



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 07:02 PM UTC

PDB ID : 1IEJ / pdb_00001iej
Title : OVOTRANSFERRIN, N-TERMINAL LOBE, HOLO FORM, AT 1.65 Å RESOLUTION
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Deposited on : 2001-04-10
Resolution : 1.65 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
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

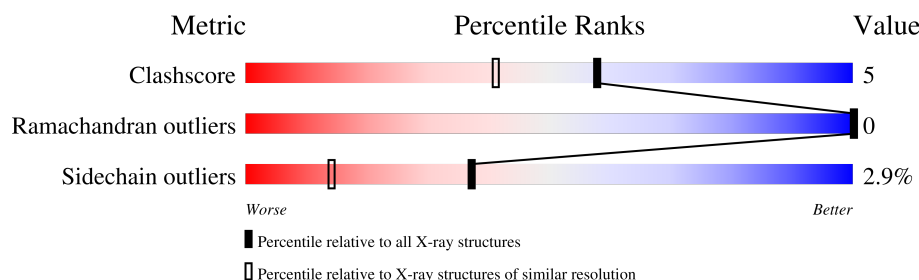
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.65 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	2662 (1.66-1.66)
Ramachandran outliers	187476	2621 (1.66-1.66)
Sidechain outliers	187428	2621 (1.66-1.66)

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	332	 83% 14% ..

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2827 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 OVOTRANSFERRIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	329	2566	1617	437	496	16	0	5	0

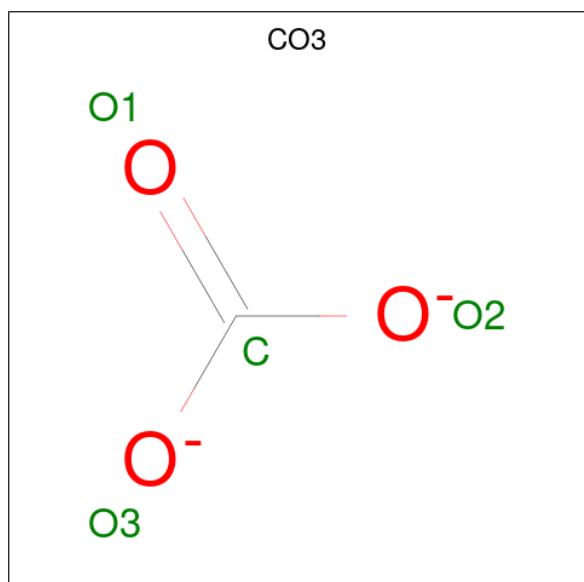
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	58	THR	SER	conflict	UNP P02789
A	64	VAL	ALA	conflict	UNP P02789

- Molecule 2 is FE (III) ION (CCD ID: FE) (formula: Fe).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Fe 1 1	0	0

- Molecule 3 is CARBONATE ION (CCD ID: CO3) (formula: CO₃).



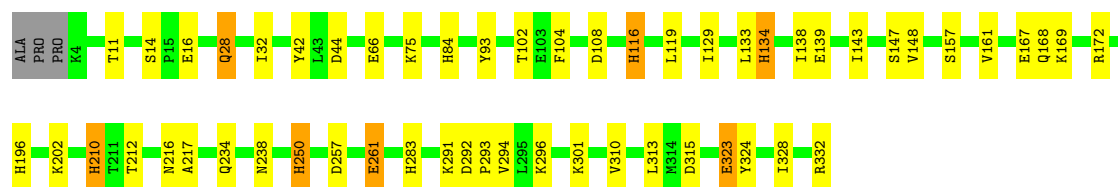
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	1	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	256	Total	O	0	0
			256	256		

Note EDS was not executed.

Chain A: 83% 14% ..



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	46.46 Å 85.95 Å 76.10 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 1.65	Depositor
% Data completeness (in resolution range)	(Not available) (10.00-1.65)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.173 , 0.242	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2827	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CO3, FE

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	0.95	8/2639 (0.3%)	1.49	23/3568 (0.6%)

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	1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	210	HIS	CD2-NE2	-7.09	1.30	1.37
1	A	116	HIS	CD2-NE2	-6.87	1.30	1.37
1	A	283	HIS	CD2-NE2	-6.66	1.30	1.37
1	A	196	HIS	CD2-NE2	-5.91	1.31	1.37
1	A	84	HIS	CD2-NE2	-5.79	1.31	1.37
1	A	116	HIS	CG-ND1	-5.76	1.31	1.38
1	A	294	VAL	CA-CB	5.56	1.61	1.54
1	A	250	HIS	CG-ND1	-5.15	1.32	1.38

