051 (0.7%)
2	X	0.70	0/775	1.20	7/1051 (0.7%)
2	Y	0.74	0/775	1.25	4/1051 (0.4%)
All	All	0.71	0/6261	1.12	34/8463 (0.4%)

There are no bond length outliers.

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Y	156	ILE	CA-C-N	11.39	134.07	119.84
2	Y	156	ILE	C-N-CA	11.39	134.07	119.84
2	T	156	ILE	CA-C-N	10.13	132.51	119.84
2	T	156	ILE	C-N-CA	10.13	132.51	119.84
2	X	156	ILE	CA-C-N	9.28	131.44	119.84

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	R	770	0	732	70	0
1	S	779	0	745	60	0
1	V	770	0	732	68	0
1	W	770	0	732	58	0
2	T	758	0	775	67	0
2	U	758	0	775	110	0
2	X	758	0	775	86	0
2	Y	758	0	775	63	0
All	All	6121	0	6041	540	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 44.

The worst 5 of 540 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)
2:U:133:ARG:HH22	2:U:139:TYR:CB	1.52	1.22
2:U:133:ARG:NH2	2:U:139:TYR:HB2	1.56	1.19
2:X:183:ARG:HG2	2:X:183:ARG:HH11	1.01	1.18
2:X:178:ILE:HD12	2:T:183:ARG:HD2	1.20	1.16
2:X:174:LEU:HD12	2:X:174:LEU:H	1.14	1.12

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	R	93/102 (91%)	83 (89%)	6 (6%)	4 (4%)	2	4
1	S	94/102 (92%)	85 (90%)	7 (7%)	2 (2%)	5	15
1	V	93/102 (91%)	85 (91%)	7 (8%)	1 (1%)	11	29
1	W	93/102 (91%)	82 (88%)	8 (9%)	3 (3%)	3	7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	T	92/101 (91%)	82 (89%)	7 (8%)	3 (3%)	3	7
2	U	92/101 (91%)	76 (83%)	12 (13%)	4 (4%)	2	4
2	X	92/101 (91%)	81 (88%)	8 (9%)	3 (3%)	3	7
2	Y	92/101 (91%)	80 (87%)	8 (9%)	4 (4%)	2	4
All	All	741/812 (91%)	654 (88%)	63 (8%)	24 (3%)	3	7

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	W	88	GLY
2	U	138	MET
1	V	64	GLU
1	R	64	GLU
1	R	88	GLY

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	R	90/96 (94%)	73 (81%)	17 (19%)	1	4
1	S	91/96 (95%)	72 (79%)	19 (21%)	1	3
1	V	90/96 (94%)	72 (80%)	18 (20%)	1	4
1	W	90/96 (94%)	72 (80%)	18 (20%)	1	4
2	T	86/93 (92%)	66 (77%)	20 (23%)	1	2
2	U	86/93 (92%)	68 (79%)	18 (21%)	1	3
2	X	86/93 (92%)	66 (77%)	20 (23%)	1	2
2	Y	86/93 (92%)	60 (70%)	26 (30%)	0	1
All	All	705/756 (93%)	549 (78%)	156 (22%)	1	3

5 of 156 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	Y	221	LEU
2	U	162	SER
2	T	140	SER
2	T	183	ARG
2	U	196	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
2	Y	196	ASN
2	Y	214	HIS
2	U	196	ASN
2	T	196	ASN
1	S	27	HIS

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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.