



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 18, 2026 – 05:07 PM UTC

PDB ID : 4KV5 / pdb_00004kv5
Title : scFv GC1009 in complex with TGF-beta1.
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Deposited on : 2013-05-22
Resolution : 3.00 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) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

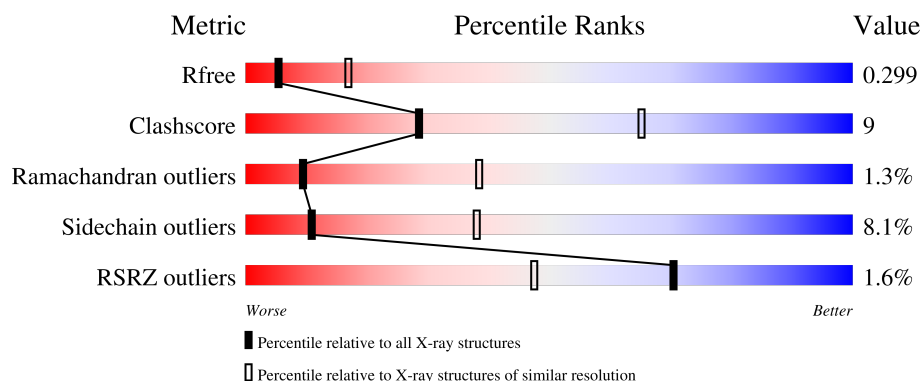
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	A	112	
1	B	112	
1	C	112	
1	D	112	
2	E	252	

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Mol	Chain	Length	Quality of chain
2	G	252	2% 67% 22% 9%
2	H	252	2% 65% 23% 9%
2	J	252	1% 69% 19% 9%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 10542 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 Transforming growth factor beta-1 proprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	112	Total	C	N	O	S	0	0	0
			897	576	152	159	10			
1	D	112	Total	C	N	O	S	0	0	0
			897	576	152	159	10			
1	A	112	Total	C	N	O	S	0	0	0
			896	576	152	158	10			
1	B	112	Total	C	N	O	S	0	0	0
			897	576	152	159	10			

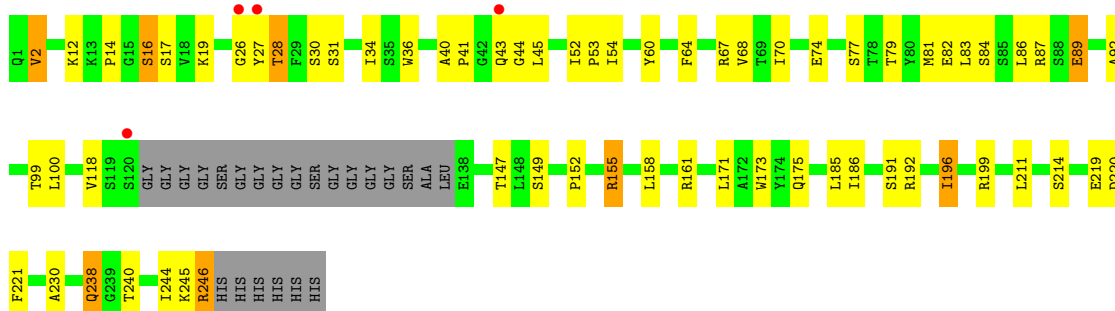
- Molecule 2 is a protein called Single-chain variable fragment GC1009.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	J	230	Total	C	N	O	S	0	0	0
			1743	1095	294	347	7			
2	H	229	Total	C	N	O	S	0	0	0
			1735	1089	293	346	7			
2	E	230	Total	C	N	O	S	0	0	0
			1743	1095	294	347	7			
2	G	229	Total	C	N	O	S	0	0	0
			1734	1090	292	345	7			

