



Full wwPDB EM Validation Report ⓘ

Apr 15, 2026 – 10:47 AM UTC

PDB ID : 1SUV / pdb_00001suv
Title : Structure of Human Transferrin Receptor-Transferrin Complex
Authors : Cheng, Y.; Zak, O.; Aisen, P.; Harrison, S.C.; Walz, T.
Deposited on : 2004-03-26
Resolution : 7.50 Å (reported)
Based on initial models : 1JNF, 1A8E, 1CX8

This is a Full wwPDB EM Validation 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.

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 : **FAILED**
Mogul : 2022.3.0, CSD as543be (2022)
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:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.50 Å.

There are no overall percentile quality scores available for this entry.

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 20612 atoms, of which 0 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 Transferrin receptor protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	639	Total	C	N	O	S	0	0
			5056	3244	846	952	14		
1	B	639	Total	C	N	O	S	0	0
			5056	3244	846	952	14		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	172	GLU	GLN	SEE REMARK 999	UNP P02786
A	613	GLU	ARG	SEE REMARK 999	UNP P02786
B	172	GLU	GLN	SEE REMARK 999	UNP P02786
B	613	GLU	ARG	SEE REMARK 999	UNP P02786

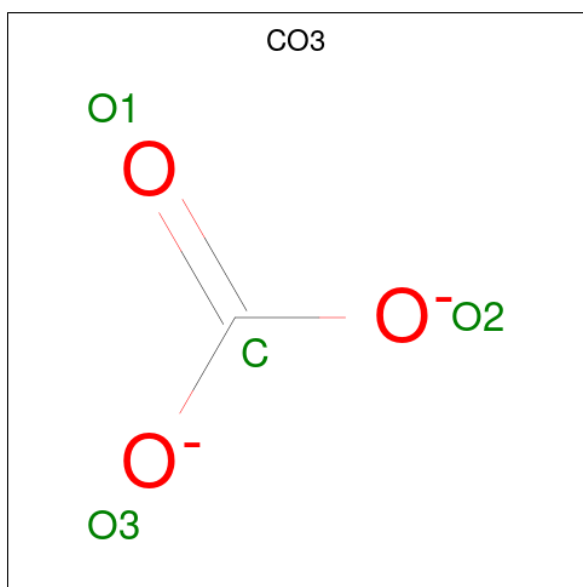
- Molecule 2 is a protein called Serotransferrin, N-lobe.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	329	Total	C	N	O	S	5	0
			2567	1621	440	485	21		
2	D	329	Total	C	N	O	S	5	0
			2567	1621	440	485	21		

- Molecule 3 is a protein called Serotransferrin, C-lobe.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	345	Total	C	N	O	S	0	0
			2669	1662	469	512	26		
3	F	345	Total	C	N	O	S	0	0
			2669	1662	469	512	26		

- Molecule 4 is CARBONATE ION (CCD ID: CO3) (formula: CO₃).



Mol	Chain	Residues	Atoms			AltConf
4	C	1	Total	C	O	1
			8	2	6	
4	D	1	Total	C	O	1
			8	2	6	
4	E	1	Total	C	O	0
			4	1	3	
4	F	1	Total	C	O	0
			4	1	3	

- Molecule 5 is FE (III) ION (CCD ID: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		AltConf
5	C	1	Total	Fe	0
			1	1	
5	D	1	Total	Fe	0
			1	1	
5	E	1	Total	Fe	0
			1	1	
5	F	1	Total	Fe	0
			1	1	

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

GLOBAL-STATISTICS INFOmissingINFO

3 Model quality [i](#)

3.1 Standard geometry [i](#)

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3.2 Too-close contacts [i](#)

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3.3 Torsion angles [i](#)

3.3.1 Protein backbone [i](#)

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

3.3.2 Protein sidechains [i](#)

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

3.3.3 RNA [i](#)

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

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

There are no non-standard protein/DNA/RNA residues in this entry.

3.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

3.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 4 are monoatomic - leaving 6 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	$\# Z > 2$
4	CO3	C	338[A]	5	3,3,3	0.22	0	2,3,3	0.16	0
4	CO3	E	701	5	3,3,3	1.21	1 (33%)	2,3,3	1.59	1 (50%)
4	CO3	C	338[B]	5	3,3,3	1.19	0	2,3,3	0.52	0
4	CO3	F	701	5	3,3,3	1.20	1 (33%)	2,3,3	1.59	1 (50%)
4	CO3	D	338[A]	5	3,3,3	0.21	0	2,3,3	0.14	0
4	CO3	D	338[B]	5	3,3,3	1.18	0	2,3,3	0.55	0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	701	CO3	O1-C	2.04	1.32	1.25
4	F	701	CO3	O1-C	2.02	1.32	1.25

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	701	CO3	O3-C-O1	2.10	125.04	119.68
4	F	701	CO3	O3-C-O1	2.10	125.04	119.68

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

3.7 Other polymers

There are no such residues in this entry.

3.8 Polymer linkage issues

There are no chain breaks in this entry.