



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 03:37 PM UTC

PDB ID : 6DSZ / pdb_00006dsz
Title : Crystal structure of DDB1 in complex with DET1- and DDB1-associated protein 1 (DDA1)
Authors : Shabek, N.; Zheng, N.
Deposited on : 2018-06-14
Resolution : 3.09 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

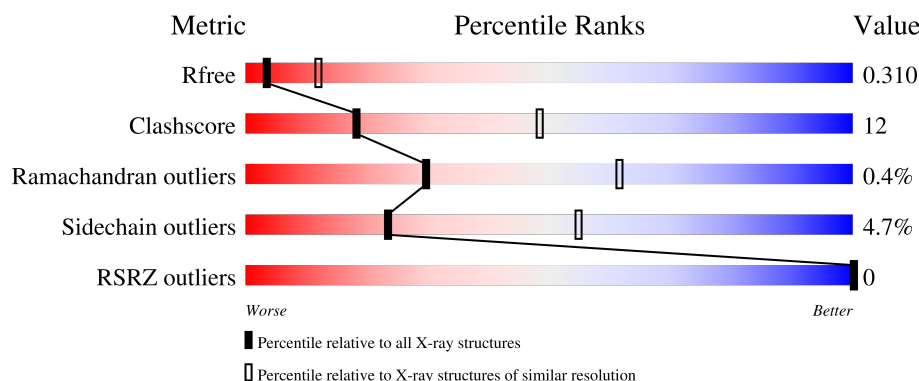
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

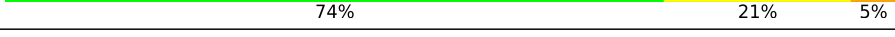
The reported resolution of this entry is 3.09 Å.

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}	180053	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	1140	 73% 22% . .
1	B	1140	 65% 24% . 6%
2	C	19	 58% 37% 5%
2	D	19	 74% 21% 5%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 34801 atoms, of which 17393 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 DNA damage-binding protein 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	1107	Total	C	H	N	O	S	0	0	0
			17329	5503	8655	1460	1664	47			
1	B	1072	Total	C	H	N	O	S	0	0	0
			16842	5356	8422	1418	1599	47			

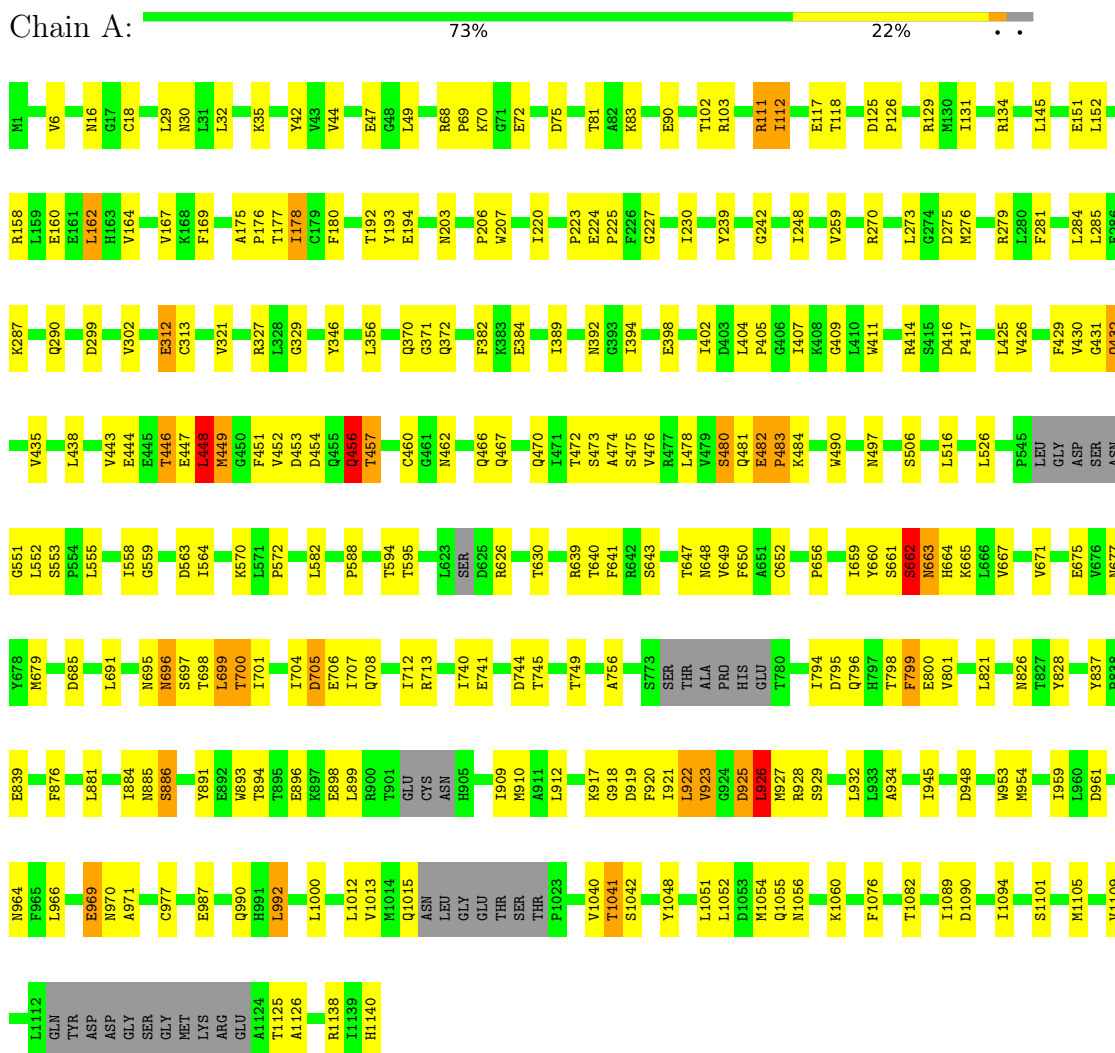
- Molecule 2 is a protein called DET1- and DDB1-associated protein 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	C	19	Total	C	H	N	O	S	0	0	0
			315	104	158	26	26	1			
2	D	19	Total	C	H	N	O	S	0	0	0
			315	104	158	26	26	1			

