



wwPDB EM Validation Summary Report ⓘ

Sep 21, 2025 – 12:54 AM JST

PDB ID : 9UTB / pdb_00009utb
EMDB ID : EMD-64487
Title : The full-length human sweet taste receptor TAS1R2 and TAS1R3 in the sucralose-bound state
Authors : Shi, Z.J.; Xu, W.X.; Yue, X.L.; Wu, L.J.; Hua, T.; Liu, Z.J.
Deposited on : 2025-05-03
Resolution : 3.59 Å(reported)

This is a wwPDB EM 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/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:

EMDB validation analysis : **FAILED**
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : **FAILED**
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.45.1

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 3.59 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

There are 3 unique types of molecules in this entry. The entry contains 12471 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 Taste receptor type 1 member 2,Taste receptor type 1 member 2,Taste receptor type 1 member 2,Engineered red fluorescent protein mScarlet3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	781	Total	C	N	O	S	0	0
			6235	4041	1021	1125	48		

There are 29 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	MET	-	initiating methionine	UNP Q8TE23
A	-2	LYS	-	expression tag	UNP Q8TE23
A	-1	THR	-	expression tag	UNP Q8TE23
A	0	ILE	-	expression tag	UNP Q8TE23
A	1	ILE	-	expression tag	UNP Q8TE23
A	2	ALA	-	expression tag	UNP Q8TE23
A	3	LEU	-	expression tag	UNP Q8TE23
A	4	SER	-	expression tag	UNP Q8TE23
A	5	TYR	-	expression tag	UNP Q8TE23
A	6	ILE	-	expression tag	UNP Q8TE23
A	7	PHE	-	expression tag	UNP Q8TE23
A	8	CYS	-	expression tag	UNP Q8TE23
A	9	LEU	-	expression tag	UNP Q8TE23
A	10	VAL	-	expression tag	UNP Q8TE23
A	11	PHE	-	expression tag	UNP Q8TE23
A	12	ALA	-	expression tag	UNP Q8TE23
A	13	GLY	-	expression tag	UNP Q8TE23
A	14	SER	-	expression tag	UNP Q8TE23
A	15	ASP	-	expression tag	UNP Q8TE23
A	16	TYR	-	expression tag	UNP Q8TE23
A	17	LYS	-	expression tag	UNP Q8TE23
A	18	ASP	-	expression tag	UNP Q8TE23
A	19	ASP	-	expression tag	UNP Q8TE23
A	20	ASP	-	expression tag	UNP Q8TE23
A	21	ASP	-	expression tag	UNP Q8TE23
A	22	LYS	-	expression tag	UNP Q8TE23
A	23	GLY	-	expression tag	UNP Q8TE23

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Chain	Residue	Modelled	Actual	Comment	Reference
A	24	SER	-	expression tag	UNP Q8TE23
A	25	ALA	-	expression tag	UNP Q8TE23

- Molecule 2 is a protein called Taste receptor type 1 member 3,mNeonGreen.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	803	Total	C	N	O	S	0	0
			6213	3982	1080	1101	50		

