



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 3, 2021 – 12:25 AM EDT

PDB ID : 3KBU
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), EMTS derivative
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	:	2.23.2
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)	:	2.23.2

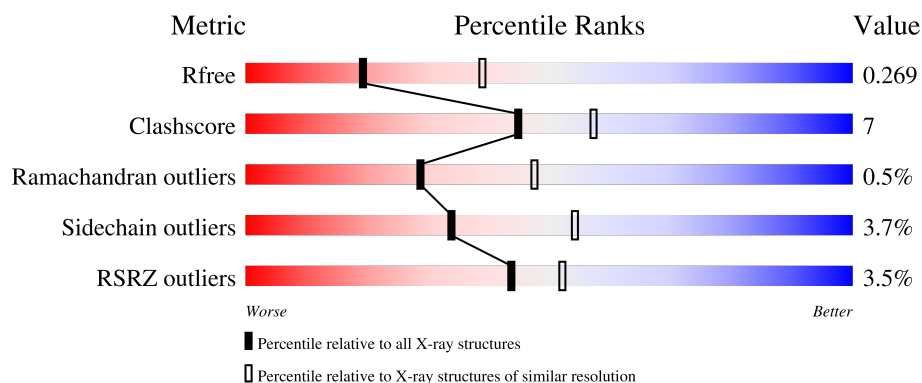
1 Overall quality at a glance

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 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 $\leq 5\%$. 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	
1	B	326	
2	C	161	
2	D	161	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 7125 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	285	Total	C	N	O	S	0	0	0
			2313	1446	409	452	6			
1	B	298	Total	C	N	O	S	0	0	0
			2402	1502	423	471	6			

There are 10 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	1680	CYS	GLU	engineered mutation	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	1680	CYS	GLU	engineered mutation	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	153	Total	C	N	O	S	0	0	0
			1188	750	215	216	7			
2	D	156	Total	C	N	O	S	0	0	0
			1214	766	219	222	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

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

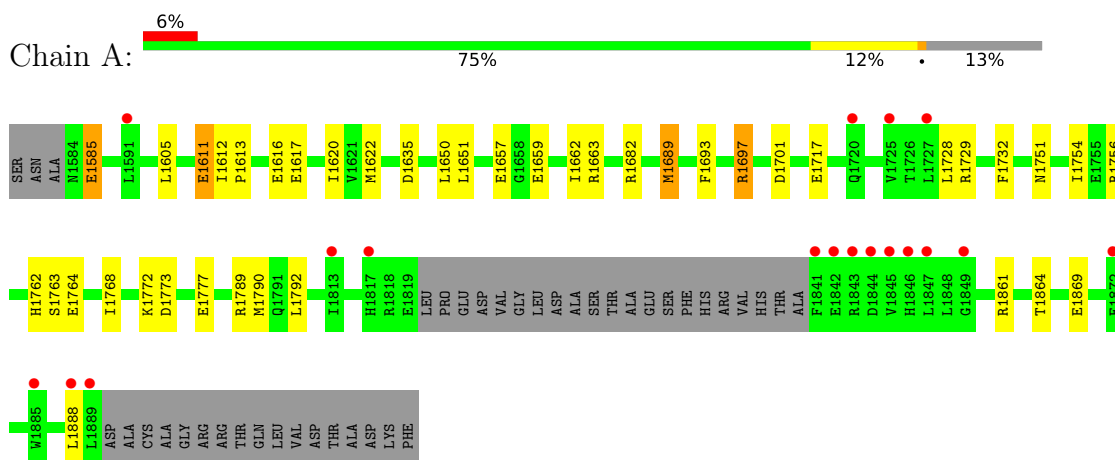
- Molecule 3 is MERCURY (II) ION (three-letter code: HG) (formula: Hg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Hg	0	0
			1	1		
3	B	1	Total	Hg	0	0
			1	1		
3	C	3	Total	Hg	0	0
			3	3		
3	D	3	Total	Hg	0	0
			3	3		

