wwPDB X-ray Structure Validation Summary Report (i)

Jun 13, 2024 – 11:11 AM EDT

PDB ID	:	1MK9
Title	:	CRYSTAL STRUCTURE OF AN INTEGRIN BETA3-TALIN CHIMERA
Authors	:	Garcia-Alvarez, B.; De Pereda, J.M.; Calderwood, D.A.; Ulmer, T.S.; Critchley, D.; Campbell, I.D.; Ginsberg, M.H.; Liddington, R.C.
Deposited on	:	2002-08-28
Resolution	:	2.80 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 (i) 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 (i)) were used in the production of this report:

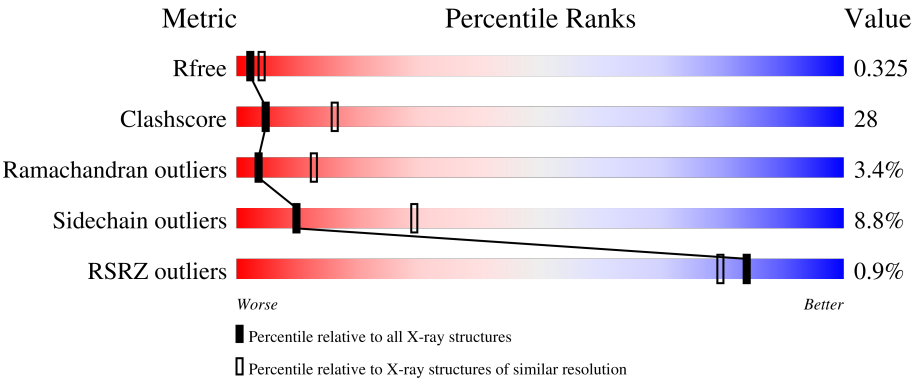
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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 <=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	16	6%, 19%, 50%, 12%, 19%
1	C	16	50%, 44%, 6%
1	E	16	44%, 38%, 6%, 12%
1	G	16	44%, 38%, 6%, 12%
2	B	192	56%, 37%, . . .

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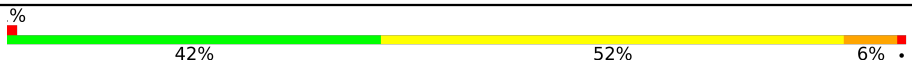
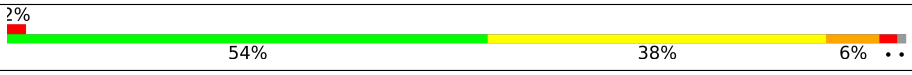
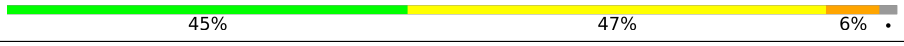
Mol	Chain	Length	Quality of chain
2	D	192	
2	F	192	
2	H	192	

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 6640 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 Integrin Beta3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	13	Total	C	N	O	S	0	0	0
			108	69	17	21	1			
1	C	15	Total	C	N	O	S	0	0	0
			124	78	21	24	1			
1	E	14	Total	C	N	O	S	0	0	0
			118	75	20	22	1			
1	G	14	Total	C	N	O	S	0	0	0
			118	75	20	22	1			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	735	GLY	-	CLONING ARTIFACT	UNP P05106
A	736	SER	-	CLONING ARTIFACT	UNP P05106
A	737	HIS	-	CLONING ARTIFACT	UNP P05106
A	738	MET	-	CLONING ARTIFACT	UNP P05106
C	735	GLY	-	CLONING ARTIFACT	UNP P05106
C	736	SER	-	CLONING ARTIFACT	UNP P05106
C	737	HIS	-	CLONING ARTIFACT	UNP P05106
C	738	MET	-	CLONING ARTIFACT	UNP P05106
E	735	GLY	-	CLONING ARTIFACT	UNP P05106
E	736	SER	-	CLONING ARTIFACT	UNP P05106
E	737	HIS	-	CLONING ARTIFACT	UNP P05106
E	738	MET	-	CLONING ARTIFACT	UNP P05106
G	735	GLY	-	CLONING ARTIFACT	UNP P05106
G	736	SER	-	CLONING ARTIFACT	UNP P05106
G	737	HIS	-	CLONING ARTIFACT	UNP P05106
G	738	MET	-	CLONING ARTIFACT	UNP P05106

