



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 15, 2020 – 06:32 pm BST

PDB ID : 4NKO  
Title : Crystal structure of engineered anti-EE scFv antibody fragment  
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Deposited on : 2013-11-12  
Resolution : 3.50 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

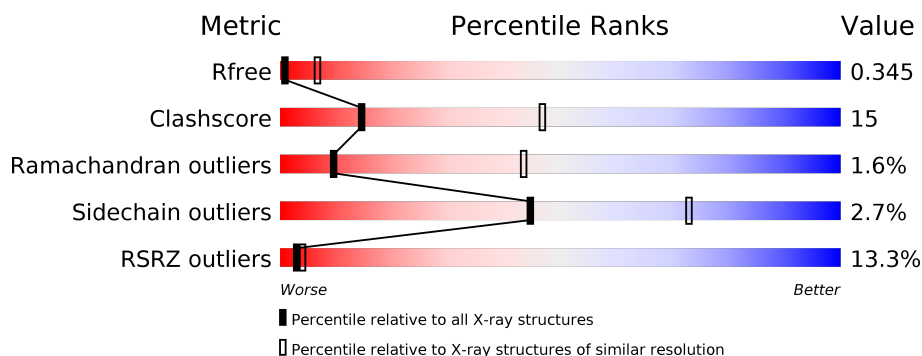
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.50 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	1659 (3.60-3.40)
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)
RSRZ outliers	127900	1559 (3.60-3.40)

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  $\geq 3$ , 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	138	<div> <div>8%</div> <div>58%</div> <div>25%</div> <div>17%</div> </div>
1	C	138	<div> <div>14%</div> <div>59%</div> <div>25%</div> <div>17%</div> </div>
1	E	138	<div> <div>9%</div> <div>60%</div> <div>23%</div> <div>17%</div> </div>
2	B	131	<div> <div>11%</div> <div>63%</div> <div>25%</div> <div>8%</div> </div>
2	D	131	<div> <div>11%</div> <div>66%</div> <div>24%</div> <div>8%</div> </div>
2	F	131	<div> <div>16%</div> <div>73%</div> <div>17%</div> <div>8%</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5394 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 Engineered scFv light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	115	Total	C	N	O	S	0	0	0
			874	552	148	171	3			
1	C	115	Total	C	N	O	S	0	0	0
			874	552	148	171	3			
1	E	115	Total	C	N	O	S	0	0	0
			874	552	148	171	3			

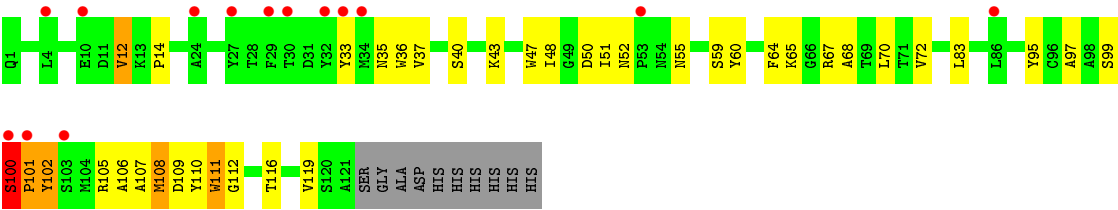
- Molecule 2 is a protein called Engineered scFv heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	121	Total	C	N	O	S	0	0	0
			924	576	153	189	6			
2	D	121	Total	C	N	O	S	0	0	0
			924	576	153	189	6			
2	F	121	Total	C	N	O	S	0	0	0
			924	576	153	189	6			



