



wwPDB X-ray Structure Validation Summary Report ⓘ

May 15, 2020 – 11:39 am BST

PDB ID : 3LH2
Title : Crystal structure of HIV epitope-scaffold 4E10_1VI7A_S0_002_N 4E10 Fv complex
Authors : Holmes, M.A.
Deposited on : 2010-01-21
Resolution : 2.65 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 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

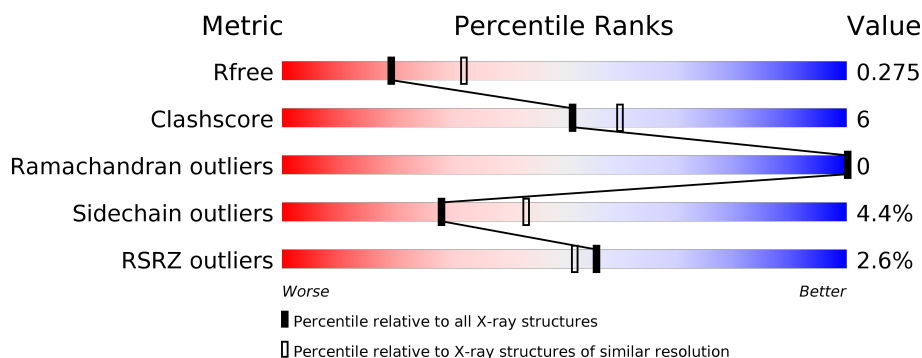
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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	1332 (2.68-2.64)
Clashscore	141614	1374 (2.68-2.64)
Ramachandran outliers	138981	1349 (2.68-2.64)
Sidechain outliers	138945	1349 (2.68-2.64)
RSRZ outliers	127900	1318 (2.68-2.64)

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 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	S	76	<div> <div>5%</div> <div> <div></div> <div>66%</div> <div>17%</div> <div>•</div> <div>16%</div> </div> </div>
1	T	76	<div> <div>75%</div> <div>9%</div> <div>•</div> <div>12%</div> </div>
1	U	76	<div> <div>76%</div> <div>12%</div> <div>•</div> <div>11%</div> </div>
1	V	76	<div> <div>7%</div> <div>76%</div> <div>11%</div> <div>•</div> <div>11%</div> </div>
2	H	137	<div> <div>3%</div> <div>80%</div> <div>12%</div> <div>7%</div> </div>
2	I	137	<div> <div>4%</div> <div>85%</div> <div>7%</div> <div>•</div> <div>7%</div> </div>

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Mol	Chain	Length	Quality of chain
2	J	137	<div><div><div></div><div></div><div></div></div><div>2%</div><div>79%</div><div>11%</div><div>9%</div></div>
2	K	137	<div><div><div></div><div></div><div></div></div><div>%</div><div>84%</div><div>7%</div><div>8%</div></div>
3	L	114	<div><div><div></div><div></div><div></div></div><div>3%</div><div>81%</div><div>16%</div><div></div></div>
3	M	114	<div><div><div></div><div></div><div></div></div><div></div><div>78%</div><div>17%</div><div>5%</div></div>
3	N	114	<div><div><div></div><div></div><div></div></div><div>3%</div><div>82%</div><div>15%</div><div></div></div>
3	O	114	<div><div><div></div><div></div><div></div></div><div>2%</div><div>82%</div><div>14%</div><div></div></div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 9151 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 4E10_1VI7A_S0_002_N (T88).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	S	64	Total	C	N	O	0	0	0
			488	323	76	89			
1	T	67	Total	C	N	O	0	1	0
			508	336	79	93			
1	V	68	Total	C	N	O	0	0	0
			498	330	78	90			
1	U	68	Total	C	N	O	0	0	0
			511	336	81	94			

- Molecule 2 is a protein called Fv 4E10 heavy chain.

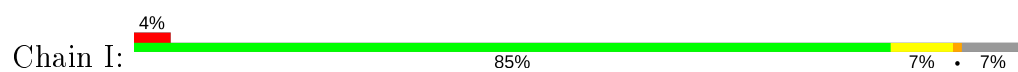
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	127	Total	C	N	O	S	0	0	0
			946	600	164	179	3			
2	I	127	Total	C	N	O	S	0	0	0
			958	603	172	180	3			
2	K	126	Total	C	N	O	S	0	1	0
			928	593	156	176	3			
2	J	125	Total	C	N	O	S	0	1	0
			911	580	155	173	3			

- Molecule 3 is a protein called Fv 4E10 light chain.

