



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 07:05 AM UTC

PDB ID : 1M7W / pdb_00001m7w
Title : HNF4a ligand binding domain with bound fatty acid
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Deposited on : 2002-07-22
Resolution : 2.80 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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
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

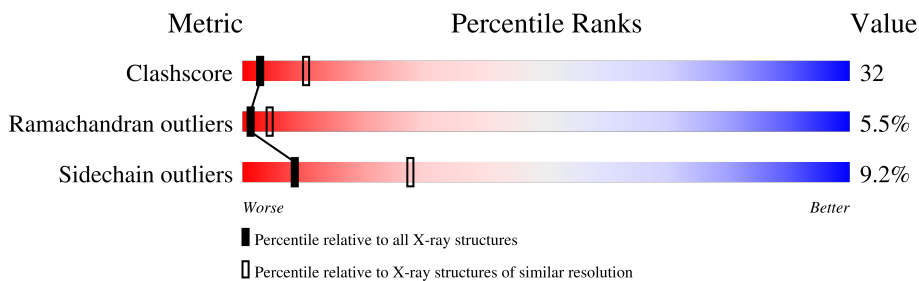
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)

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 was not executed.

Mol	Chain	Length	Quality of chain
1	A	250	48% 32% 7% • 11%
1	B	250	36% 37% 14% 13%
1	C	250	39% 38% 9% • 12%
1	D	250	39% 41% 8% 12%

2 Entry composition [i](#)

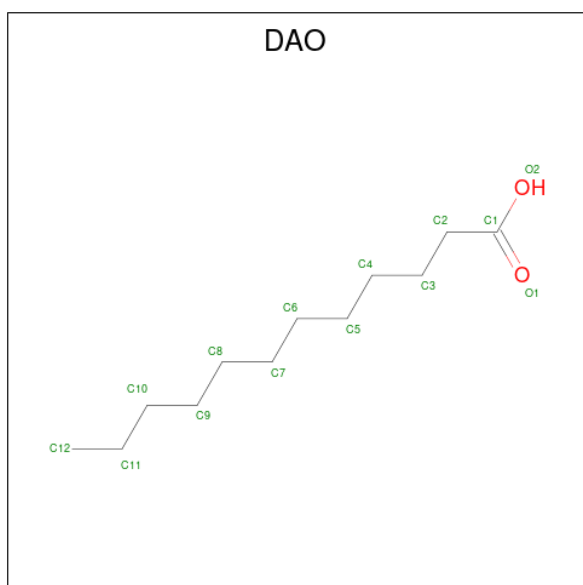
There are 3 unique types of molecules in this entry. The entry contains 7176 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Hepatocyte nuclear factor 4-alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	223	Total	C	N	O	S	0	0	0
			1777	1140	298	329	10			
1	B	218	Total	C	N	O	S	0	0	0
			1745	1122	293	320	10			
1	C	220	Total	C	N	O	S	0	0	0
			1759	1131	295	323	10			
1	D	221	Total	C	N	O	S	0	0	0
			1765	1134	296	325	10			

- Molecule 2 is LAURIC ACID (CCD ID: DAO) (formula: C₁₂H₂₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			14	12	2		
2	B	1	Total	C	O	0	0
			14	12	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	C	O	0	0
			14	12	2		
2	D	1	Total	C	O	0	0
			14	12	2		

- Molecule 3 is water.

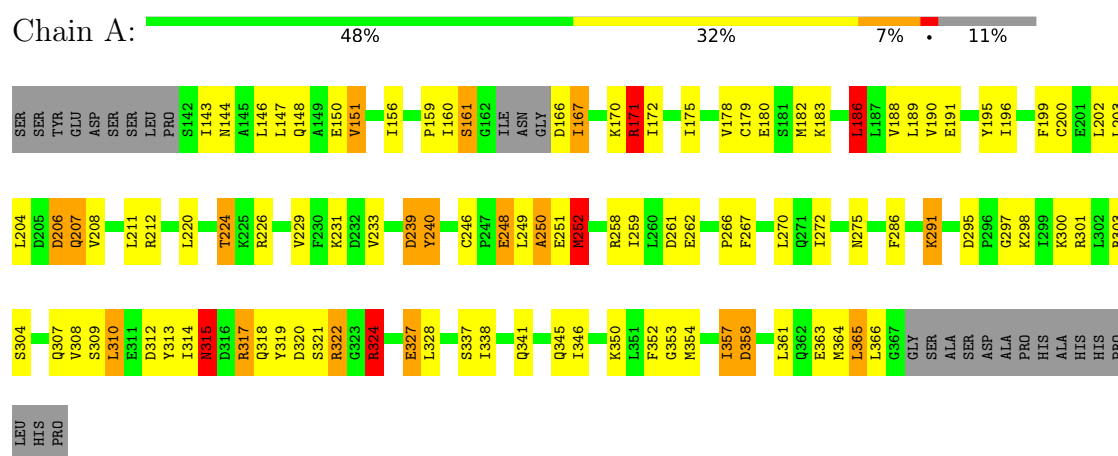
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	17	Total	O	0	0
			17	17		
3	B	22	Total	O	0	0
			22	22		
3	C	19	Total	O	0	0
			19	19		
3	D	16	Total	O	0	0
			16	16		

