



wwPDB/EMDatabank EM Map/Model Validation Summary Report ⓘ

Jul 13, 2019 – 11:11 AM EDT

PDB ID : 6N2P
EMDB ID: : EMD-9332
Title : Helical assembly of the CARD9 CARD
Authors : Holliday, M.J.; Rohou, A.; Arthur, C.P.; Dueber, E.C.; Fairbrother, W.J.
Deposited on : 2018-11-13
Resolution : 4.00 Å(reported)
Based on PDB ID : 6E26

This is a wwPDB/EMDatabank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : 2.3.2

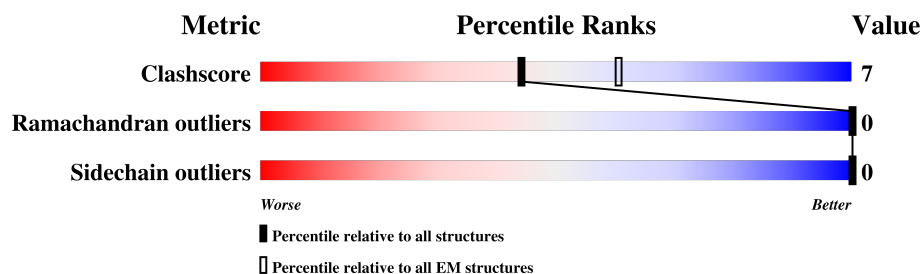
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

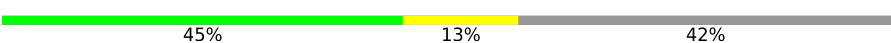
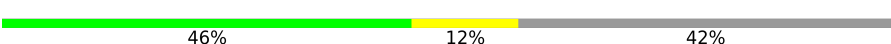
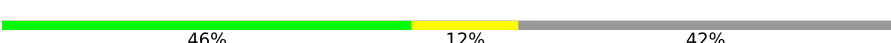
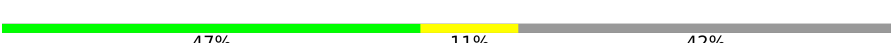
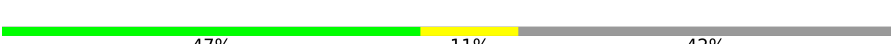
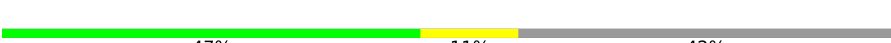
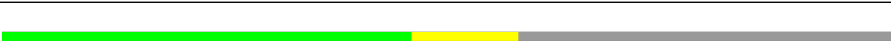
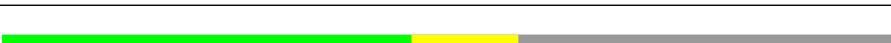
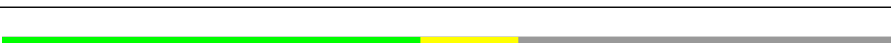
The reported resolution of this entry is 4.00 Å.

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)	EM structures (#Entries)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	152	 45% 13% 42%
1	B	152	 46% 12% 42%
1	C	152	 46% 12% 42%
1	D	152	 47% 11% 42%
1	E	152	 47% 11% 42%
1	F	152	 47% 11% 42%
1	G	152	 46% 12% 42%
1	H	152	 46% 12% 42%
1	I	152	 47% 11% 42%

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Mol	Chain	Length	Quality of chain
1	J	152	<div><div></div><div></div><div></div><div>47%</div><div>11%</div><div>42%</div></div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 14570 atoms, of which 7380 are hydrogens and 0 are deuteriums.