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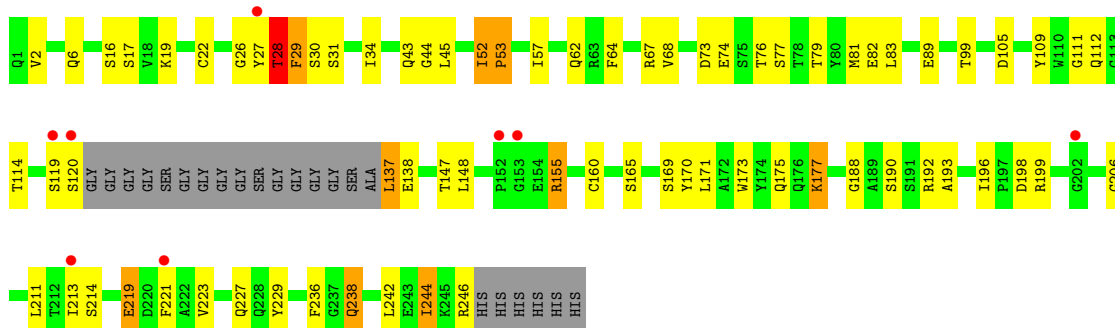
• Molecule 2: Single-chain variable fragment GC1009

Chain H: 



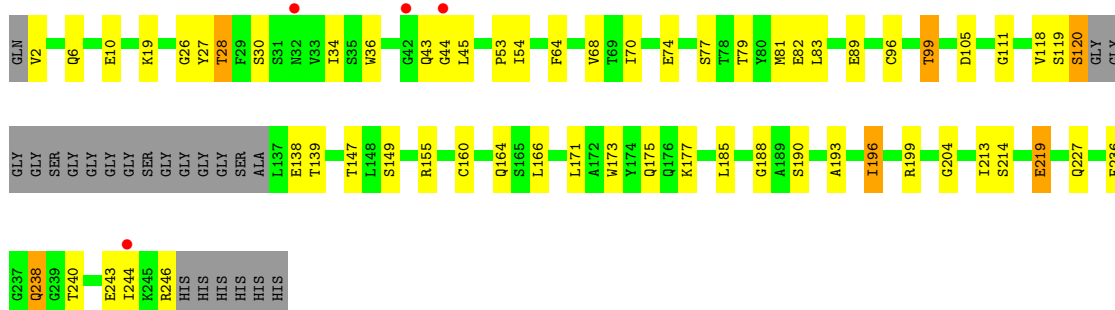
• Molecule 2: Single-chain variable fragment GC1009

Chain E: 



• Molecule 2: Single-chain variable fragment GC1009

Chain G: 



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	108.19Å 171.77Å 109.88Å 90.00° 111.30° 90.00°	Depositor
Resolution (Å)	30.96 – 3.00 30.96 – 3.00	Depositor EDS
% Data completeness (in resolution range)	91.5 (30.96-3.00) 91.5 (30.96-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 3.00Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.229 , 0.300 0.233 , 0.299	Depositor DCC
R_{free} test set	2000 reflections (5.35%)	wwPDB-VP
Wilson B-factor (Å ²)	73.9	Xtriage
Anisotropy	0.461	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 32.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.57$, $\langle L^2 \rangle = 0.41$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	10542	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.68% 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](#)

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	0.71	0/924	1.06	2/1258 (0.2%)
1	B	0.74	0/925	1.05	2/1258 (0.2%)
1	C	0.73	1/925 (0.1%)	1.09	5/1258 (0.4%)
1	D	0.71	0/925	0.99	2/1258 (0.2%)
2	E	0.59	0/1778	0.97	4/2415 (0.2%)
2	G	0.64	0/1769	1.00	5/2403 (0.2%)
2	H	0.65	0/1770	0.98	7/2404 (0.3%)
2	J	0.67	0/1778	0.99	5/2415 (0.2%)
All	All	0.67	1/10794 (0.0%)	1.01	32/14669 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	51	ILE	CA-CB	5.12	1.61	1.54

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	E	28	THR	N-CA-C	7.98	127.80	110.80
2	H	28	THR	N-CA-C	7.34	120.64	108.96
2	H	196	ILE	CA-C-N	7.11	127.14	119.89
2	H	196	ILE	C-N-CA	7.11	127.14	119.89
2	G	28	THR	N-CA-C	7.04	121.15	109.46

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	896	0	871	17	0
1	B	897	0	871	15	0
1	C	897	0	871	12	0
1	D	897	0	871	8	0
2	E	1743	0	1711	44	0
2	G	1734	0	1700	31	0
2	H	1735	0	1700	37	0
2	J	1743	0	1711	30	0
All	All	10542	0	10306	183	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 9.