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	102	THR	N-CA-C	-8.95	98.47	110.55
1	A	257	ASP	CA-CB-CG	7.86	120.46	112.60
1	A	167	GLU	N-CA-C	7.14	120.37	108.73
1	A	292	ASP	CA-CB-CG	7.11	119.71	112.60
1	A	134	HIS	CA-CB-CG	7.09	120.89	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	212	THR	N-CA-C	6.57	118.44	111.28
1	A	14	SER	CA-C-O	-6.56	112.49	118.79
1	A	196	HIS	CA-CB-CG	-6.00	107.80	113.80
1	A	102	THR	CA-C-N	-5.74	112.96	122.08
1	A	102	THR	C-N-CA	-5.74	112.96	122.08
1	A	283	HIS	CB-CG-CD2	-5.40	124.19	131.20
1	A	196	HIS	CB-CG-CD2	-5.37	124.22	131.20
1	A	315	ASP	CA-CB-CG	5.33	117.93	112.60
1	A	32	ILE	CA-C-O	5.30	125.90	120.39
1	A	102	THR	O-C-N	-5.27	116.84	122.85
1	A	216	ASN	N-CA-C	5.19	120.47	114.04
1	A	147	SER	N-CA-C	5.04	117.19	110.53
1	A	44	ASP	CA-CB-CG	-5.03	107.57	112.60
1	A	217	ALA	CA-C-N	5.02	124.80	119.28
1	A	217	ALA	C-N-CA	5.02	124.80	119.28
1	A	310	VAL	CA-C-N	5.01	125.01	119.90
1	A	310	VAL	C-N-CA	5.01	125.01	119.90
1	A	323	GLU	CB-CG-CD	5.00	121.11	112.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	42	TYR	Sidechain

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	2566	0	2510	23	0
2	A	1	0	0	0	0
3	A	4	0	0	0	0
4	A	256	0	0	4	0
All	All	2827	0	2510	23	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 5.

All (23) 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:202:LYS:HA	1:A:202:LYS:HE2	1.72	0.71
1:A:129:ILE:O	1:A:133:LEU:HD13	2.04	0.58
1:A:293:PRO:HA	1:A:296:LYS:HD2	1.85	0.58
1:A:133:LEU:HD12	1:A:138:ILE:HB	1.88	0.56
1:A:168:GLN:HB3	4:A:599:HOH:O	2.10	0.52
1:A:261[B]:GLU:HG2	4:A:498:HOH:O	2.09	0.52
1:A:157:SER:O	1:A:169:LYS:HE3	2.11	0.51
1:A:104:PHE:HB2	1:A:108:ASP:HB2	1.93	0.51
1:A:66:GLU:HG2	1:A:332:ARG:HH12	1.75	0.50
1:A:250:HIS:CE1	1:A:301:LYS:HD2	2.47	0.49
1:A:324:TYR:CZ	1:A:328:ILE:HD11	2.49	0.48
1:A:28:GLN:HE21	1:A:28:GLN:HA	1.79	0.48
1:A:93:TYR:H	1:A:210:HIS:CD2	2.33	0.46
1:A:11:THR:HB	1:A:16:GLU:HB3	1.97	0.46
1:A:134:HIS:HB2	4:A:384:HOH:O	2.16	0.45
1:A:234:GLN:HE21	1:A:238:ASN:HD22	1.63	0.45
1:A:332:ARG:HA	1:A:332:ARG:HD3	1.71	0.44
1:A:168:GLN:HE22	1:A:172:ARG:HE	1.65	0.43
1:A:116:HIS:CD2	1:A:161:VAL:HG22	2.53	0.43
1:A:291:LYS:HG2	1:A:296:LYS:HE2	2.01	0.43
1:A:234:GLN:NE2	1:A:238:ASN:HD22	2.19	0.41
1:A:148:VAL:HG21	4:A:433:HOH:O	2.20	0.41
1:A:168:GLN:NE2	1:A:172:ARG:HE	2.18	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	332/332 (100%)	322 (97%)	10 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	280/277 (101%)	270 (96%)	10 (4%)	31 9

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	GLN
1	A	75	LYS
1	A	119	LEU
1	A	139	GLU
1	A	143	ILE
1	A	261[A]	GLU
1	A	261[B]	GLU
1	A	313[A]	LEU
1	A	313[B]	LEU
1	A	323	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	28	GLN
1	A	29	GLN
1	A	51	ASN
1	A	63	GLN
1	A	168	GLN
1	A	173	GLN
1	A	210	HIS
1	A	216	ASN
1	A	220	GLN
1	A	234	GLN
1	A	238	ASN
1	A	243	ASN

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Mol	Chain	Res	Type
1	A	258	ASN
1	A	329	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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	$\# Z > 2$
3	CO3	A	334	2	3,3,3	1.14	0	2,3,3	0.23	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.