



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 10:12 AM UTC

PDB ID : 1H6O / pdb_00001h6o
Title : Dimerisation domain from human TRF1
Authors : Fairall, L.; Chapman, L.; Rhodes, D.
Deposited on : 2001-06-20
Resolution : 2.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 : **FAILED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

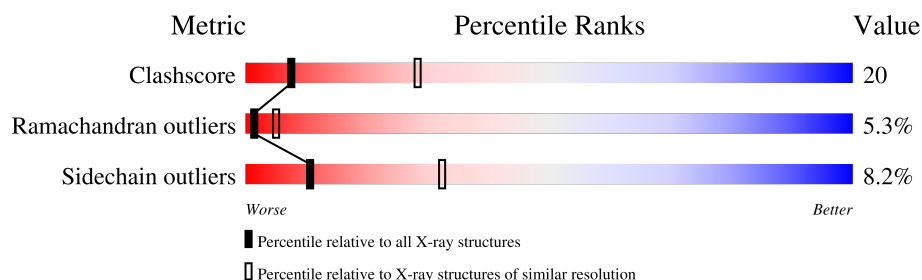
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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))
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)

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 $\leq 5\%$.

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	204	 52% 37% 6% .

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1475 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 TELOMERIC REPEAT BINDING FACTOR 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	195	1475	936	251	276	12	0	0	0

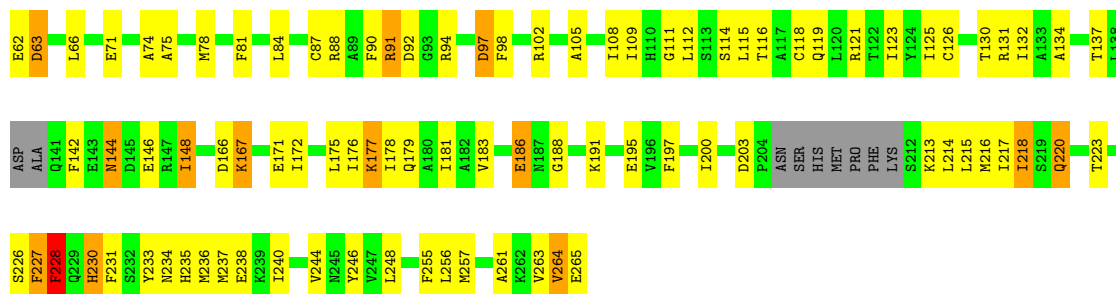
3 Residue-property plots

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. 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.

Note EDS failed to run properly.

• Molecule 1: TELOMERIC REPEAT BINDING FACTOR 1

Chain A: 



4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	85.39Å 85.39Å 91.63Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	24.84 – 2.90	Depositor
% Data completeness (in resolution range)	92.1 (24.84-2.90)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.00 (at 2.31Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.250 , 0.303	Depositor
Wilson B-factor (Å ²)	35.2	Xtriage
Anisotropy	0.948	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.032 for -h,-k,l	Xtriage
Total number of atoms	1475	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.51% 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	0.54	0/1500	1.04	10/2025 (0.5%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	144	ASN	N-CA-C	7.48	120.38	111.33
1	A	66	LEU	N-CA-C	-7.11	104.07	112.89
1	A	228	PHE	N-CA-C	6.87	125.42	110.80
1	A	167	LYS	N-CA-C	-6.81	103.94	111.36
1	A	98	PHE	N-CA-C	-6.71	103.89	111.07
1	A	227	PHE	N-CA-C	6.60	121.02	107.37
1	A	231	PHE	N-CA-C	-6.14	102.15	110.68
1	A	246	TYR	N-CA-C	-6.03	104.33	111.03
1	A	227	PHE	CB-CA-C	-5.77	103.86	111.82
1	A	178	ILE	N-CA-C	5.15	115.37	110.53

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	1475	0	1383	58	0
All	All	1475	0	1383	58	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 20.

