



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 11:33 AM GMT

PDB ID : 3P9W
Title : Crystal structure of an engineered human autonomous VH Domain in complex with VEGF
Authors : Ma, X.; Wiesmann, C.
Deposited on : 2010-10-18
Resolution : 2.41 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

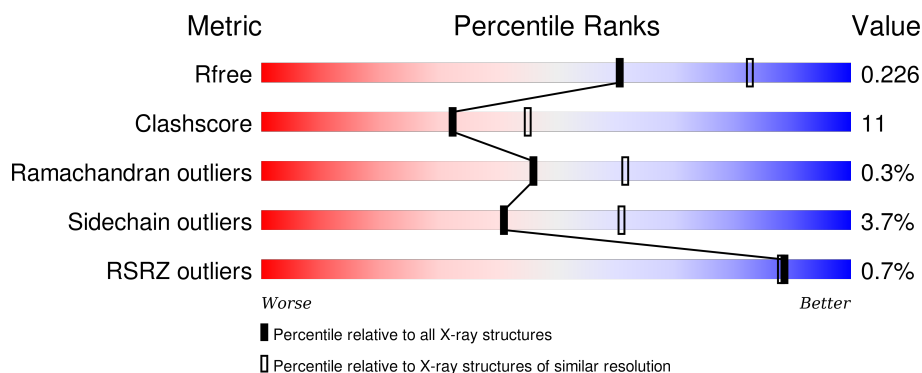
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.41 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}	91344	3386 (2.44-2.40)
Clashscore	102246	3897 (2.44-2.40)
Ramachandran outliers	100387	3837 (2.44-2.40)
Sidechain outliers	100360	3838 (2.44-2.40)
RSRZ outliers	91569	3396 (2.44-2.40)

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. 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	106	<div> <div>71%</div> <div>19%</div> <div>9%</div> </div>
1	C	106	<div> <div>70%</div> <div>21%</div> <div>8%</div> </div>
1	E	106	<div> <div>76%</div> <div>15%</div> <div>8%</div> </div>
1	G	106	<div> <div>61%</div> <div>28%</div> <div>8%</div> </div>
2	B	123	<div> <div>89%</div> <div>10%</div> <div>1%</div> </div>

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Mol	Chain	Length	Quality of chain
2	D	123	<div> <div>4%</div> <div>73%</div> <div>24%</div> <div>..</div> </div>
2	F	123	<div> <div>77%</div> <div>18%</div> <div>..</div> </div>
2	H	123	<div> <div>73%</div> <div>24%</div> <div>..</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7350 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 A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	96	Total	C	N	O	S	0	0	0
			780	489	132	146	13			
1	C	97	Total	C	N	O	S	0	0	0
			789	495	134	147	13			
1	E	97	Total	C	N	O	S	0	0	0
			789	495	134	147	13			
1	G	97	Total	C	N	O	S	0	0	0
			790	495	135	147	13			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	GLY	-	EXPRESSION TAG	UNP P15692
A	8	SER	-	EXPRESSION TAG	UNP P15692
C	7	GLY	-	EXPRESSION TAG	UNP P15692
C	8	SER	-	EXPRESSION TAG	UNP P15692
E	7	GLY	-	EXPRESSION TAG	UNP P15692
E	8	SER	-	EXPRESSION TAG	UNP P15692
G	7	GLY	-	EXPRESSION TAG	UNP P15692
G	8	SER	-	EXPRESSION TAG	UNP P15692

- Molecule 2 is a protein called human VEGF.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	123	Total	C	N	O	S	0	0	0
			949	600	162	184	3			
2	D	121	Total	C	N	O	S	0	0	0
			934	592	160	179	3			
2	F	122	Total	C	N	O	S	0	0	0
			940	595	161	181	3			
2	H	122	Total	C	N	O	S	0	0	0
			940	595	161	181	3			

- Molecule 3 is water.