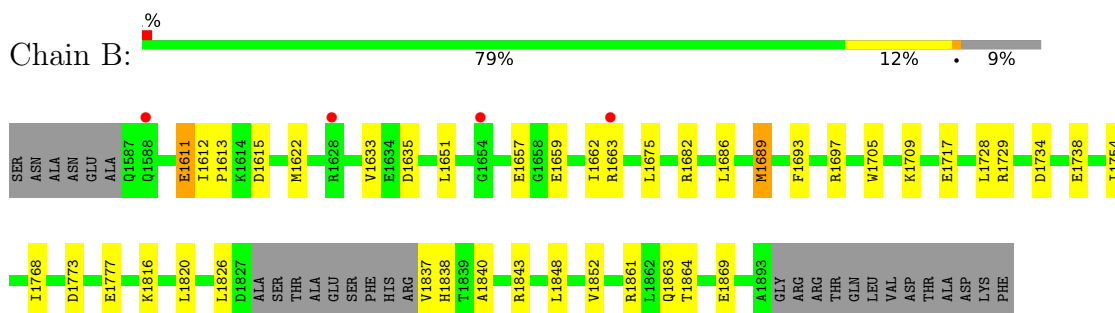
3 Residue-property plots [i](#)

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.

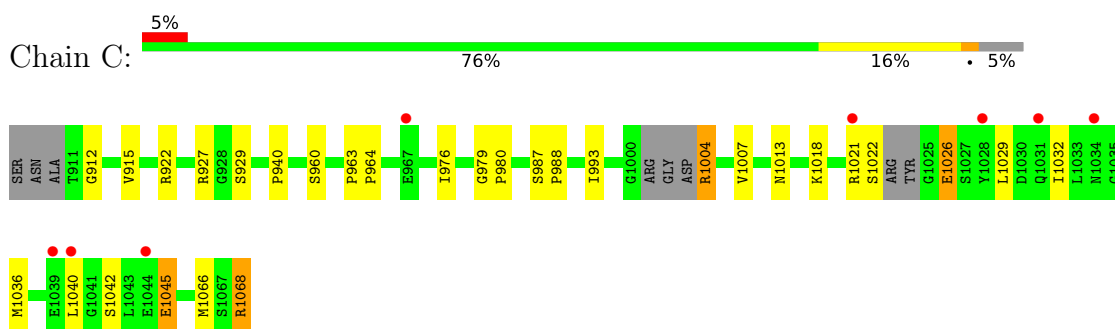
- Molecule 1: Spectrin beta chain, erythrocyte



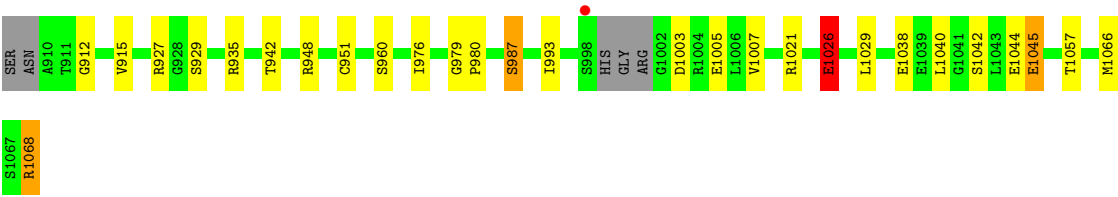
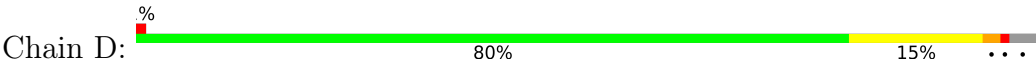
- Molecule 1: Spectrin beta chain, erythrocyte



- 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	90.13Å 98.54Å 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)	99.8 (37.82-2.75) 99.8 (37.82-2.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.94 (at 2.77Å)	Xtriage
Refinement program	REFMAC 5.5.0088	Depositor
R, R_{free}	0.225 , 0.277 0.222 , 0.269	Depositor DCC
R_{free} test set	1681 reflections (5.17%)	wwPDB-VP
Wilson B-factor (Å ²)	53.2	Xtriage
Anisotropy	0.411	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 38.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7125	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.05% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: HG