3 Residue-property plots

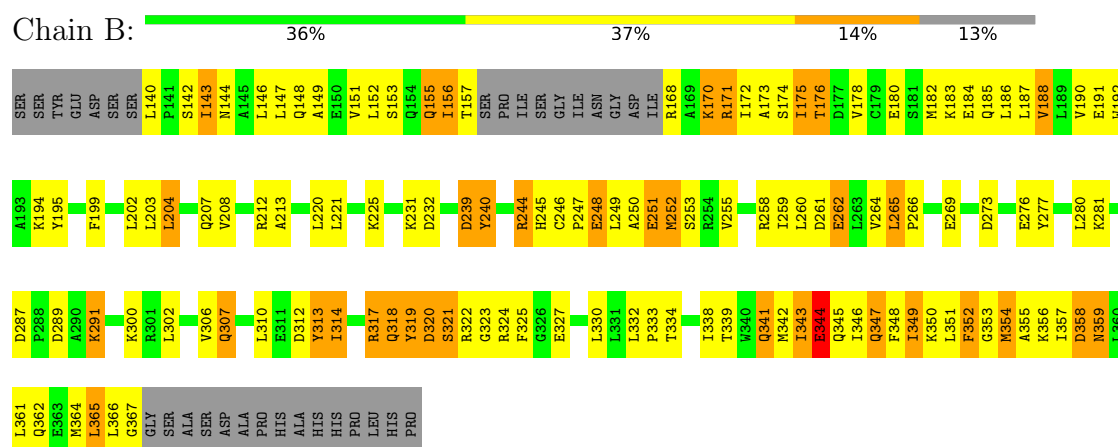
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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 was not executed.

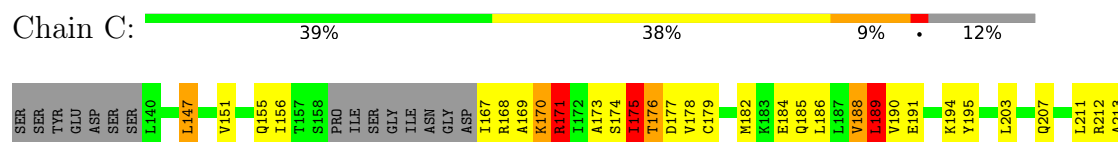
• Molecule 1: Hepatocyte nuclear factor 4-alpha

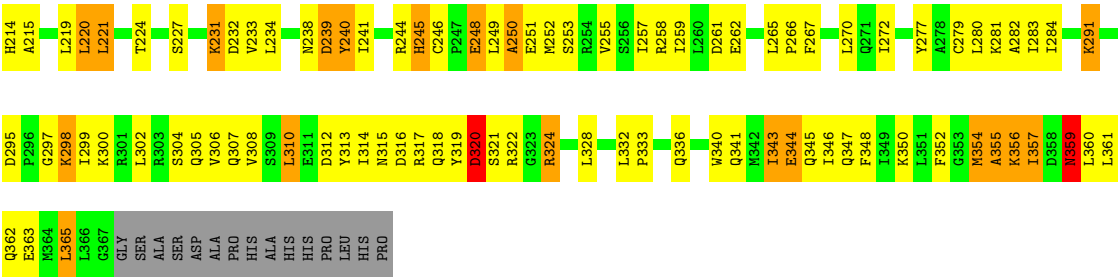


• Molecule 1: Hepatocyte nuclear factor 4-alpha

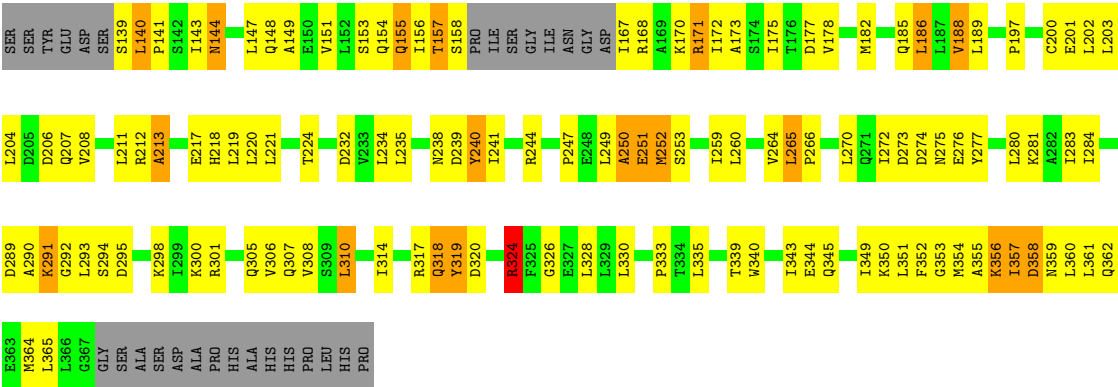
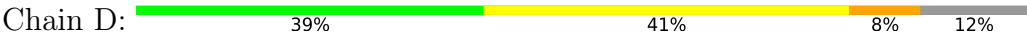


• Molecule 1: Hepatocyte nuclear factor 4-alpha





● Molecule 1: Hepatocyte nuclear factor 4-alpha



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	102.29Å 102.29Å 227.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.80	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.237 , 0.282	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7176	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

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: DAO

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	0.49	0/1803	1.03	8/2435 (0.3%)
1	B	0.50	0/1771	1.03	11/2392 (0.5%)
1	C	0.51	0/1785	1.08	9/2411 (0.4%)
1	D	0.47	0/1791	0.98	5/2419 (0.2%)
All	All	0.49	0/7150	1.03	33/9657 (0.3%)

There are no bond length outliers.