In the tables below, 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 Caspase recruitment domain-containing protein 9.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	88	Total	C	H	N	O	S	0	0
			1457	463	738	121	133	2		
1	B	88	Total	C	H	N	O	S	0	0
			1457	463	738	121	133	2		
1	C	88	Total	C	H	N	O	S	0	0
			1457	463	738	121	133	2		
1	D	88	Total	C	H	N	O	S	0	0
			1457	463	738	121	133	2		
1	E	88	Total	C	H	N	O	S	0	0
			1457	463	738	121	133	2		
1	F	88	Total	C	H	N	O	S	0	0
			1457	463	738	121	133	2		
1	G	88	Total	C	H	N	O	S	0	0
			1457	463	738	121	133	2		
1	H	88	Total	C	H	N	O	S	0	0
			1457	463	738	121	133	2		
1	I	88	Total	C	H	N	O	S	0	0
			1457	463	738	121	133	2		
1	J	88	Total	C	H	N	O	S	0	0
			1457	463	738	121	133	2		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP Q9H257
A	107	GLU	ILE	engineered mutation	UNP Q9H257
B	1	GLY	-	expression tag	UNP Q9H257
B	107	GLU	ILE	engineered mutation	UNP Q9H257
C	1	GLY	-	expression tag	UNP Q9H257
C	107	GLU	ILE	engineered mutation	UNP Q9H257
D	1	GLY	-	expression tag	UNP Q9H257
D	107	GLU	ILE	engineered mutation	UNP Q9H257
E	1	GLY	-	expression tag	UNP Q9H257
E	107	GLU	ILE	engineered mutation	UNP Q9H257

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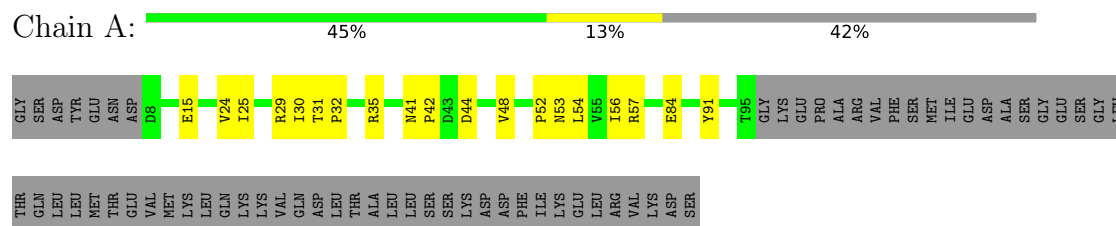
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Chain	Residue	Modelled	Actual	Comment	Reference
F	1	GLY	-	expression tag	UNP Q9H257
F	107	GLU	ILE	engineered mutation	UNP Q9H257
G	1	GLY	-	expression tag	UNP Q9H257
G	107	GLU	ILE	engineered mutation	UNP Q9H257
H	1	GLY	-	expression tag	UNP Q9H257
H	107	GLU	ILE	engineered mutation	UNP Q9H257
I	1	GLY	-	expression tag	UNP Q9H257
I	107	GLU	ILE	engineered mutation	UNP Q9H257
J	1	GLY	-	expression tag	UNP Q9H257
J	107	GLU	ILE	engineered mutation	UNP Q9H257

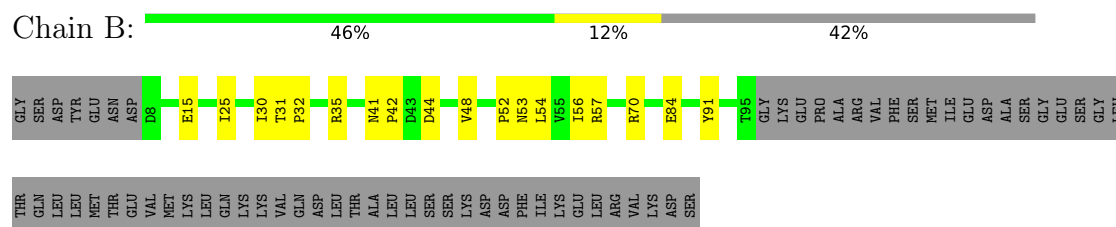
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

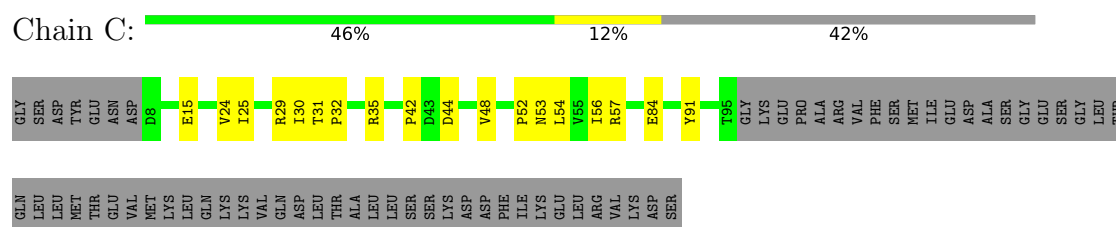
- Molecule 1: Caspase recruitment domain-containing protein 9