All (58) 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:261:ALA:O	1:A:264:VAL:HG12	1.71	0.91
1:A:220:GLN:HE21	1:A:220:GLN:N	1.69	0.89
1:A:175:LEU:HD13	1:A:236:MET:HA	1.61	0.82
1:A:234:ASN:O	1:A:238:GLU:HG3	1.80	0.81
1:A:220:GLN:HE21	1:A:220:GLN:H	1.24	0.80
1:A:126:CYS:O	1:A:130:THR:HG23	1.83	0.79
1:A:227:PHE:O	1:A:228:PHE:HB3	1.90	0.71
1:A:115:LEU:HD13	1:A:123:ILE:CD1	2.21	0.71
1:A:105:ALA:O	1:A:109:ILE:HG13	1.95	0.67
1:A:240:ILE:O	1:A:244:VAL:HG23	1.95	0.66
1:A:146:GLU:HG2	1:A:148:ILE:HB	1.77	0.65
1:A:84:LEU:HD12	1:A:248:LEU:HD12	1.78	0.65
1:A:111:GLY:O	1:A:112:LEU:HD23	1.97	0.63
1:A:167:LYS:O	1:A:171:GLU:HG3	1.98	0.63
1:A:75:ALA:HB1	1:A:112:LEU:HD21	1.81	0.61
1:A:230:HIS:O	1:A:235:HIS:HD2	1.83	0.61
1:A:263:VAL:C	1:A:265:GLU:H	2.09	0.61
1:A:197:PHE:CE2	1:A:218:ILE:HG23	2.36	0.60
1:A:116:THR:OG1	1:A:119:GLN:HG3	2.02	0.59
1:A:91:ARG:HG2	1:A:92:ASP:N	2.18	0.59
1:A:90:PHE:CZ	1:A:132:ILE:HD11	2.39	0.58
1:A:115:LEU:HD13	1:A:123:ILE:HD11	1.86	0.57
1:A:215:LEU:HA	1:A:218:ILE:HD11	1.86	0.57
1:A:244:VAL:O	1:A:248:LEU:HB2	2.06	0.55
1:A:74:ALA:O	1:A:78:MET:HG3	2.06	0.54
1:A:179:GLN:O	1:A:183:VAL:HG23	2.08	0.53
1:A:92:ASP:HB2	1:A:94:ARG:NH1	2.25	0.52
1:A:264:VAL:O	1:A:264:VAL:HG13	2.10	0.52
1:A:87:CYS:HB2	1:A:248:LEU:HD13	1.94	0.50
1:A:191:LYS:O	1:A:195:GLU:HG3	2.12	0.50
1:A:90:PHE:CZ	1:A:237:MET:HE1	2.46	0.49
1:A:81:PHE:CG	1:A:256:LEU:HD23	2.47	0.49
1:A:115:LEU:HD13	1:A:123:ILE:HD12	1.93	0.49
1:A:62:GLU:O	1:A:63:ASP:C	2.56	0.48
1:A:175:LEU:HD13	1:A:236:MET:CA	2.39	0.48
1:A:132:ILE:CD1	1:A:240:ILE:HG21	2.43	0.48
1:A:223:THR:O	1:A:223:THR:HG22	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:121:ARG:O	1:A:125:ILE:HG13	2.15	0.47
1:A:172:ILE:O	1:A:176:ILE:HG13	2.16	0.46
1:A:179:GLN:HE21	1:A:233:TYR:HD1	1.64	0.45
1:A:131:ARG:HH11	1:A:131:ARG:HG2	1.82	0.45
1:A:216:MET:O	1:A:220:GLN:NE2	2.50	0.45
1:A:220:GLN:H	1:A:220:GLN:NE2	2.01	0.44
1:A:134:ALA:O	1:A:137:THR:HB	2.17	0.44
1:A:263:VAL:C	1:A:265:GLU:N	2.75	0.43
1:A:88:ARG:HH12	1:A:257:MET:HE3	1.83	0.43
1:A:81:PHE:CB	1:A:256:LEU:HD23	2.48	0.43
1:A:177:LYS:HG2	1:A:200:ILE:HG21	2.01	0.43
1:A:181:ILE:HD13	1:A:217:ILE:HG21	2.01	0.43
1:A:186:GLU:C	1:A:188:GLY:N	2.76	0.42
1:A:186:GLU:C	1:A:188:GLY:H	2.28	0.42
1:A:71:GLU:O	1:A:75:ALA:N	2.50	0.42
1:A:92:ASP:CB	1:A:94:ARG:NH1	2.83	0.41
1:A:87:CYS:CB	1:A:248:LEU:HD13	2.51	0.41
1:A:114:SER:C	1:A:115:LEU:HG	2.45	0.41
1:A:214:LEU:C	1:A:216:MET:N	2.76	0.41
1:A:220:GLN:HE21	1:A:220:GLN:CA	2.34	0.40
1:A:115:LEU:CD1	1:A:123:ILE:CD1	2.95	0.40

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	189/204 (93%)	162 (86%)	17 (9%)	10 (5%)	1 5

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	228	PHE
1	A	255	PHE
1	A	63	ASP
1	A	97	ASP
1	A	264	VAL
1	A	142	PHE
1	A	166	ASP
1	A	213	LYS
1	A	226	SER
1	A	203	ASP

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	146/176 (83%)	134 (92%)	12 (8%)	10	32

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	91	ARG
1	A	97	ASP
1	A	102	ARG
1	A	108	ILE
1	A	118	CYS
1	A	144	ASN
1	A	148	ILE
1	A	177	LYS
1	A	186	GLU
1	A	218	ILE
1	A	220	GLN
1	A	230	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	127	GLN
1	A	179	GLN
1	A	220	GLN
1	A	234	ASN
1	A	235	HIS
1	A	245	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 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 [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS failed to run properly - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS failed to run properly - this section is therefore empty.

6.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

6.4 Ligands

EDS failed to run properly - this section is therefore empty.

6.5 Other polymers

EDS failed to run properly - this section is therefore empty.