There are 63 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-7	MET	-	initiating methionine	UNP Q7RTX0
B	-6	LYS	-	expression tag	UNP Q7RTX0
B	-5	THR	-	expression tag	UNP Q7RTX0
B	-4	ILE	-	expression tag	UNP Q7RTX0
B	-3	ILE	-	expression tag	UNP Q7RTX0
B	-2	ALA	-	expression tag	UNP Q7RTX0
B	-1	LEU	-	expression tag	UNP Q7RTX0
B	0	SER	-	expression tag	UNP Q7RTX0
B	1	TYR	-	expression tag	UNP Q7RTX0
B	2	ILE	-	expression tag	UNP Q7RTX0
B	3	PHE	-	expression tag	UNP Q7RTX0
B	4	CYS	-	expression tag	UNP Q7RTX0
B	5	LEU	-	expression tag	UNP Q7RTX0
B	6	VAL	-	expression tag	UNP Q7RTX0
B	7	PHE	-	expression tag	UNP Q7RTX0
B	8	ALA	-	expression tag	UNP Q7RTX0
B	9	GLY	-	expression tag	UNP Q7RTX0
B	10	SER	-	expression tag	UNP Q7RTX0
B	11	ASP	-	expression tag	UNP Q7RTX0
B	12	TYR	-	expression tag	UNP Q7RTX0
B	13	LYS	-	expression tag	UNP Q7RTX0
B	14	ASP	-	expression tag	UNP Q7RTX0
B	15	ASP	-	expression tag	UNP Q7RTX0
B	16	ASP	-	expression tag	UNP Q7RTX0
B	17	ASP	-	expression tag	UNP Q7RTX0
B	18	LYS	-	expression tag	UNP Q7RTX0
B	19	GLY	-	expression tag	UNP Q7RTX0
B	20	SER	-	expression tag	UNP Q7RTX0
B	853	GLY	-	linker	UNP Q7RTX0
B	854	SER	-	linker	UNP Q7RTX0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	855	SER	-	linker	UNP Q7RTX0
B	856	GLY	-	linker	UNP Q7RTX0
B	857	LEU	-	linker	UNP Q7RTX0
B	858	GLU	-	linker	UNP Q7RTX0
B	859	VAL	-	linker	UNP Q7RTX0
B	860	LEU	-	linker	UNP Q7RTX0
B	861	PHE	-	linker	UNP Q7RTX0
B	862	GLN	-	linker	UNP Q7RTX0
B	863	GLY	-	linker	UNP Q7RTX0
B	864	PRO	-	linker	UNP Q7RTX0
B	865	SER	-	linker	UNP Q7RTX0
B	866	GLY	-	linker	UNP Q7RTX0
B	867	GLY	-	linker	UNP Q7RTX0
B	1103	GLY	-	expression tag	UNP A0A1S4NYF2
B	1104	SER	-	expression tag	UNP A0A1S4NYF2
B	1105	GLU	-	expression tag	UNP A0A1S4NYF2
B	1106	ASN	-	expression tag	UNP A0A1S4NYF2
B	1107	LEU	-	expression tag	UNP A0A1S4NYF2
B	1108	TYR	-	expression tag	UNP A0A1S4NYF2
B	1109	PHE	-	expression tag	UNP A0A1S4NYF2
B	1110	GLN	-	expression tag	UNP A0A1S4NYF2
B	1111	SER	-	expression tag	UNP A0A1S4NYF2
B	1112	SER	-	expression tag	UNP A0A1S4NYF2
B	1113	GLY	-	expression tag	UNP A0A1S4NYF2
B	1114	HIS	-	expression tag	UNP A0A1S4NYF2
B	1115	HIS	-	expression tag	UNP A0A1S4NYF2
B	1116	HIS	-	expression tag	UNP A0A1S4NYF2
B	1117	HIS	-	expression tag	UNP A0A1S4NYF2
B	1118	HIS	-	expression tag	UNP A0A1S4NYF2
B	1119	HIS	-	expression tag	UNP A0A1S4NYF2
B	1120	HIS	-	expression tag	UNP A0A1S4NYF2
B	1121	HIS	-	expression tag	UNP A0A1S4NYF2
B	1122	HIS	-	expression tag	UNP A0A1S4NYF2

- Molecule 3 is an oligosaccharide called 4-chloro-4-deoxy-alpha-D-galactopyranose-(1-2)-1,6-dichloro-1,6-dideoxy-beta-D-fructofuranose.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	2	Total	C	Cl	O	0	0
			23	12	3	8		

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

3 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	139714	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor

4 Model quality [i](#)

4.1 Standard geometry [i](#)

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4.2 Too-close contacts [i](#)

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

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

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

4.3.2 Protein sidechains [i](#)

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

4.3.3 RNA [i](#)

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

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

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

4.5 Carbohydrates [i](#)

2 monosaccharides 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
3	RRY	C	1	3	10,12,12	0.74	0	8,18,18	0.61	0
3	RRJ	C	2	3	10,11,12	1.21	1 (10%)	11,15,17	1.07	0

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
3	RRY	C	1	3	-	1/5/24/24	0/1/1/1
3	RRJ	C	2	3	-	0/2/19/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	2	RRJ	C4-C5	2.64	1.55	1.52

There are no bond angle outliers.