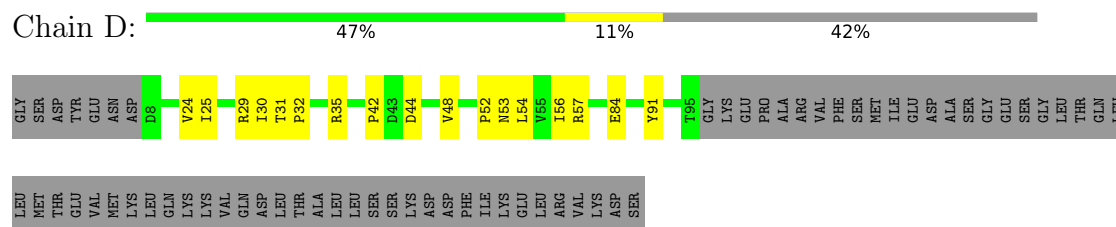
- Molecule 1: Caspase recruitment domain-containing protein 9



- Molecule 1: Caspase recruitment domain-containing protein 9



- Molecule 1: Caspase recruitment domain-containing protein 9



- Molecule 1: Caspase recruitment domain-containing protein 9

Chain E:  47% 11% 42%

GLY SER ASP TYR TRP MET ASN ASP D8 I25 I26 R29 I30 T31 P32 R35 P42 P43 D44 V48 P52 N53 L54 V55 I56 R57 E84 Y91 T95 GLY LYS GLU PRO ARG ALA VAL PHE SER MET ILE GLU ASP ALA SER GLY GLN LEU THR LEU LEU

MET THR GLU VAL MET LYS LEU GLN LYS VAL GLN ASP LEU THR ALA LEU LEU SER SER ASP ASP PHE ILE LYS GLU LEU ARG VAL ASP SER

- Molecule 1: Caspase recruitment domain-containing protein 9

Chain F:  47% 11% 42%

GLY SER ASP TYR TRP MET ASN ASP D8 I25 I26 R29 I30 T31 P32 R35 P42 P43 D44 V48 P52 N53 L54 V55 I56 R57 E84 Y91 T95 GLY LYS GLU PRO ARG ALA VAL PHE SER MET ILE GLU ASP ALA SER GLY GLN LEU THR LEU LEU

LEU MET THR GLU VAL MET LYS LEU GLN LYS VAL GLN ASP LEU THR ALA LEU LEU SER SER ASP ASP PHE ILE LYS GLU LEU ARG VAL ASP SER

- Molecule 1: Caspase recruitment domain-containing protein 9

Chain G:  46% 12% 42%

GLY SER ASP TYR TRP MET ASN ASP D8 E15 I25 I30 T31 P32 R35 N41 P42 D43 D44 V48 P52 N53 L54 V55 I56 R57 R70 E84 Y91 T95 GLY LYS GLU PRO ARG ALA VAL PHE SER MET ILE GLU ASP ALA SER GLY GLN LEU THR LEU LEU

THR GLN LEU LEU MET THR MET GLU VAL MET LYS LEU GLN LYS VAL GLN ASP LEU THR ALA LEU LEU SER SER LYS ASP ASP PHE ILE LYS GLU LEU ARG VAL ASP SER

- Molecule 1: Caspase recruitment domain-containing protein 9

Chain H:  46% 12% 42%

GLY SER ASP TYR TRP MET ASN ASP D8 E15 I25 I30 T31 P32 R35 N41 P42 D43 D44 V48 P52 N53 L54 V55 I56 R57 R70 E84 Y91 T95 GLY LYS GLU PRO ARG ALA VAL PHE SER MET ILE GLU ASP ALA SER GLY GLN LEU THR LEU LEU

THR GLN LEU LEU MET THR MET GLU VAL MET LYS LEU GLN LYS VAL GLN ASP LEU THR ALA LEU LEU SER SER LYS ASP ASP PHE ILE LYS GLU LEU ARG VAL ASP SER