- Molecule 2 is a protein called TALIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	187	Total	C	N	O	S	26	0	0
			1515	975	256	276	8			
2	D	192	Total	C	N	O	S	26	0	0
			1557	1003	264	282	8			
2	F	190	Total	C	N	O	S	30	0	0
			1541	991	262	280	8			
2	H	188	Total	C	N	O	S	12	0	0
			1528	984	258	279	7			

- Molecule 3 is water.

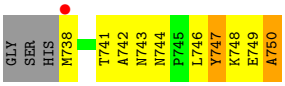
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	9	Total	O	0	0
			9	9		
3	C	2	Total	O	0	0
			2	2		
3	D	8	Total	O	0	0
			8	8		
3	F	7	Total	O	0	0
			7	7		
3	G	1	Total	O	0	0
			1	1		
3	H	4	Total	O	0	0
			4	4		

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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: Integrin Beta3

Chain A:

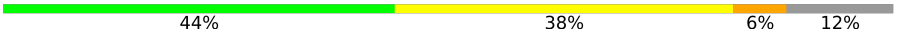


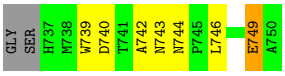
• Molecule 1: Integrin Beta3

Chain C:

• Molecule 1: Integrin Beta3

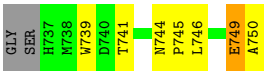
Chain E:





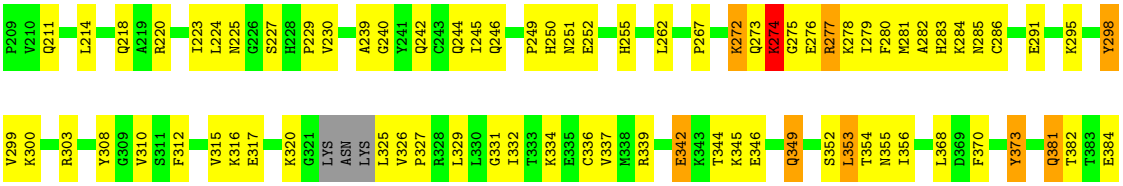
• Molecule 1: Integrin Beta3

Chain G:



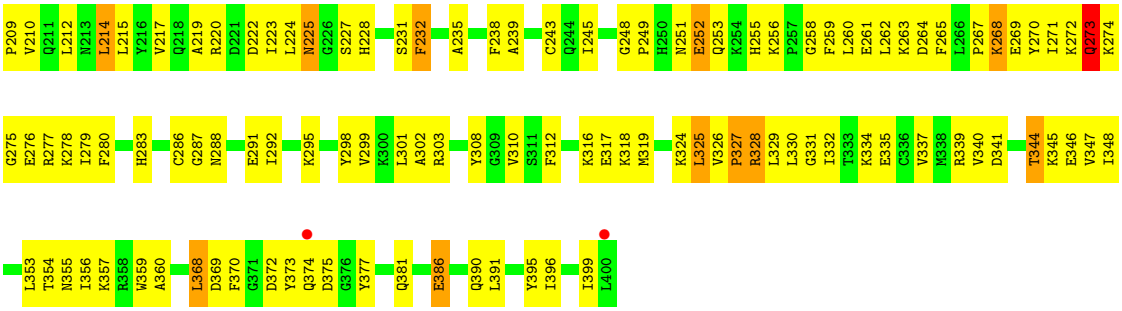
• Molecule 2: TALIN

Chain B:



