



wwPDB X-ray Structure Validation Summary Report ⓘ

May 21, 2020 – 02:03 pm BST

PDB ID : 3KBT
Title : Crystal structure of the ankyrin binding domain of human erythroid beta spectrin (repeats 13-15) in complex with the spectrin binding domain of human erythroid ankyrin (ZU5-ANK)
Authors : Ipsaro, J.J.; Mondragon, A.
Deposited on : 2009-10-20
Resolution : 2.75 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

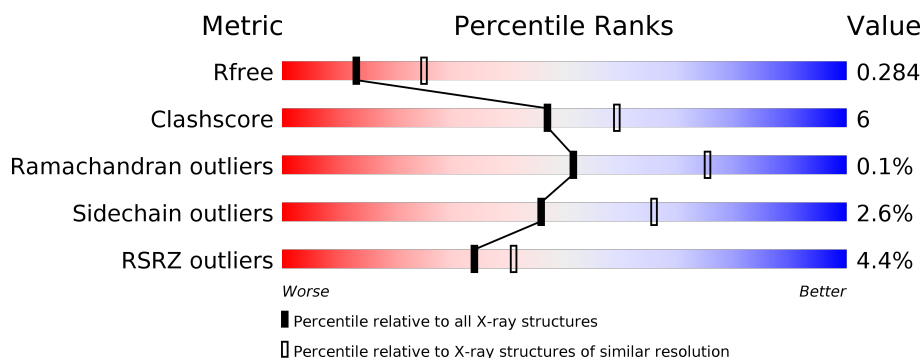
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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	A	326	<div> <div>5%</div> <div> <div></div> <div>73%</div> <div>13%</div> <div>13%</div> </div> </div>
1	B	326	<div> <div>2%</div> <div> <div></div> <div>76%</div> <div>14%</div> <div>10%</div> </div> </div>
2	C	161	<div> <div>7%</div> <div> <div></div> <div>78%</div> <div>19%</div> <div>•</div> </div> </div>
2	D	161	<div> <div>4%</div> <div> <div></div> <div>81%</div> <div>11%</div> <div>•</div> <div>6%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7076 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 Spectrin beta chain, erythrocyte.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	284	Total	C	N	O	S	0	0	0
			2308	1444	407	452	5			
1	B	294	Total	C	N	O	S	0	0	0
			2377	1486	417	468	6			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1581	SER	-	EXPRESSION TAG	UNP P11277
A	1582	ASN	-	EXPRESSION TAG	UNP P11277
A	1844	ASP	GLU	SEE REMARK 999	UNP P11277
A	1845	VAL	LEU	SEE REMARK 999	UNP P11277
B	1581	SER	-	EXPRESSION TAG	UNP P11277
B	1582	ASN	-	EXPRESSION TAG	UNP P11277
B	1844	ASP	GLU	SEE REMARK 999	UNP P11277
B	1845	VAL	LEU	SEE REMARK 999	UNP P11277

- Molecule 2 is a protein called Ankyrin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	157	Total	C	N	O	S	0	0	0
			1216	765	222	222	7			
2	D	151	Total	C	N	O	S	0	0	0
			1175	743	211	214	7			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	908	SER	-	EXPRESSION TAG	UNP P16157
C	909	ASN	-	EXPRESSION TAG	UNP P16157
C	910	ALA	-	EXPRESSION TAG	UNP P16157
D	908	SER	-	EXPRESSION TAG	UNP P16157