3 Residue-property plots

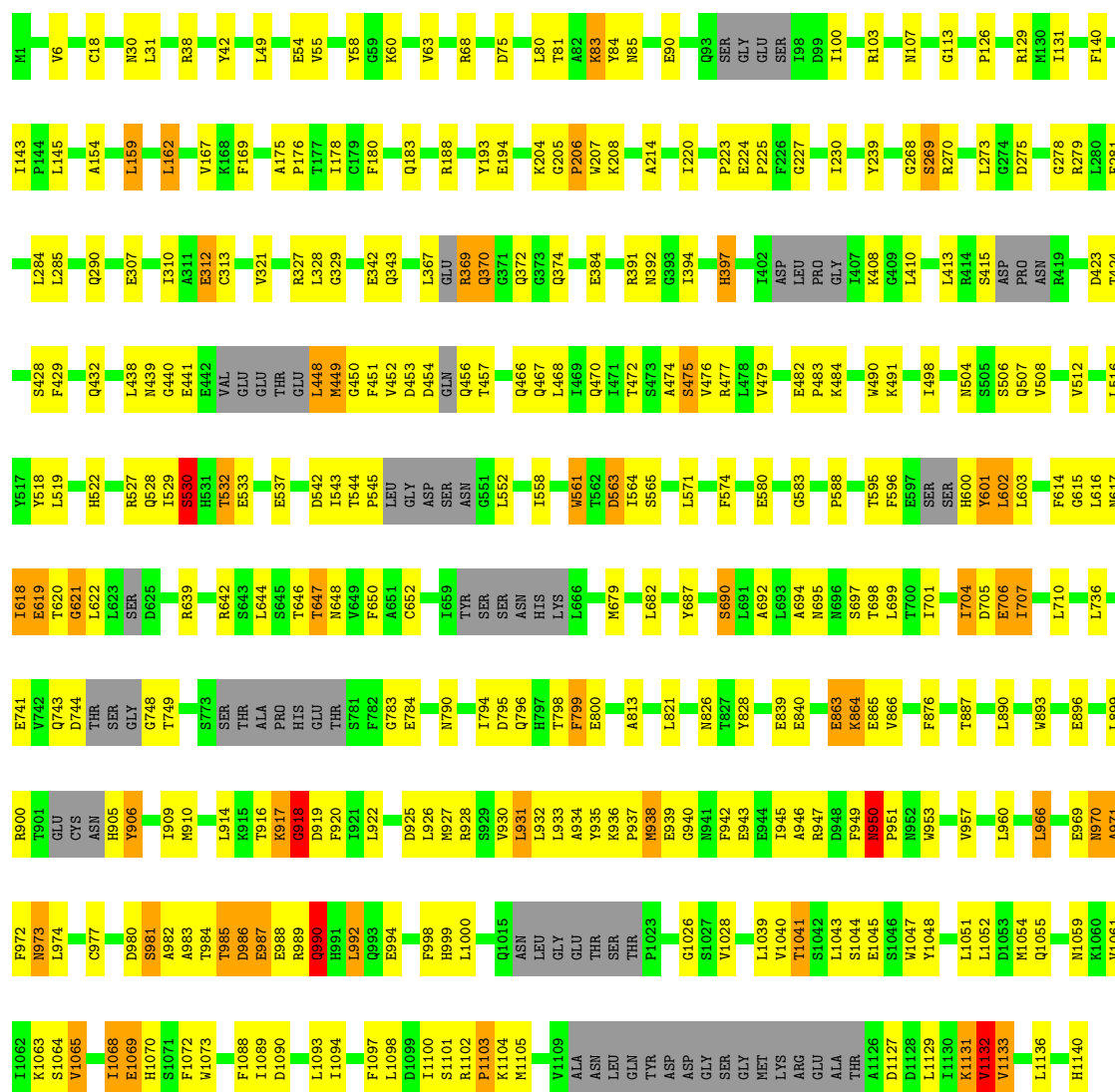
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: DNA damage-binding protein 1