• Molecule 2: TALIN

Chain D:

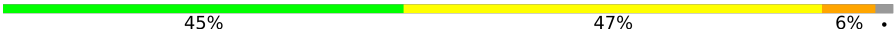


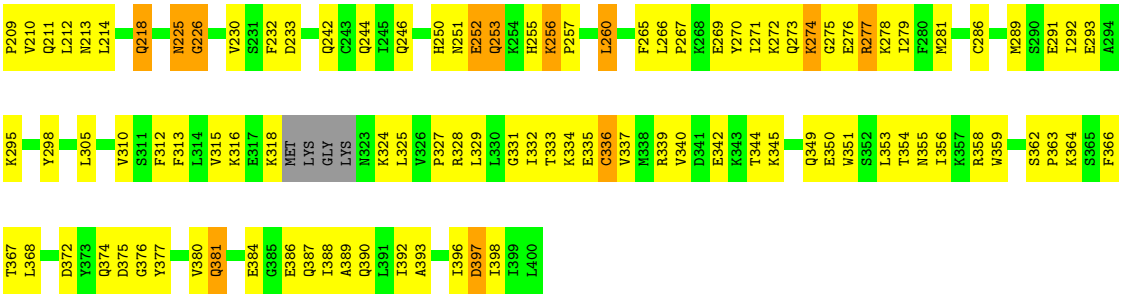
• Molecule 2: TALIN

Chain F:

• Molecule 2: TALIN

Chain H:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	50.26Å 141.76Å 59.60Å 90.00° 90.11° 90.00°	Depositor
Resolution (Å)	29.83 – 2.80 29.83 – 2.80	Depositor EDS
% Data completeness (in resolution range)	91.7 (29.83-2.80) 91.4 (29.83-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$< I/\sigma(I) >$ [1]	3.68 (at 2.80Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.242 , 0.327 0.242 , 0.325	Depositor DCC
R_{free} test set	1387 reflections (7.37%)	wwPDB-VP
Wilson B-factor (Å^2)	33.5	Xtriage
Anisotropy	0.488	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 5.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.43$, $< L^2 > = 0.25$	Xtriage
Estimated twinning fraction	0.369 for h,-k,-l	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	6640	wwPDB-VP
Average B, all atoms (Å^2)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.43% 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	A	0.63	0/111	1.13	1/151 (0.7%)
1	C	0.43	0/128	0.85	0/174
1	E	0.61	0/122	1.11	1/166 (0.6%)
1	G	0.54	0/122	0.88	0/166
2	B	0.49	0/1547	0.73	1/2077 (0.0%)
2	D	0.44	0/1590	0.66	0/2135
2	F	0.52	0/1574	0.85	5/2113 (0.2%)
2	H	0.47	0/1560	0.71	2/2095 (0.1%)
All	All	0.49	0/6754	0.76	10/9077 (0.1%)

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	F	277	ARG	NE-CZ-NH2	-11.70	114.45	120.30
2	F	277	ARG	NE-CZ-NH1	9.14	124.87	120.30
1	E	749	GLU	N-CA-C	7.06	130.07	111.00
2	F	277	ARG	CG-CD-NE	-6.95	97.22	111.80
1	A	750	ALA	N-CA-C	-6.26	94.09	111.00

There are no chirality outliers.

There are no planarity outliers.

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	108	0	97	14	0
1	C	124	0	109	4	1
1	E	118	0	104	7	0
1	G	118	0	104	7	0
2	B	1515	0	1525	66	0
2	D	1557	0	1580	107	0
2	F	1541	0	1558	81	4
2	H	1528	0	1541	98	3
3	B	9	0	0	0	0
3	C	2	0	0	0	0
3	D	8	0	0	1	0
3	F	7	0	0	0	0
3	G	1	0	0	0	0
3	H	4	0	0	0	0
All	All	6640	0	6618	360	4

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 28.