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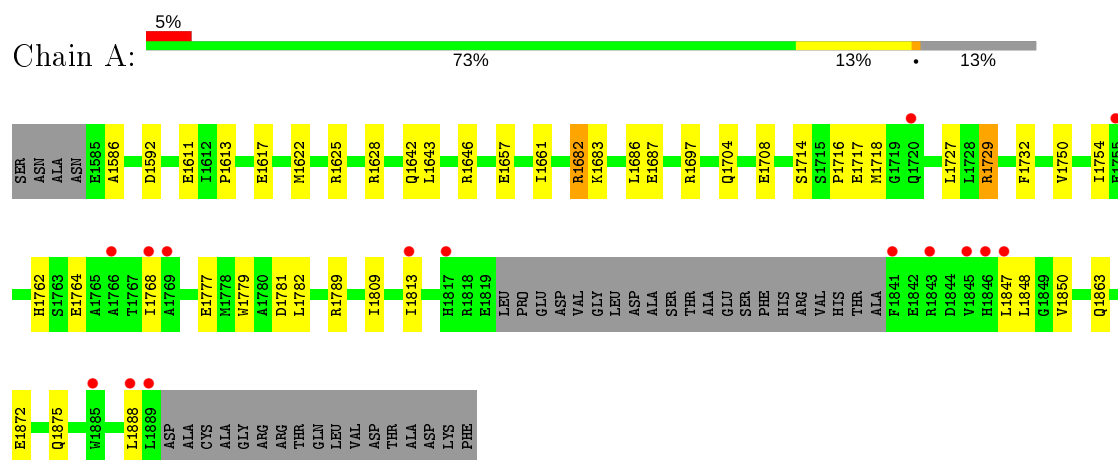
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Chain	Residue	Modelled	Actual	Comment	Reference
D	909	ASN	-	EXPRESSION TAG	UNP P16157
D	910	ALA	-	EXPRESSION TAG	UNP P16157

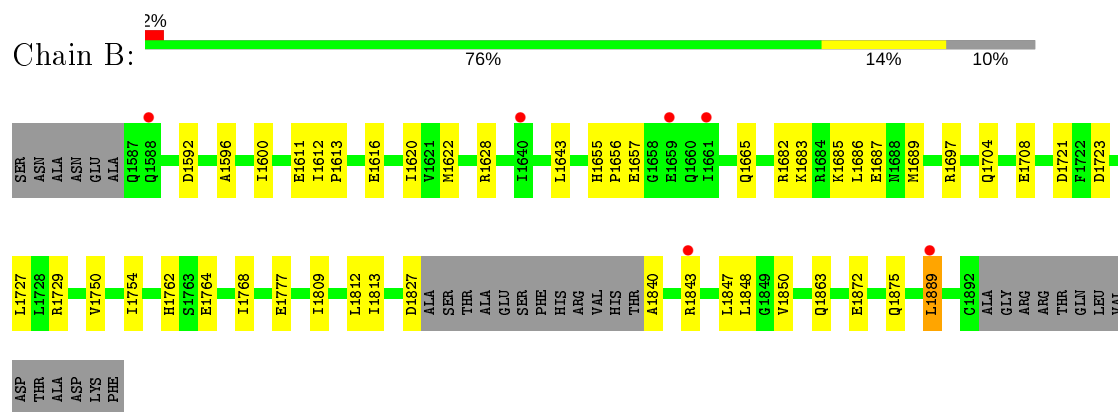
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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 ($\text{RSRZ} > 2$). 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.

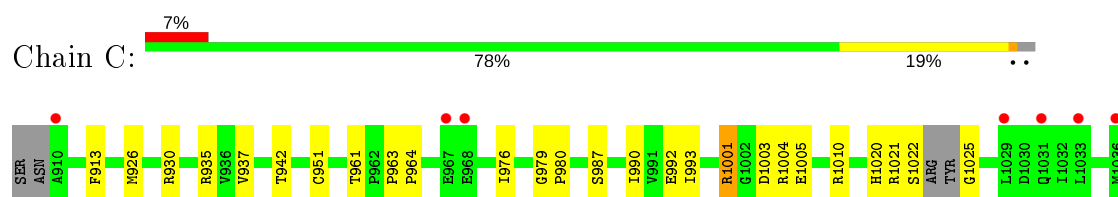
- Molecule 1: Spectrin beta chain, erythrocyte

