wwPDB X-ray Structure Validation Summary Report (i)

Feb 2, 2017 – 11:26 AM EST

PDB ID	:	1E4X
Title	:	crossreactive binding of a circularized peptide to an anti-TGFalpha antibody Fab-fragment
Authors	:	Hahn, M.; Winkler, D.; Misselwitz, R.; Wessner, H.; Welfle, K.; Zahn, G.; Schneider-Mergener, J.; Hoehne, W.
Deposited on	:	2000-07-12
Resolution	:	1.90 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

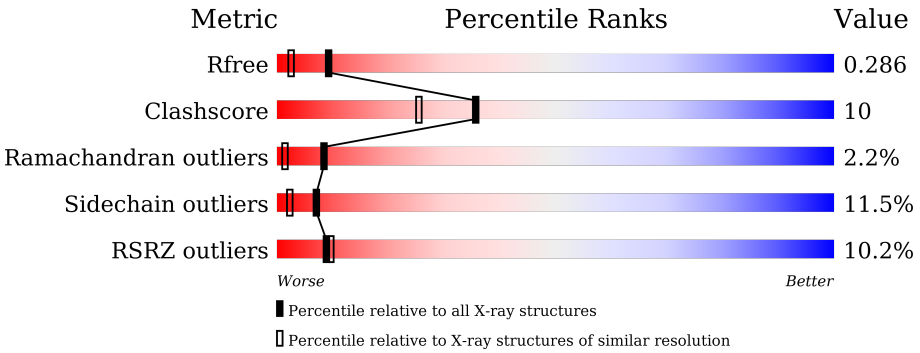
MolProbity	:	4.02b-467
Mogul	:	unknown
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20028442
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20028442

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (1.90-1.90)

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 <=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	H	217	16% 60% 28% 10%
2	I	217	12% 71% 17% 9%
3	L	214	8% 74% 22%
3	M	214	5% 74% 21%
4	P	7	71% 29%
4	Q	7	86% 14%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7115 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 TAB2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	216	Total	C	N	O	S	0	0	0
			1634	1032	270	325	7			

- Molecule 2 is a protein called TAB2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	I	217	Total	C	N	O	S	0	0	0
			1644	1040	271	326	7			

- Molecule 3 is a protein called TAB2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	214	Total	C	N	O	S	0	0	0
			1657	1032	276	342	7			
3	M	214	Total	C	N	O	S	0	0	0
			1657	1032	276	342	7			

- Molecule 4 is a protein called CYCLIC PEPTIDE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	P	7	Total	C	N	O	0	0	0
			58	36	10	12			
4	Q	7	Total	C	N	O	0	0	0
			58	36	10	12			

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	67	Total	O	0	0
			67	67		
5	I	91	Total	O	0	0
			91	91		

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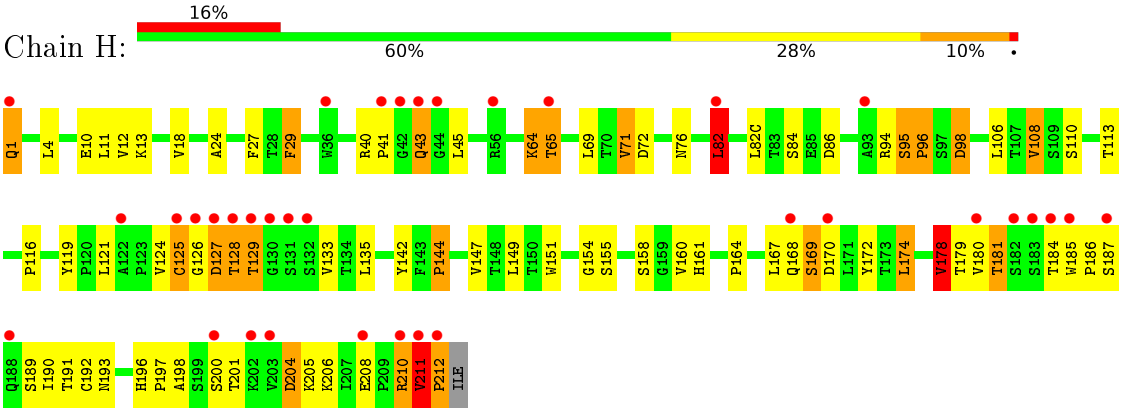
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	L	130	Total O 130 130	0	0
5	M	116	Total O 116 116	0	0
5	P	2	Total O 2 2	0	0
5	Q	1	Total O 1 1	0	0

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.