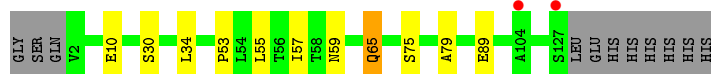
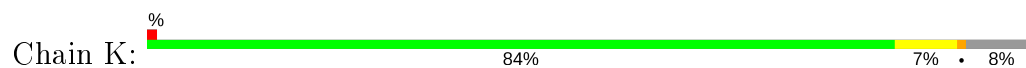
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	110	Total	C	N	O	S	0	0	0
			823	512	144	165	2			
3	M	108	Total	C	N	O	S	0	1	0
			813	507	143	161	2			
3	O	110	Total	C	N	O	S	0	0	0
			819	510	142	165	2			
3	N	110	Total	C	N	O	S	0	0	0
			816	510	140	164	2			

- Molecule 4 is water.

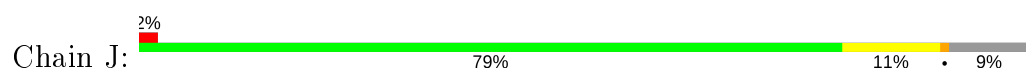
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	S	5	Total 5	O 5	0	0
4	H	16	Total 16	O 16	0	0
4	T	9	Total 9	O 9	0	0
4	I	10	Total 10	O 10	0	0
4	V	5	Total 5	O 5	0	0
4	K	13	Total 13	O 13	0	0
4	L	14	Total 14	O 14	0	0
4	M	11	Total 11	O 11	0	0
4	O	15	Total 15	O 15	0	0
4	U	7	Total 7	O 7	0	0
4	N	15	Total 15	O 15	0	0
4	J	12	Total 12	O 12	0	0



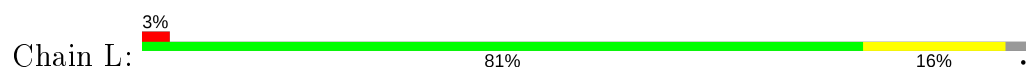
- Molecule 2: Fv 4E10 heavy chain



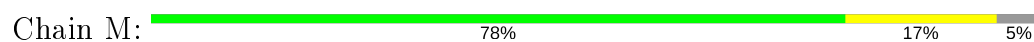
- Molecule 2: Fv 4E10 heavy chain



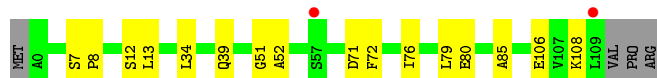
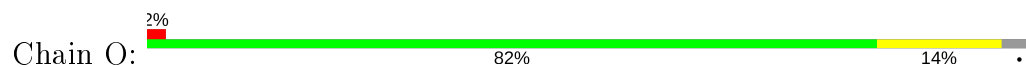
- Molecule 3: Fv 4E10 light chain



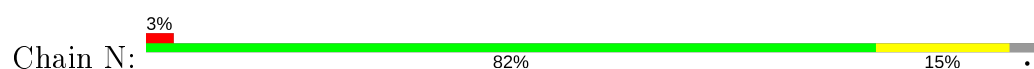
- Molecule 3: Fv 4E10 light chain



- Molecule 3: Fv 4E10 light chain



- Molecule 3: Fv 4E10 light chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	75.85Å 145.95Å 78.55Å 90.00° 92.43° 90.00°	Depositor
Resolution (Å)	26.70 – 2.65 26.70 – 2.65	Depositor EDS
% Data completeness (in resolution range)	98.5 (26.70-2.65) 98.5 (26.70-2.65)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.55 (at 2.64Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.222 , 0.270 0.231 , 0.275	Depositor DCC
R_{free} test set	2478 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	45.1	Xtriage
Anisotropy	0.079	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 33.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for l,k,-h 0.050 for h,-k,-l 0.019 for l,-k,h	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	9151	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.77% 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	S	0.32	0/495	0.47	0/671
1	T	0.31	0/520	0.49	0/709
1	U	0.33	0/520	0.47	0/709
1	V	0.31	0/507	0.49	0/692
2	H	0.34	0/968	0.50	0/1318
2	I	0.33	0/981	0.49	0/1334
2	J	0.31	0/935	0.48	0/1275
2	K	0.34	0/953	0.51	0/1300
3	L	0.36	0/839	0.51	0/1137
3	M	0.34	0/832	0.50	0/1127
3	N	0.34	0/832	0.49	0/1128
3	O	0.36	0/835	0.50	0/1132
All	All	0.33	0/9217	0.49	0/12532

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	S	488	0	486	12	0
1	T	508	0	509	14	0
1	U	511	0	509	13	0
1	V	498	0	486	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	H	946	0	912	11	0
2	I	958	0	931	5	0
2	J	911	0	882	11	0
2	K	928	0	902	8	0
3	L	823	0	792	8	0
3	M	813	0	790	11	0
3	N	816	0	788	7	0
3	O	819	0	784	8	0
4	H	16	0	0	0	0
4	I	10	0	0	0	0
4	J	12	0	0	0	0
4	K	13	0	0	0	0
4	L	14	0	0	0	0
4	M	11	0	0	1	0
4	N	15	0	0	0	0
4	O	15	0	0	0	0
4	S	5	0	0	1	0
4	T	9	0	0	1	0
4	U	7	0	0	1	0
4	V	5	0	0	0	0
All	All	9151	0	8771	99	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 6.