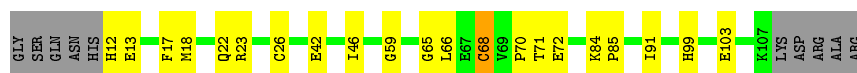
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	61	Total 61	O 61	0	0
3	B	81	Total 81	O 81	0	0
3	C	54	Total 54	O 54	0	0
3	D	24	Total 24	O 24	0	0
3	E	42	Total 42	O 42	0	0
3	F	90	Total 90	O 90	0	0
3	G	58	Total 58	O 58	0	0
3	H	29	Total 29	O 29	0	0

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 errors 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: Vascular endothelial growth factor A

Chain A: 




- Molecule 1: Vascular endothelial growth factor A

Chain C: 



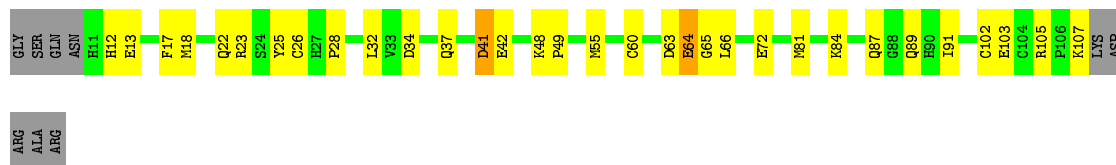
- Molecule 1: Vascular endothelial growth factor A

Chain E: 




- Molecule 1: Vascular endothelial growth factor A

Chain G: 

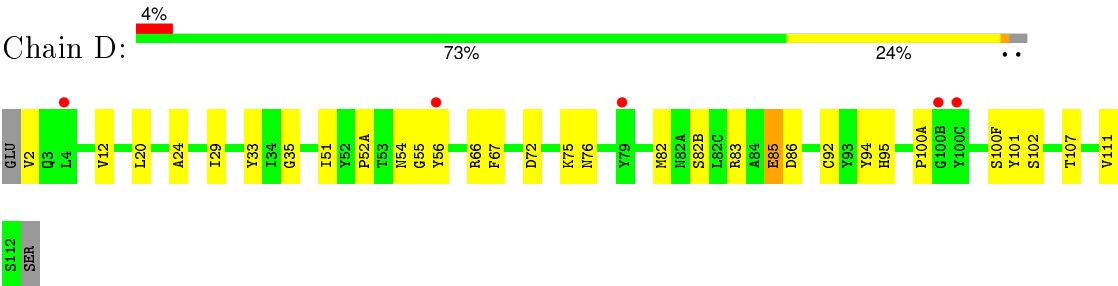


- Molecule 2: human VEGF

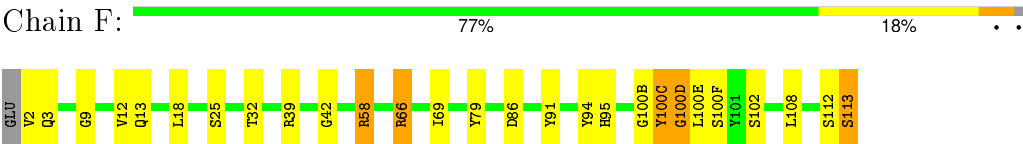
Chain B: 



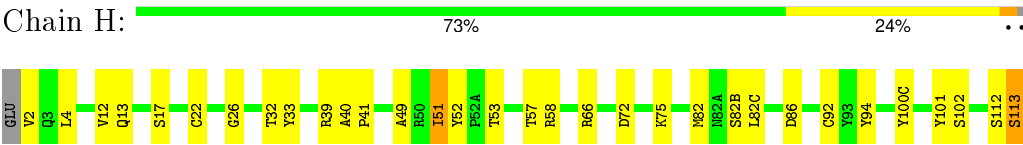
- Molecule 2: human VEGF



• Molecule 2: human VEGF



• Molecule 2: human VEGF



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	52.73Å 132.91Å 175.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.41 45.19 – 2.41	Depositor EDS
% Data completeness (in resolution range)	91.7 (50.00-2.41) 91.7 (45.19-2.41)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.52 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.193 , 0.233 0.189 , 0.226	Depositor DCC
R_{free} test set	2281 reflections (5.37%)	DCC
Wilson B-factor (Å ²)	39.5	Xtriage
Anisotropy	0.391	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 55.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 44896 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7350	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.16% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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	0.53	1/799 (0.1%)	0.55	0/1077
1	C	0.41	0/808	0.52	0/1088
1	E	0.42	0/808	0.54	0/1088
1	G	0.36	0/810	0.48	0/1092
2	B	0.46	0/973	0.58	1/1321 (0.1%)
2	D	0.31	0/958	0.46	0/1301
2	F	0.45	0/964	0.65	2/1309 (0.2%)
2	H	0.31	0/964	0.46	0/1309
All	All	0.41	1/7084 (0.0%)	0.54	3/9585 (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
2	B	0	1
2	D	0	1
2	F	0	2
2	H	0	1
All	All	0	5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	68	CYS	CB-SG	8.57	1.96	1.82