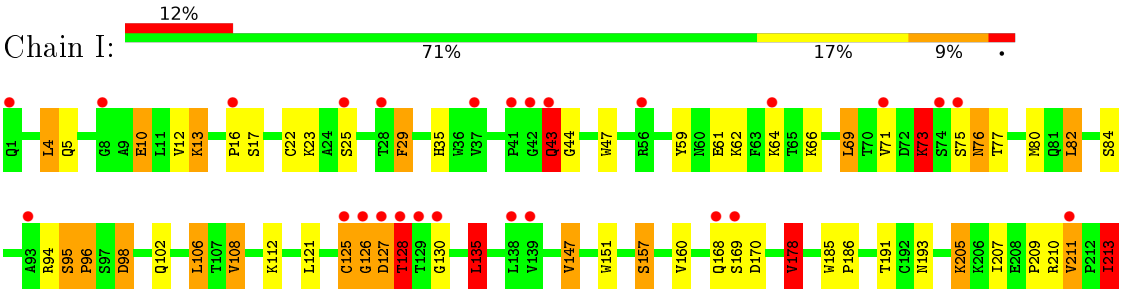
- Molecule 1: TAB2

Chain H:



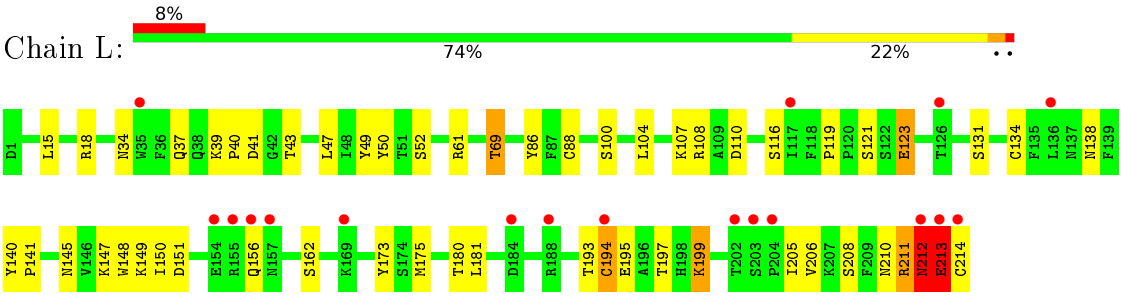
- Molecule 2: TAB2

Chain I:



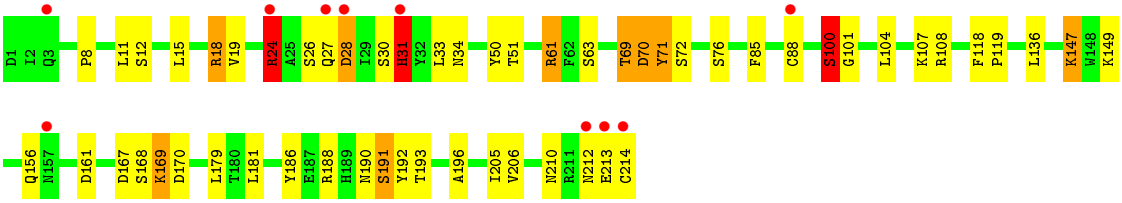
- Molecule 3: TAB2

Chain L:



- Molecule 3: TAB2

Chain M:



• Molecule 4: CYCLIC PEPTIDE

Chain P:

• Molecule 4: CYCLIC PEPTIDE

Chain Q:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	173.82Å 45.09Å 120.41Å 90.00° 99.13° 90.00°	Depositor
Resolution (Å)	20.00 – 1.90 19.90 – 1.90	Depositor EDS
% Data completeness (in resolution range)	94.6 (20.00-1.90) 92.8 (19.90-1.90)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.65 (at 1.90Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.245 , 0.311 0.231 , 0.286	Depositor DCC
R_{free} test set	3426 reflections (5.30%)	DCC
Wilson B-factor (Å^2)	23.9	Xtriage
Anisotropy	0.151	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 46.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	7115	wwPDB-VP
Average B, all atoms (Å^2)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.04% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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	H	0.65	0/1677	1.54	24/2293 (1.0%)
2	I	0.68	0/1688	1.58	30/2309 (1.3%)
3	L	0.69	0/1694	1.48	21/2298 (0.9%)
3	M	0.72	0/1694	1.56	19/2298 (0.8%)
4	P	0.99	0/59	1.55	2/78 (2.6%)
4	Q	0.94	1/59 (1.7%)	1.18	0/78
All	All	0.69	1/6871 (0.0%)	1.54	96/9354 (1.0%)