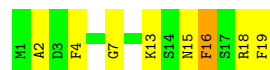
• Molecule 1: DNA damage-binding protein 1





• Molecule 2: DET1- and DDB1-associated protein 1

Chain C: 58% 37% 5%



• Molecule 2: DET1- and DDB1-associated protein 1

Chain D: 74% 21% 5%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	63.20Å 219.18Å 89.32Å 90.00° 89.98° 90.00°	Depositor
Resolution (Å)	47.80 – 3.09 47.80 – 3.09	Depositor EDS
% Data completeness (in resolution range)	88.7 (47.80-3.09) 88.7 (47.80-3.09)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.10 (at 3.07Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.247 , 0.307 0.249 , 0.310	Depositor DCC
R_{free} test set	1999 reflections (4.52%)	wwPDB-VP
Wilson B-factor (Å ²)	53.4	Xtriage
Anisotropy	0.587	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 44.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.458 for h,-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	34801	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.59% 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

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	0.21	1/8830 (0.0%)	0.59	15/11954 (0.1%)
1	B	0.26	1/8563 (0.0%)	0.85	36/11575 (0.3%)
2	C	0.21	0/161	0.67	0/214
2	D	0.15	0/161	0.38	0/214
All	All	0.24	2/17715 (0.0%)	0.73	51/23957 (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
1	A	0	6
1	B	1	6
All	All	1	12

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	456	GLN	C-N	-9.98	1.20	1.33
1	B	113	GLY	C-N	5.02	1.44	1.33

The worst 5 of 51 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	985	THR	N-CA-C	25.00	145.92	112.68
1	A	456	GLN	CA-C-N	21.85	151.90	120.87
1	A	456	GLN	C-N-CA	21.85	151.90	120.87
1	B	983	ALA	CA-C-N	20.23	164.67	123.20
1	B	983	ALA	C-N-CA	20.23	164.67	123.20

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	B	983	ALA	CA

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	448	LEU	Peptide
1	A	456	GLN	Mainchain,Peptide
1	A	705	ASP	Peptide
1	A	925	ASP	Peptide
1	A	926	LEU	Peptide

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	8674	8655	8663	197	0
1	B	8420	8422	8433	225	0
2	C	157	158	158	6	0
2	D	157	158	158	3	0
All	All	17408	17393	17412	422	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 12.

The worst 5 of 422 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:A:456:GLN:HG2	1:A:456:GLN:O	1.24	1.05
1:A:456:GLN:O	1:A:456:GLN:CG	2.05	1.02
1:B:799:PHE:O	1:B:800:GLU:HG3	1.63	0.99
1:A:398:GLU:CD	1:A:700:THR:HG21	1.87	0.98
1:A:407:ILE:CD1	1:A:699:LEU:CD1	2.44	0.95

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 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	1093/1140 (96%)	931 (85%)	157 (14%)	5 (0%)	24	57
1	B	1040/1140 (91%)	885 (85%)	151 (14%)	4 (0%)	30	61
2	C	17/19 (90%)	12 (71%)	5 (29%)	0	100	100
2	D	17/19 (90%)	13 (76%)	4 (24%)	0	100	100
All	All	2167/2318 (94%)	1841 (85%)	317 (15%)	9 (0%)	30	61

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	405	PRO
1	A	482	GLU
1	A	970	ASN
1	B	1065	VAL
1	B	223	PRO

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	971/999 (97%)	939 (97%)	32 (3%)	33	63
1	B	941/999 (94%)	884 (94%)	57 (6%)	17	46
2	C	17/17 (100%)	16 (94%)	1 (6%)	18	48
2	D	17/17 (100%)	15 (88%)	2 (12%)	5	21
All	All	1946/2032 (96%)	1854 (95%)	92 (5%)	23	55

5 of 92 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	644	LEU
1	B	950	ASN
1	B	704	ILE
1	B	909	ILE
1	B	973	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	209	GLN
1	B	731	GLN
1	B	677	ASN
1	B	805	HIS
1	A	600	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 oligosaccharides 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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	456:GLN	C	457:THR	N	1.20

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	1107/1140 (97%)	-1.27	0 100 100	14, 53, 96, 140	0
1	B	1072/1140 (94%)	-1.26	0 100 100	13, 53, 94, 117	0
2	C	19/19 (100%)	-1.32	0 100 100	36, 45, 74, 85	0
2	D	19/19 (100%)	-1.40	0 100 100	36, 51, 66, 84	0
All	All	2217/2318 (95%)	-1.26	0 100 100	13, 53, 95, 140	0

There are no RSRZ outliers to report.

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 oligosaccharides 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.