The worst 5 of 183 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:G:34:ILE:HG21	2:G:79:THR:HG21	1.65	0.79
2:H:2:VAL:HA	2:H:26:GLY:HA3	1.66	0.78
2:G:2:VAL:HA	2:G:26:GLY:HA3	1.69	0.74
1:C:98:VAL:HG23	1:A:87:PRO:HB3	1.68	0.73
2:H:34:ILE:HG21	2:H:79:THR:HG21	1.70	0.73

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	110/112 (98%)	98 (89%)	10 (9%)	2 (2%)	6	31
1	B	110/112 (98%)	98 (89%)	10 (9%)	2 (2%)	6	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	110/112 (98%)	98 (89%)	10 (9%)	2 (2%)	6	31
1	D	110/112 (98%)	99 (90%)	9 (8%)	2 (2%)	6	31
2	E	226/252 (90%)	212 (94%)	11 (5%)	3 (1%)	9	38
2	G	225/252 (89%)	211 (94%)	13 (6%)	1 (0%)	30	65
2	H	225/252 (89%)	211 (94%)	11 (5%)	3 (1%)	9	38
2	J	226/252 (90%)	212 (94%)	12 (5%)	2 (1%)	14	48
All	All	1342/1456 (92%)	1239 (92%)	86 (6%)	17 (1%)	9	38

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	70	PRO
1	A	51	ILE
1	B	70	PRO
2	J	29	PHE
2	E	28	THR

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	100/100 (100%)	95 (95%)	5 (5%)	22	56
1	B	100/100 (100%)	94 (94%)	6 (6%)	17	50
1	C	100/100 (100%)	92 (92%)	8 (8%)	11	38
1	D	100/100 (100%)	92 (92%)	8 (8%)	11	38
2	E	191/200 (96%)	173 (91%)	18 (9%)	8	32
2	G	190/200 (95%)	173 (91%)	17 (9%)	9	34
2	H	190/200 (95%)	175 (92%)	15 (8%)	11	39
2	J	191/200 (96%)	174 (91%)	17 (9%)	9	34
All	All	1162/1200 (97%)	1068 (92%)	94 (8%)	11	38

5 of 94 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	238	GLN
2	E	171	LEU
2	E	30	SER
2	E	89	GLU
2	E	244	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	66	ASN
2	J	59	ASN
2	G	228	GLN
2	G	43	GLN
1	D	66	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 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 ⓘ

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	112/112 (100%)	-0.10	0 100 100	43, 57, 80, 93	0
1	B	112/112 (100%)	-0.23	0 100 100	39, 53, 76, 83	0
1	C	112/112 (100%)	-0.19	2 (1%) 67 44	42, 58, 87, 93	0
1	D	112/112 (100%)	-0.23	1 (0%) 81 61	44, 56, 81, 89	0
2	E	230/252 (91%)	0.16	8 (3%) 47 27	50, 74, 104, 163	0
2	G	229/252 (90%)	0.25	4 (1%) 69 45	47, 76, 104, 136	0
2	H	229/252 (90%)	0.06	4 (1%) 69 45	48, 68, 97, 135	0
2	J	230/252 (91%)	-0.12	3 (1%) 75 53	41, 59, 88, 117	0
All	All	1366/1456 (93%)	-0.00	22 (1%) 70 47	39, 64, 96, 163	0

The worst 5 of 22 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	120	SER	2.9
1	C	1	ALA	2.8
2	E	27	TYR	2.7
2	J	27	TYR	2.7
1	C	53	SER	2.6

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 oligosaccharides 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.