- Molecule 1: Caspase recruitment domain-containing protein 9

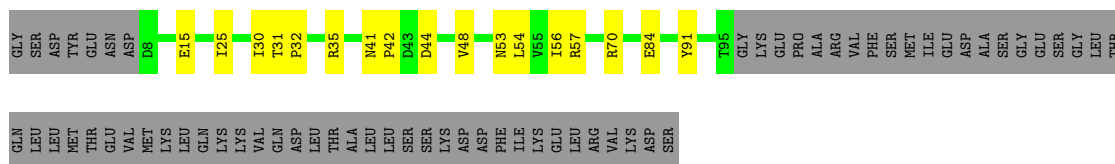
Chain I:  47% 11% 42%

GLY SER ASP TYR TRP MET ASN ASP D8 E15 I25 I30 T31 P32 R35 P42 P43 D44 V48 P52 N53 L54 V55 I56 R57 E84 Y91 T95 GLY LYS GLU PRO ARG ALA VAL PHE SER MET ILE GLU ASP ALA SER GLY GLN LEU THR LEU LEU

LEU MET THR GLU VAL MET LYS LEU GLN LYS VAL GLN ASP LEU THR ALA LEU LEU SER SER ASP ASP PHE ILE LYS GLU LEU ARG VAL ASP SER

- Molecule 1: Caspase recruitment domain-containing protein 9

Chain J:  47% 11% 42%



4 Experimental information

Property	Value	Source
Reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=-101.6°, rise=5.11 Å, axial sym=C1	Depositor
Number of segments used	31908	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.9	Depositor
Minimum defocus (nm)	1250	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

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 >2	RMSZ	# Z >2
1	A	0.44	0/733	0.52	0/995
1	B	0.44	0/733	0.52	0/995
1	C	0.44	0/733	0.52	0/995
1	D	0.44	0/733	0.52	0/995
1	E	0.44	0/733	0.52	0/995
1	F	0.44	0/733	0.52	0/995
1	G	0.44	0/733	0.52	0/995
1	H	0.44	0/733	0.52	0/995
1	I	0.44	0/733	0.52	0/995
1	J	0.44	0/733	0.52	0/995
All	All	0.44	0/7330	0.52	0/9950

There are no bond length outliers.

There are no bond angle outliers.

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	719	738	738	17	0
1	B	719	738	738	14	0
1	C	719	738	738	15	0
1	D	719	738	738	14	0
1	E	719	738	738	13	0
1	F	719	738	738	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	719	738	738	15	0
1	H	719	738	738	14	0
1	I	719	738	738	11	0
1	J	719	738	738	13	0
All	All	7190	7380	7380	109	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 109 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:B:15:GLU:OE2	1:E:35:ARG:NE	2.20	0.75
1:A:15:GLU:OE2	1:D:35:ARG:NE	2.22	0.72
1:B:35:ARG:NE	1:H:15:GLU:OE2	2.23	0.72
1:D:53:ASN:ND2	1:E:52:PRO:O	2.24	0.69
1:C:15:GLU:OE2	1:F:35:ARG:NE	2.26	0.69

There are no symmetry-related clashes.

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 PDB entries followed by that with respect to all EM entries.

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	86/152 (57%)	75 (87%)	11 (13%)	0	100	100
1	B	86/152 (57%)	75 (87%)	11 (13%)	0	100	100
1	C	86/152 (57%)	75 (87%)	11 (13%)	0	100	100
1	D	86/152 (57%)	75 (87%)	11 (13%)	0	100	100
1	E	86/152 (57%)	75 (87%)	11 (13%)	0	100	100
1	F	86/152 (57%)	75 (87%)	11 (13%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	86/152 (57%)	75 (87%)	11 (13%)	0	100	100
1	H	86/152 (57%)	75 (87%)	11 (13%)	0	100	100
1	I	86/152 (57%)	75 (87%)	11 (13%)	0	100	100
1	J	86/152 (57%)	75 (87%)	11 (13%)	0	100	100
All	All	860/1520 (57%)	750 (87%)	110 (13%)	0	100	100

There are no Ramachandran outliers to report.

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 PDB entries followed by that with respect to all EM entries.

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	83/140 (59%)	83 (100%)	0	100	100
1	B	83/140 (59%)	83 (100%)	0	100	100
1	C	83/140 (59%)	83 (100%)	0	100	100
1	D	83/140 (59%)	83 (100%)	0	100	100
1	E	83/140 (59%)	83 (100%)	0	100	100
1	F	83/140 (59%)	83 (100%)	0	100	100
1	G	83/140 (59%)	83 (100%)	0	100	100
1	H	83/140 (59%)	83 (100%)	0	100	100
1	I	83/140 (59%)	83 (100%)	0	100	100
1	J	83/140 (59%)	83 (100%)	0	100	100
All	All	830/1400 (59%)	830 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.