



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 02:19 AM GMT

PDB ID : 2GL7
Title : Crystal Structure of a beta-catenin/BCL9/Tcf4 complex
Authors : Sampietro, J.
Deposited on : 2006-04-04
Resolution : 2.60 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
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) : trunk26865

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X-RAY DIFFRACTION

A.




Similar resolution
(#Entries, resolution range(Å))

Quality of chain

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Mol	Chain	Length	Quality of chain
3	F	46	 A horizontal bar chart showing the quality of chain F. The bar is divided into four segments: red (4%), green (24%), yellow (9%), and grey (63%). A small black dot is located on the grey segment.

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8429 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 Beta-catenin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	512	Total	C	N	O	S	0	0	0
			3830	2409	688	708	25			
1	D	506	Total	C	N	O	S	0	0	0
			3753	2363	679	686	25			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	137	SER	-	CLONING ARTIFACT	UNP P35222
A	142	GLU	TYR	ENGINEERED	UNP P35222
D	137	SER	-	CLONING ARTIFACT	UNP P35222
D	142	GLU	TYR	ENGINEERED	UNP P35222

- Molecule 2 is a protein called Transcription factor 7-like 2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	30	Total	C	N	O	0	0	0
			218	134	35	49			
2	E	28	Total	C	N	O	0	0	0
			201	123	32	46			

- Molecule 3 is a protein called B-cell lymphoma 9 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	23	Total	C	N	O	S	0	0	0
			167	104	32	30	1			
3	F	17	Total	C	N	O		0	0	0
			132	80	27	25				

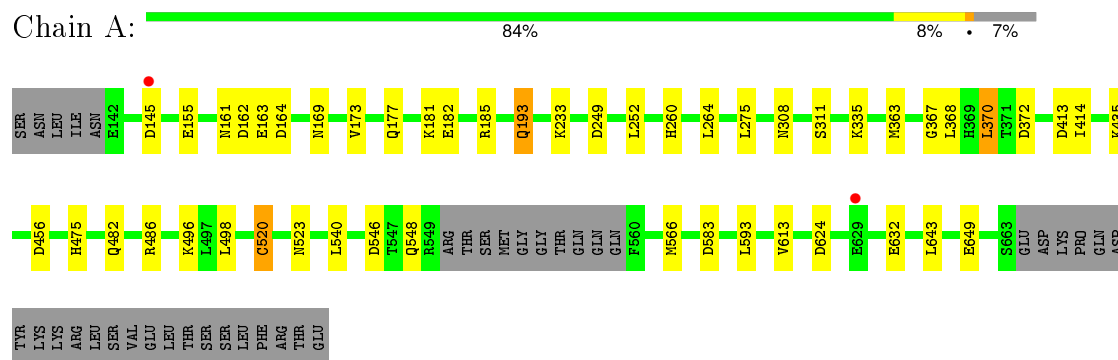
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	70	Total 70	O 70	0	0
4	B	1	Total 1	O 1	0	0
4	D	56	Total 56	O 56	0	0
4	E	1	Total 1	O 1	0	0

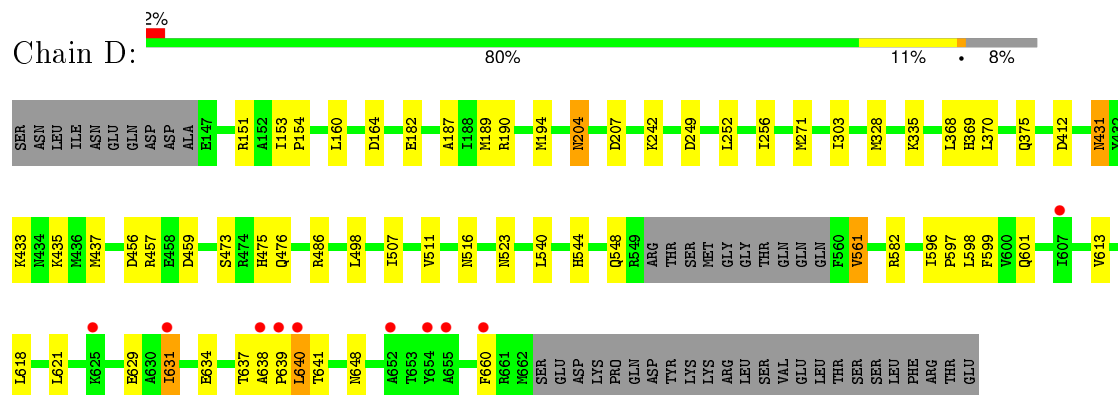
3 Residue-property plots

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 ($\text{RSRZ} > 2$). 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.