- Molecule 1: Engineered scFv light chain

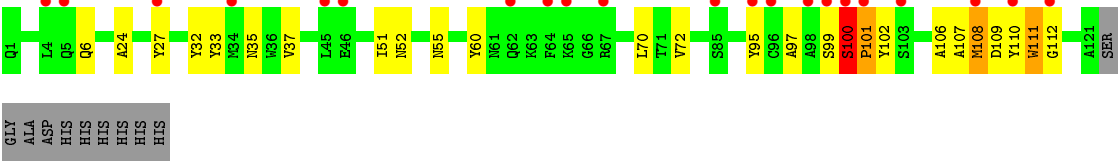




• Molecule 2: Engineered scFv heavy chain



• Molecule 2: Engineered scFv heavy chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	60.59Å 104.92Å 284.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.20 – 3.50 42.22 – 3.50	Depositor EDS
% Data completeness (in resolution range)	(Not available) (42.20-3.50) 93.1 (42.22-3.50)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.10 (at 3.48Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, $R_{free}$	0.308 , 0.344 0.309 , 0.345	Depositor DCC
$R_{free}$ test set	526 reflections (4.74%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	104.4	Xtriage
Anisotropy	0.148	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 39.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.388 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.408 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
$F_o, F_c$ correlation	0.87	EDS
Total number of atoms	5394	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.78% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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	0.27	0/893	0.47	0/1208
1	C	0.25	0/893	0.48	0/1208
1	E	0.26	0/893	0.51	0/1208
2	B	0.30	0/945	0.65	1/1281 (0.1%)
2	D	0.29	0/945	0.64	1/1281 (0.1%)
2	F	0.30	0/945	0.66	1/1281 (0.1%)
All	All	0.28	0/5514	0.57	3/7467 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	100	SER	C-N-CD	-5.82	107.80	120.60
2	D	100	SER	C-N-CD	-5.75	107.96	120.60
2	B	100	SER	C-N-CD	-5.71	108.03	120.60

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	874	0	866	25	0
1	C	874	0	866	22	0
1	E	874	0	866	20	0
2	B	924	0	882	38	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	924	0	880	36	0
2	F	924	0	880	35	0
All	All	5394	0	5240	164	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 15.

The worst 5 of 164 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:B:35:ASN:HB2	2:B:97:ALA:HB3	1.46	0.95
2:D:35:ASN:HB2	2:D:97:ALA:HB3	1.48	0.95
2:F:35:ASN:HB2	2:F:97:ALA:HB3	1.52	0.90
2:F:97:ALA:HA	2:F:110:TYR:HB2	1.66	0.77
2:F:100:SER:HB3	2:F:101:PRO:HA	1.67	0.77

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	113/138 (82%)	109 (96%)	3 (3%)	1 (1%)	17	56
1	C	113/138 (82%)	110 (97%)	2 (2%)	1 (1%)	17	56
1	E	113/138 (82%)	110 (97%)	3 (3%)	0	100	100
2	B	119/131 (91%)	104 (87%)	11 (9%)	4 (3%)	3	28
2	D	119/131 (91%)	106 (89%)	10 (8%)	3 (2%)	5	34
2	F	119/131 (91%)	104 (87%)	13 (11%)	2 (2%)	9	42
All	All	696/807 (86%)	643 (92%)	42 (6%)	11 (2%)	9	43



5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	56	VAL
1	C	56	VAL
2	B	102	TYR
2	D	100	SER
2	F	100	SER

### 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	99/108 (92%)	97 (98%)	2 (2%)	55	79
1	C	99/108 (92%)	97 (98%)	2 (2%)	55	79
1	E	99/108 (92%)	98 (99%)	1 (1%)	76	88
2	B	101/109 (93%)	97 (96%)	4 (4%)	31	64
2	D	101/109 (93%)	97 (96%)	4 (4%)	31	64
2	F	101/109 (93%)	98 (97%)	3 (3%)	41	71
All	All	600/651 (92%)	584 (97%)	16 (3%)	44	73

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	111	LEU
2	D	12	VAL
1	E	111	LEU
1	C	22	SER
2	F	100	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
2	F	5	GLN

### 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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	115/138 (83%)	0.71	11 (9%) 8 8	67, 86, 102, 114	0
1	C	115/138 (83%)	0.77	20 (17%) 1 1	68, 90, 106, 114	0
1	E	115/138 (83%)	0.71	13 (11%) 5 6	72, 88, 103, 114	0
2	B	121/131 (92%)	0.66	14 (11%) 4 5	75, 92, 110, 121	0
2	D	121/131 (92%)	0.73	15 (12%) 4 5	73, 92, 112, 131	0
2	F	121/131 (92%)	1.03	21 (17%) 1 1	71, 91, 111, 119	0
All	All	708/807 (87%)	0.77	94 (13%) 3 4	67, 90, 109, 131	0

The worst 5 of 94 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	100	SER	10.4
2	F	45	LEU	8.6
1	C	97	SER	7.2
2	F	103	SER	6.5
2	F	101	PRO	6.0

### 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 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.