There are no chirality outliers.

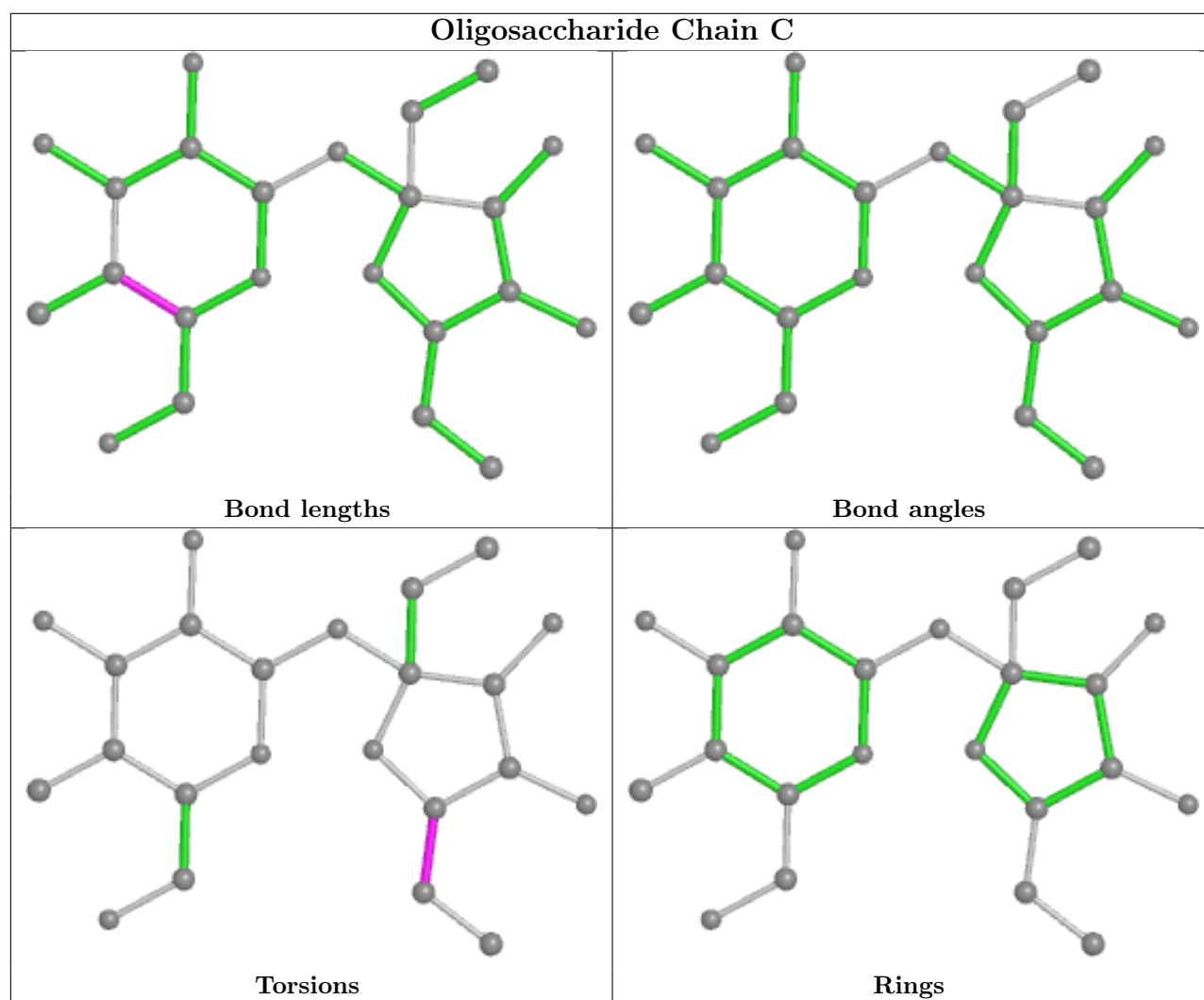
All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	1	RRY	C4-C5-C6-CL6

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



4.6 Ligand geometry [i](#)

There are no ligands in this entry.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.