The worst 5 of 360 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:G:749:GLU:O	2:H:209:PRO:HD3	1.56	1.06
2:B:277:ARG:HH11	2:B:277:ARG:HB3	1.21	1.04
2:F:262:LEU:HD21	2:F:276:GLU:CD	1.79	1.03
2:F:316:LYS:HB3	2:F:325:LEU:HB3	1.42	1.00
2:H:277:ARG:O	2:H:281:MET:HG3	1.63	0.98

All (4) 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)
2:F:323:ASN:ND2	2:H:214:LEU:CD2[1_455]	1.55	0.65
2:F:323:ASN:ND2	2:H:214:LEU:CD1[1_455]	1.89	0.31
2:F:323:ASN:ND2	2:H:214:LEU:CG[1_455]	1.93	0.27
1:C:740:ASP:OD1	2:F:364:LYS:NZ[2_556]	2.06	0.14

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	11/16 (69%)	9 (82%)	1 (9%)	1 (9%)	1 1
1	C	13/16 (81%)	10 (77%)	3 (23%)	0	100 100
1	E	12/16 (75%)	10 (83%)	1 (8%)	1 (8%)	1 2
1	G	12/16 (75%)	9 (75%)	2 (17%)	1 (8%)	1 2
2	B	183/192 (95%)	161 (88%)	18 (10%)	4 (2%)	6 22
2	D	190/192 (99%)	156 (82%)	28 (15%)	6 (3%)	4 13
2	F	188/192 (98%)	165 (88%)	18 (10%)	5 (3%)	5 17
2	H	184/192 (96%)	143 (78%)	32 (17%)	9 (5%)	2 7
All	All	793/832 (95%)	663 (84%)	103 (13%)	27 (3%)	3 13

5 of 27 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	232	PHE
2	D	373	TYR
1	E	749	GLU
2	H	334	LYS
2	H	376	GLY

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	A	11/13 (85%)	9 (82%)	2 (18%)	1 5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	C	13/13 (100%)	12 (92%)	1 (8%)	13 35
1	E	12/13 (92%)	11 (92%)	1 (8%)	11 32
1	G	12/13 (92%)	11 (92%)	1 (8%)	11 32
2	B	164/169 (97%)	151 (92%)	13 (8%)	12 34
2	D	169/169 (100%)	157 (93%)	12 (7%)	14 39
2	F	167/169 (99%)	146 (87%)	21 (13%)	4 14
2	H	166/169 (98%)	154 (93%)	12 (7%)	14 38
All	All	714/728 (98%)	651 (91%)	63 (9%)	10 29

5 of 63 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	740	ASP
2	H	256	LYS
2	F	269	GLU
2	H	253	GLN
2	H	336	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
2	F	225	ASN
2	F	349	GLN
2	H	253	GLN
2	F	285	ASN
2	F	374	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 monosaccharides 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, 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	A	13/16 (81%)	0.09	1 (7%) 13 7	18, 28, 45, 81	0
1	C	15/16 (93%)	-0.38	0 100 100	13, 16, 34, 34	0
1	E	14/16 (87%)	0.34	0 100 100	31, 43, 67, 71	0
1	G	14/16 (87%)	-0.49	0 100 100	13, 17, 45, 46	0
2	B	187/192 (97%)	-0.40	0 100 100	13, 19, 32, 47	6 (3%)
2	D	192/192 (100%)	-0.15	2 (1%) 82 77	13, 31, 52, 71	6 (3%)
2	F	190/192 (98%)	-0.25	4 (2%) 63 54	13, 21, 42, 65	8 (4%)
2	H	188/192 (97%)	-0.19	0 100 100	13, 27, 47, 78	3 (1%)
All	All	813/832 (97%)	-0.24	7 (0%) 84 80	13, 23, 48, 81	23 (2%)

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	323	ASN	3.8
2	F	321	GLY	3.4
2	F	275	GLY	2.6
2	F	276	GLU	2.5
1	A	738	MET	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 monosaccharides in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.