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
1	H	0	2
2	I	0	2
All	All	0	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	Q	7	ASP	C-OXT	5.64	1.34	1.23

The worst 5 of 96 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	M	18	ARG	CD-NE-CZ	14.59	144.02	123.60
3	M	31	HIS	CA-CB-CG	13.00	135.70	113.60
3	M	24	ARG	NE-CZ-NH1	12.48	126.54	120.30
2	I	127	ASP	C-N-CA	11.41	150.24	121.70
2	I	98	ASP	CB-CG-OD2	-10.89	108.50	118.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	H	95	SER	Mainchain,Peptide
2	I	95	SER	Mainchain,Peptide

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	H	1634	0	1603	40	0
2	I	1644	0	1615	41	0
3	L	1657	0	1576	27	0
3	M	1657	0	1576	28	0
4	P	58	0	51	0	0
4	Q	58	0	51	0	0
5	H	67	0	0	1	0
5	I	91	0	0	3	0
5	L	130	0	0	3	0
5	M	116	0	0	6	0
5	P	2	0	0	0	0
5	Q	1	0	0	0	0
All	All	7115	0	6472	128	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 10.

The worst 5 of 128 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:H:211:VAL:HG22	1:H:212:PRO:HD3	1.45	0.97
1:H:191:THR:HG22	1:H:206:LYS:HG3	1.51	0.91
2:I:126:GLY:H	2:I:211:VAL:HG21	1.35	0.89
2:I:125:CYS:HA	2:I:211:VAL:HG11	1.64	0.79
3:M:8:PRO:HG3	3:M:11:LEU:HD13	1.65	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	H	214/217 (99%)	191 (89%)	15 (7%)	8 (4%)	4 0
2	I	215/217 (99%)	199 (93%)	9 (4%)	7 (3%)	5 0
3	L	212/214 (99%)	205 (97%)	5 (2%)	2 (1%)	21 9
3	M	212/214 (99%)	206 (97%)	4 (2%)	2 (1%)	21 9
4	P	5/7 (71%)	5 (100%)	0	0	100 100
4	Q	5/7 (71%)	5 (100%)	0	0	100 100
All	All	863/876 (98%)	811 (94%)	33 (4%)	19 (2%)	8 1

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	126	GLY
1	H	129	THR
1	H	211	VAL
2	I	126	GLY
2	I	128	THR

5.3.2 Protein sidechains (i)

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	H	188/189 (100%)	154 (82%)	34 (18%)	2 0
2	I	190/190 (100%)	163 (86%)	27 (14%)	4 1
3	L	190/190 (100%)	180 (95%)	10 (5%)	28 16

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	M	190/190 (100%)	172 (90%)	18 (10%)	11 4
4	P	7/7 (100%)	7 (100%)	0	100 100
4	Q	7/7 (100%)	7 (100%)	0	100 100
All	All	772/773 (100%)	683 (88%)	89 (12%)	7 2

5 of 89 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	I	62	LYS
2	I	108	VAL
3	M	156	GLN
2	I	69	LEU
2	I	84	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
2	I	43	GLN
2	I	102	GLN
3	L	212	ASN
2	I	5	GLN
3	M	27	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

There are no ligands in this entry.

5.7 Other polymers

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

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, 95^{th} 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	H	216/217 (99%)	0.80	35 (16%) 3 3	23, 38, 58, 79	0
2	I	217/217 (100%)	0.85	26 (11%) 6 6	21, 36, 59, 79	0
3	L	214/214 (100%)	0.60	18 (8%) 14 15	21, 35, 53, 69	0
3	M	214/214 (100%)	0.32	10 (4%) 35 38	21, 32, 47, 68	0
4	P	7/7 (100%)	-0.03	0 100 100	23, 25, 27, 27	0
4	Q	7/7 (100%)	0.56	0 100 100	34, 35, 38, 42	0
All	All	875/876 (99%)	0.64	89 (10%) 9 10	21, 35, 55, 79	0

The worst 5 of 89 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	L	214	CYS	12.9
2	I	126	GLY	11.2
2	I	128	THR	10.9
1	H	129	THR	8.8
1	H	211	VAL	8.2

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

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.