The worst 5 of 99 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)
3:N:34:LEU:HD13	3:N:72:PHE:CD1	2.15	0.81
2:H:18:VAL:HG12	2:H:86:LEU:HD11	1.65	0.78
3:L:38:GLN:HB2	3:L:48:LEU:HD11	1.70	0.74
1:T:22:ILE:HD11	1:U:68:LEU:HD21	1.71	0.72
1:V:64:SER:HB3	1:V:68:LEU:HD22	1.71	0.71

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	S	58/76 (76%)	58 (100%)	0	0	100	100
1	T	66/76 (87%)	66 (100%)	0	0	100	100
1	U	66/76 (87%)	64 (97%)	2 (3%)	0	100	100
1	V	66/76 (87%)	65 (98%)	1 (2%)	0	100	100
2	H	123/137 (90%)	119 (97%)	4 (3%)	0	100	100
2	I	123/137 (90%)	122 (99%)	1 (1%)	0	100	100
2	J	124/137 (90%)	123 (99%)	1 (1%)	0	100	100
2	K	125/137 (91%)	122 (98%)	3 (2%)	0	100	100
3	L	108/114 (95%)	104 (96%)	4 (4%)	0	100	100
3	M	107/114 (94%)	103 (96%)	4 (4%)	0	100	100
3	N	108/114 (95%)	103 (95%)	5 (5%)	0	100	100
3	O	108/114 (95%)	105 (97%)	3 (3%)	0	100	100
All	All	1182/1308 (90%)	1154 (98%)	28 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	S	49/62 (79%)	46 (94%)	3 (6%)	18	29
1	T	50/62 (81%)	46 (92%)	4 (8%)	12	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	U	50/62 (81%)	47 (94%)	3 (6%)	19	30
1	V	45/62 (73%)	42 (93%)	3 (7%)	16	25
2	H	96/108 (89%)	93 (97%)	3 (3%)	40	57
2	I	100/108 (93%)	96 (96%)	4 (4%)	31	47
2	J	90/108 (83%)	87 (97%)	3 (3%)	38	54
2	K	93/108 (86%)	88 (95%)	5 (5%)	22	34
3	L	87/94 (93%)	84 (97%)	3 (3%)	37	53
3	M	87/94 (93%)	85 (98%)	2 (2%)	50	68
3	N	86/94 (92%)	81 (94%)	5 (6%)	20	31
3	O	86/94 (92%)	83 (96%)	3 (4%)	36	52
All	All	919/1056 (87%)	878 (96%)	41 (4%)	28	42

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	K	65[A]	GLN
3	L	20	THR
3	N	61	ASP
2	K	65[B]	GLN
2	K	75	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
2	H	65	GLN
1	T	35	ASN
2	I	133	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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, 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	S	64/76 (84%)	0.24	4 (6%) 20 17	46, 61, 86, 93	0
1	T	67/76 (88%)	0.00	0 100 100	44, 58, 70, 75	0
1	U	68/76 (89%)	0.11	0 100 100	45, 63, 79, 82	0
1	V	68/76 (89%)	0.19	5 (7%) 14 12	48, 60, 81, 84	0
2	H	127/137 (92%)	0.09	4 (3%) 49 45	44, 56, 68, 82	0
2	I	127/137 (92%)	0.16	5 (3%) 39 35	44, 56, 69, 81	0
2	J	125/137 (91%)	0.10	3 (2%) 59 54	45, 58, 68, 71	0
2	K	126/137 (91%)	0.08	2 (1%) 72 69	44, 55, 65, 71	0
3	L	110/114 (96%)	0.07	3 (2%) 54 50	44, 55, 64, 69	0
3	M	108/114 (94%)	0.02	0 100 100	44, 54, 62, 67	0
3	N	110/114 (96%)	-0.01	3 (2%) 54 50	46, 55, 65, 71	0
3	O	110/114 (96%)	0.00	2 (1%) 68 65	44, 54, 64, 71	0
All	All	1210/1308 (92%)	0.08	31 (2%) 56 52	44, 56, 74, 93	0

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	V	7	LEU	4.1
3	O	109	LEU	3.8
2	H	27	GLY	3.7
2	I	76	THR	3.2
1	V	30	ASP	2.9

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.