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	66	ARG	NE-CZ-NH2	-6.38	117.11	120.30
2	B	66	ARG	NE-CZ-NH2	-5.62	117.49	120.30
2	F	58	ARG	NE-CZ-NH1	-5.02	117.79	120.30

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	32	THR	Peptide
2	D	100(A)	PRO	Peptide
2	F	32	THR	Peptide
2	F	42	GLY	Peptide
2	H	32	THR	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	A	780	0	739	14	0
1	C	789	0	752	19	0
1	E	789	0	752	17	0
1	G	790	0	746	27	0
2	B	949	0	906	10	0
2	D	934	0	892	24	0
2	F	940	0	897	25	0
2	H	940	0	897	20	0
3	A	61	0	0	3	0
3	B	81	0	0	4	1
3	C	54	0	0	6	0
3	D	24	0	0	3	0
3	E	42	0	0	9	0
3	F	90	0	0	5	1
3	G	58	0	0	7	0
3	H	29	0	0	4	0
All	All	7350	0	6581	142	1

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.

The worst 5 of 142 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:C:106:PRO:HG2	1:G:18:MET:HE1	1.41	1.01
2:H:113:SER:C	3:H:424:HOH:O	1.98	1.00
2:D:94:TYR:CE1	2:D:102:SER:HB2	1.99	0.96
2:D:72:ASP:OD2	2:D:75:LYS:HG3	1.67	0.95
1:E:73:GLU:CD	2:F:58:ARG:HH12	1.70	0.95

All (1) 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)
3:B:116:HOH:O	3:F:119:HOH:O[2_564]	2.12	0.08

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	94/106 (89%)	87 (93%)	6 (6%)	1 (1%)	17	24
1	C	95/106 (90%)	90 (95%)	4 (4%)	1 (1%)	17	24
1	E	95/106 (90%)	92 (97%)	3 (3%)	0	100	100
1	G	95/106 (90%)	92 (97%)	3 (3%)	0	100	100
2	B	121/123 (98%)	119 (98%)	2 (2%)	0	100	100
2	D	119/123 (97%)	115 (97%)	4 (3%)	0	100	100
2	F	120/123 (98%)	119 (99%)	0	1 (1%)	24	33
2	H	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
All	All	859/916 (94%)	832 (97%)	24 (3%)	3 (0%)	46	62

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F	100(D)	GLY

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Mol	Chain	Res	Type
1	A	26	CYS
1	C	26	CYS

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	91/99 (92%)	87 (96%)	4 (4%)	35	52
1	C	92/99 (93%)	88 (96%)	4 (4%)	35	54
1	E	92/99 (93%)	89 (97%)	3 (3%)	45	65
1	G	92/99 (93%)	87 (95%)	5 (5%)	27	42
2	B	98/98 (100%)	96 (98%)	2 (2%)	63	80
2	D	96/98 (98%)	94 (98%)	2 (2%)	61	79
2	F	97/98 (99%)	94 (97%)	3 (3%)	47	68
2	H	97/98 (99%)	92 (95%)	5 (5%)	29	45
All	All	755/788 (96%)	727 (96%)	28 (4%)	41	61

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	19	ASP
2	F	100(C)	TYR
2	H	92	CYS
1	E	43	ILE
1	E	60	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	22	GLN
1	E	100	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 carbohydrates 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 ⓘ

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	96/106 (90%)	-0.30	0 100 100	20, 33, 57, 67	0
1	C	97/106 (91%)	-0.25	1 (1%) 84 83	23, 34, 65, 75	0
1	E	97/106 (91%)	-0.27	0 100 100	18, 32, 59, 67	0
1	G	97/106 (91%)	-0.24	0 100 100	25, 39, 61, 71	0
2	B	123/123 (100%)	-0.42	0 100 100	13, 28, 41, 66	0
2	D	121/123 (98%)	0.41	5 (4%) 41 41	39, 60, 72, 78	0
2	F	122/123 (99%)	-0.41	0 100 100	13, 25, 44, 62	0
2	H	122/123 (99%)	-0.22	0 100 100	37, 51, 64, 76	0
All	All	875/916 (95%)	-0.21	6 (0%) 89 88	13, 37, 66, 78	0

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	100(C)	TYR	4.5
2	D	100(B)	GLY	2.9
2	D	56	TYR	2.8
2	D	79	TYR	2.7
1	C	45	TYR	2.1

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 ⓘ

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.