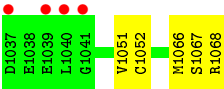


- Molecule 1: Spectrin beta chain, erythrocyte

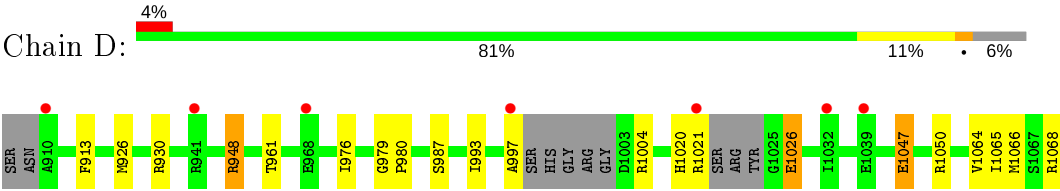


- Molecule 2: Ankyrin-1





● Molecule 2: Ankyrin-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	90.45Å 95.66Å 137.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.82 – 2.75 37.82 – 2.75	Depositor EDS
% Data completeness (in resolution range)	95.7 (37.82-2.75) 95.7 (37.82-2.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.17 (at 2.77Å)	Xtriage
Refinement program	REFMAC 5.5.0088	Depositor
R, R_{free}	0.245 , 0.292 0.238 , 0.284	Depositor DCC
R_{free} test set	1576 reflections (5.19%)	wwPDB-VP
Wilson B-factor (Å ²)	55.9	Xtriage
Anisotropy	0.374	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 32.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7076	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.55% 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	0.73	1/2346 (0.0%)	0.81	9/3161 (0.3%)
1	B	0.72	0/2416	0.80	6/3258 (0.2%)
2	C	0.67	2/1239 (0.2%)	0.78	0/1673
2	D	0.66	0/1196	0.77	0/1615
All	All	0.71	3/7197 (0.0%)	0.79	15/9707 (0.2%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1052	CYS	CB-SG	-6.63	1.71	1.82
1	A	1617	GLU	CG-CD	5.28	1.59	1.51
2	C	951	CYS	CB-SG	-5.19	1.73	1.81

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1628	ARG	NE-CZ-NH1	10.51	125.56	120.30
1	A	1628	ARG	NE-CZ-NH1	-9.99	115.31	120.30
1	A	1697	ARG	NE-CZ-NH1	-7.91	116.35	120.30
1	A	1628	ARG	NE-CZ-NH2	7.66	124.13	120.30
1	A	1697	ARG	NE-CZ-NH2	7.56	124.08	120.30

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	2308	0	2230	30	0
1	B	2377	0	2293	29	1
2	C	1216	0	1238	20	0
2	D	1175	0	1201	12	1
All	All	7076	0	6962	87	1

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 87 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:C:1001:ARG:HH11	2:C:1001:ARG:HG3	1.13	1.05
1:A:1754:ILE:HG23	1:A:1768:ILE:CG2	2.00	0.92
1:B:1754:ILE:HG23	1:B:1768:ILE:CG2	2.05	0.85
1:B:1611:GLU:O	1:B:1622:MET:HE1	1.77	0.84
2:C:1001:ARG:HH11	2:C:1001:ARG:CG	1.93	0.80

All (1) 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)
1:B:1723:ASP:OD2	2:D:1047:GLU:OE2[4_555]	2.19	0.01

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	280/326 (86%)	277 (99%)	3 (1%)	0	100	100
1	B	290/326 (89%)	287 (99%)	3 (1%)	0	100	100
2	C	153/161 (95%)	137 (90%)	16 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	145/161 (90%)	134 (92%)	10 (7%)	1 (1%)	22	39
All	All	868/974 (89%)	835 (96%)	32 (4%)	1 (0%)	51	75

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	1026	GLU

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	236/269 (88%)	231 (98%)	5 (2%)	53	71
1	B	244/269 (91%)	238 (98%)	6 (2%)	47	67
2	C	134/138 (97%)	132 (98%)	2 (2%)	65	78
2	D	130/138 (94%)	124 (95%)	6 (5%)	27	46
All	All	744/814 (91%)	725 (97%)	19 (3%)	46	66

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	1827	ASP
1	B	1889	LEU
2	D	987	SER
1	B	1812	LEU
2	D	1004	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1856	GLN
1	A	1875	GLN
1	B	1875	GLN

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Mol	Chain	Res	Type
1	A	1694	GLN
1	B	1688	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 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	A	284/326 (87%)	0.24	15 (5%) 26 31	18, 33, 46, 51	0
1	B	294/326 (90%)	0.20	6 (2%) 65 73	18, 33, 47, 51	0
2	C	157/161 (97%)	0.42	11 (7%) 16 19	24, 32, 45, 54	0
2	D	151/161 (93%)	0.25	7 (4%) 32 39	24, 31, 45, 54	0
All	All	886/974 (90%)	0.26	39 (4%) 34 41	18, 32, 46, 54	0

The worst 5 of 39 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1843	ARG	6.4
2	C	967	GLU	6.1
2	C	1031	GLN	5.5
2	D	910	ALA	4.6
1	B	1659	GLU	4.5

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.