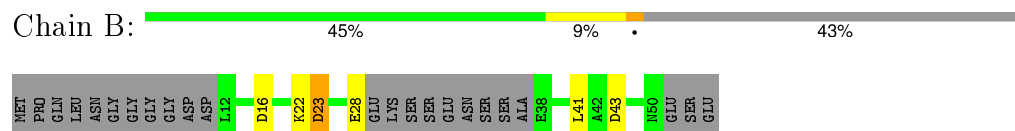
• Molecule 1: Beta-catenin



• Molecule 1: Beta-catenin

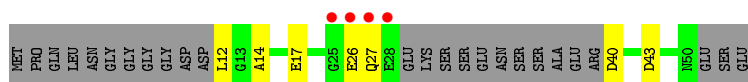


• Molecule 2: Transcription factor 7-like 2

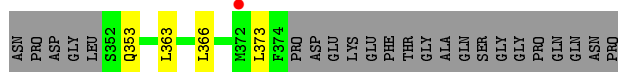
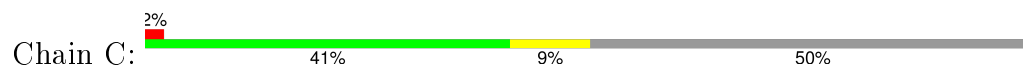


• Molecule 2: Transcription factor 7-like 2

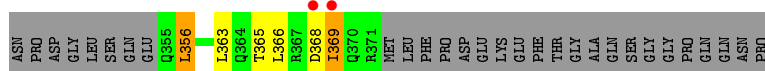




• Molecule 3: B-cell lymphoma 9 protein



• Molecule 3: B-cell lymphoma 9 protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	96.76Å 119.44Å 130.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.60 48.38 – 2.39	Depositor EDS
% Data completeness (in resolution range)	99.1 (30.00-2.60) 91.1 (48.38-2.39)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.60 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.221 , 0.267 0.217 , 0.263	Depositor DCC
R_{free} test set	2361 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	41.8	Xtriage
Anisotropy	0.750	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 45.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 55440 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8429	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.99% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.40	0/3883	0.63	8/5284 (0.2%)
1	D	0.40	0/3806	0.63	6/5180 (0.1%)
2	B	0.45	0/217	0.87	3/290 (1.0%)
2	E	0.40	0/200	0.73	1/268 (0.4%)
3	C	0.40	0/168	0.48	0/226
3	F	0.39	0/132	0.76	0/177
All	All	0.40	0/8406	0.64	18/11425 (0.2%)

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
2	B	1	0

There are no bond length outliers.

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	412	ASP	CB-CG-OD2	7.27	124.84	118.30
1	A	456	ASP	CB-CG-OD2	7.07	124.67	118.30
1	D	459	ASP	CB-CG-OD2	7.00	124.60	118.30
1	A	249	ASP	CB-CG-OD2	6.12	123.81	118.30
1	D	456	ASP	CB-CG-OD2	5.89	123.60	118.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	39	ARG	CA

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	3830	0	3909	10	0
1	D	3753	0	3819	21	0
2	B	218	0	199	0	0
2	E	201	0	180	4	0
3	C	167	0	146	0	0
3	F	132	0	122	9	0
4	A	70	0	0	1	1
4	B	1	0	0	0	0
4	D	56	0	0	0	1
4	E	1	0	0	0	0
All	All	8429	0	8375	40	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 2.

The worst 5 of 40 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:F:365:THR:O	3:F:369:ILE:CG1	1.88	1.21
3:F:365:THR:O	3:F:369:ILE:HG12	1.40	1.20
3:F:365:THR:O	3:F:369:ILE:HG13	1.85	0.77
3:F:365:THR:HG22	3:F:369:ILE:HD11	1.74	0.70
3:F:365:THR:O	3:F:369:ILE:CD1	2.46	0.63

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)
4:A:4:HOH:O	4:D:1:HOH:O[2_655]	2.12	0.08

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	A	508/550 (92%)	500 (98%)	8 (2%)	0	100	100
1	D	502/550 (91%)	496 (99%)	5 (1%)	1 (0%)	52	77
2	B	26/53 (49%)	25 (96%)	1 (4%)	0	100	100
2	E	24/53 (45%)	21 (88%)	3 (12%)	0	100	100
3	C	21/46 (46%)	21 (100%)	0	0	100	100
3	F	15/46 (33%)	15 (100%)	0	0	100	100
All	All	1096/1298 (84%)	1078 (98%)	17 (2%)	1 (0%)	56	81

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	561	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	407/460 (88%)	379 (93%)	28 (7%)	19	38
1	D	393/460 (85%)	359 (91%)	34 (9%)	13	24
2	B	23/44 (52%)	19 (83%)	4 (17%)	2	3
2	E	21/44 (48%)	18 (86%)	3 (14%)	4	7
3	C	15/41 (37%)	11 (73%)	4 (27%)	0	1
3	F	13/41 (32%)	9 (69%)	4 (31%)	0	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	872/1090 (80%)	795 (91%)	77 (9%)	12	24

5 of 77 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	366	LEU
1	D	256	ILE
2	E	26	GLU
3	C	373	LEU
1	D	190	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	169	ASN
1	D	369	HIS
1	D	578	HIS
1	D	204	ASN
1	D	260	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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	512/550 (93%)	-0.38	2 (0%) 93 91	8, 21, 43, 56	0
1	D	506/550 (92%)	-0.28	10 (1%) 68 63	9, 21, 47, 59	0
2	B	30/53 (56%)	-0.29	0 100 100	22, 29, 46, 50	0
2	E	28/53 (52%)	0.27	4 (14%) 4 2	24, 30, 40, 41	0
3	C	23/46 (50%)	0.09	1 (4%) 39 31	18, 36, 40, 41	0
3	F	17/46 (36%)	0.72	2 (11%) 6 4	35, 43, 48, 48	0
All	All	1116/1298 (85%)	-0.29	19 (1%) 73 68	8, 22, 46, 59	0

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	655	ALA	4.9
1	D	638	ALA	4.8
1	D	654	TYR	3.9
1	D	639	PRO	3.2
1	D	631	ILE	3.2

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.