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	0.80	0/2351	0.82	6/3168 (0.2%)
1	B	0.82	0/2442	0.88	5/3295 (0.2%)
2	C	0.73	0/1210	0.88	2/1633 (0.1%)
2	D	0.75	1/1237 (0.1%)	0.94	2/1671 (0.1%)
All	All	0.79	1/7240 (0.0%)	0.87	15/9767 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	951	CYS	CB-SG	-7.17	1.70	1.82

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1068	ARG	NE-CZ-NH1	8.10	124.35	120.30
2	C	1068	ARG	NE-CZ-NH2	7.58	124.09	120.30
1	B	1697	ARG	NE-CZ-NH1	7.05	123.82	120.30
1	B	1729	ARG	NE-CZ-NH2	-6.71	116.94	120.30
2	D	1068	ARG	NE-CZ-NH2	-6.62	116.99	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	2313	0	2234	23	0
1	B	2402	0	2316	27	0
2	C	1188	0	1209	25	0
2	D	1214	0	1234	21	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	3	0	0	0	0
3	D	3	0	0	0	0
All	All	7125	0	6993	92	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 7.

The worst 5 of 92 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:1004:ARG:HH11	2:C:1004:ARG:HG3	1.31	0.93
2:C:1042:SER:HB2	2:C:1045:GLU:HB2	1.59	0.82
1:A:1622:MET:HE3	1:A:1682:ARG:HH22	1.48	0.79
1:B:1861:ARG:O	1:B:1864:THR:HB	1.82	0.79
2:D:1003:ASP:O	2:D:1068:ARG:O	2.05	0.74

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	281/326 (86%)	278 (99%)	2 (1%)	1 (0%)	34	53
1	B	294/326 (90%)	289 (98%)	5 (2%)	0	100	100
2	C	147/161 (91%)	141 (96%)	5 (3%)	1 (1%)	22	39
2	D	152/161 (94%)	146 (96%)	4 (3%)	2 (1%)	12	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	874/974 (90%)	854 (98%)	16 (2%)	4 (0%)	29 47

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1763	SER
2	D	1026	GLU
2	C	915	VAL
2	D	915	VAL

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	237/269 (88%)	229 (97%)	8 (3%)	37 58
1	B	246/269 (91%)	239 (97%)	7 (3%)	43 63
2	C	132/138 (96%)	125 (95%)	7 (5%)	22 38
2	D	134/138 (97%)	128 (96%)	6 (4%)	27 46
All	All	749/814 (92%)	721 (96%)	28 (4%)	34 54

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	1869	GLU
2	D	1057	THR
2	C	987	SER
2	D	987	SER
2	C	960	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	984	GLN

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Mol	Chain	Res	Type
2	C	984	GLN
1	B	1694	GLN
1	B	1667	GLN
2	C	931	HIS

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](#)

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	285/326 (87%)	0.28	18 (6%) 20 24	13, 26, 38, 62	0
1	B	298/326 (91%)	0.01	4 (1%) 77 84	12, 26, 38, 71	0
2	C	153/161 (95%)	0.09	8 (5%) 27 33	6, 28, 39, 51	0
2	D	156/161 (96%)	0.02	1 (0%) 89 92	17, 29, 41, 75	0
All	All	892/974 (91%)	0.11	31 (3%) 44 52	6, 27, 39, 75	0

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1843	ARG	6.2
1	A	1845	VAL	6.0
1	A	1842	GLU	6.0
1	A	1841	PHE	5.7
1	A	1847	LEU	5.0

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 monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	HG	C	6	1/1	0.93	0.34	89,89,89,89	1
3	HG	D	2	1/1	0.95	0.07	78,78,78,78	0
3	HG	C	5	1/1	0.96	0.04	100,100,100,100	0
3	HG	C	1	1/1	0.97	0.06	73,73,73,73	0
3	HG	B	8	1/1	0.97	0.13	130,130,130,130	0
3	HG	D	3	1/1	0.98	0.04	69,69,69,69	0
3	HG	D	4	1/1	0.98	0.06	67,67,67,67	0
3	HG	A	7	1/1	1.00	0.08	123,123,123,123	0

6.5 Other polymers [i](#)

There are no such residues in this entry.