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	347	GLN	N-CA-C	-13.90	96.33	113.01
1	A	206	ASP	N-CA-C	-11.11	101.95	114.62
1	C	359	ASN	N-CA-C	-10.43	100.29	113.23
1	B	358	ASP	N-CA-C	-9.35	101.63	113.23
1	D	238	ASN	N-CA-C	-8.45	101.11	112.26

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	1777	0	1834	94	0
1	B	1745	0	1806	130	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1759	0	1822	129	0
1	D	1765	0	1827	127	0
2	A	14	0	23	1	0
2	B	14	0	23	3	0
2	C	14	0	23	1	0
2	D	14	0	23	1	0
3	A	17	0	0	3	0
3	B	22	0	0	3	0
3	C	19	0	0	3	0
3	D	16	0	0	4	0
All	All	7176	0	7381	470	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 32.

The worst 5 of 470 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:D:340:TRP:NE1	3:D:48:HOH:O	1.86	1.07
1:C:291:LYS:HD2	1:C:291:LYS:H	1.24	1.01
1:C:324:ARG:HH11	1:C:324:ARG:HG2	1.25	1.01
1:D:356:LYS:HE3	1:D:356:LYS:HA	1.41	1.00
1:C:170:LYS:O	1:C:171:ARG:HB2	1.64	0.98

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	219/250 (88%)	189 (86%)	19 (9%)	11 (5%)	1 5
1	B	214/250 (86%)	180 (84%)	19 (9%)	15 (7%)	1 2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	216/250 (86%)	186 (86%)	20 (9%)	10 (5%)	2	6
1	D	217/250 (87%)	183 (84%)	22 (10%)	12 (6%)	1	4
All	All	866/1000 (87%)	738 (85%)	80 (9%)	48 (6%)	1	4

5 of 48 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	161	SER
1	A	250	ALA
1	A	358	ASP
1	B	143	ILE
1	B	175	ILE

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	198/220 (90%)	176 (89%)	22 (11%)	6	20
1	B	194/220 (88%)	178 (92%)	16 (8%)	10	33
1	C	196/220 (89%)	176 (90%)	20 (10%)	7	23
1	D	197/220 (90%)	183 (93%)	14 (7%)	13	39
All	All	785/880 (89%)	713 (91%)	72 (9%)	8	27

5 of 72 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	359	ASN
1	D	360	LEU
1	D	168	ARG
1	D	300	LYS
1	B	188	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	268	GLN
1	C	341	GLN
1	D	341	GLN
1	C	315	ASN
1	C	345	GLN

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](#)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	DAO	B	701	-	13,13,13	1.39	2 (15%)	13,13,13	1.73	3 (23%)
2	DAO	A	700	-	13,13,13	1.42	2 (15%)	13,13,13	1.72	3 (23%)
2	DAO	C	702	-	13,13,13	1.23	2 (15%)	13,13,13	1.85	3 (23%)
2	DAO	D	703	-	13,13,13	1.35	2 (15%)	13,13,13	1.71	2 (15%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	DAO	B	701	-	-	6/11/11/11	-
2	DAO	A	700	-	-	6/11/11/11	-
2	DAO	C	702	-	-	8/11/11/11	-
2	DAO	D	703	-	-	8/11/11/11	-

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	700	DAO	O1-C1	4.06	1.35	1.22
2	B	701	DAO	O1-C1	3.62	1.33	1.22
2	D	703	DAO	O1-C1	3.41	1.33	1.22
2	C	702	DAO	O1-C1	3.20	1.32	1.22
2	B	701	DAO	O2-C1	-2.91	1.21	1.30

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	702	DAO	O1-C1-C2	-4.62	108.42	123.09
2	D	703	DAO	O1-C1-C2	-4.42	109.07	123.09
2	A	700	DAO	O1-C1-C2	-4.37	109.22	123.09
2	B	701	DAO	O1-C1-C2	-4.21	109.73	123.09
2	C	702	DAO	O2-C1-C2	3.97	126.56	114.00

There are no chirality outliers.

5 of 28 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	703	DAO	C1-C2-C3-C4
2	A	700	DAO	C1-C2-C3-C4
2	C	702	DAO	C4-C5-C6-C7
2	C	702	DAO	C11-C10-C9-C8
2	D	703	DAO	C3-C4-C5-C6

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	701	DAO	3	0
2	A	700	DAO	1	0
2	C	702	DAO	1	0
2	D	703	DAO	1	0

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](#)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.