

# wwPDB EM Validation Summary Report (i)

#### Dec 24, 2023 – 12:07 AM JST

PDB ID	:	8W8A
EMDB ID	:	EMD-37350
Title	:	Cryo-EM structure of the RO5256390-TAAR1 complex
Authors	:	Liu, H.; Zheng, Y.; Wang, Y.; Wang, Y.; He, X.; Xu, P.; Huang, S.; Yuan, Q.;
		Zhang, X.; Wang, S.; Xu, H.E.; Xu, F.
Deposited on		
Resolution	:	2.80 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 (i) 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 (i)) were used in the production of this report:

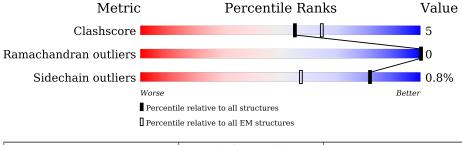
EMDB validation analysis	:	FAILED
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	FAILED
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

## 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $ELECTRON\ MICROSCOPY$ 

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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${ m EM~structures}\ (\#{ m Entries})$
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 <=5%

Mol	Chain	Length	Quality of chain		
1	А	246	82%	1	.4% •
2	В	345	83%		14% •
3	G	71	77%	•	20%
4	Ν	139	76%	15%	• 9%
5	R	339	73%	12%	15%



# 2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 8260 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.

 $\bullet\,$  Molecule 1 is a protein called Guanine nucleotide-binding protein G(s) subunit alpha isoforms short.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	А	236	Total 1934	C 1216	N 349	O 362	${ m S} 7$	0	0

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms				AltConf	Trace	
2	В	338	Total 2597	C 1601	N 467	O 508	S 21	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
В	-4	MET	-	initiating methionine	UNP P62873
В	-3	GLY	-	expression tag	UNP P62873
В	-2	SER	-	expression tag	UNP P62873
В	-1	LEU	-	expression tag	UNP P62873
В	0	LEU	-	expression tag	UNP P62873
В	1	GLN	-	expression tag	UNP P62873

- Molecule 3 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms				AltConf	Trace	
3	G	57	Total 436	C 273	N 77	O 83	${ m S} { m 3}$	0	0

• Molecule 4 is a protein called Nanobody35.

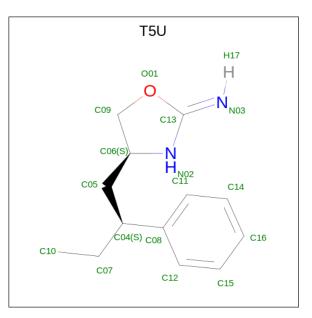
Mol	Chain	Residues	Atoms					AltConf	Trace
4	Ν	127	Total 967	C 602	N 169	0 190	S 6	0	0



• Molecule 5 is a protein called Trace amine-associated receptor 1.

Mol	Chain	Residues	Atoms				AltConf	Trace	
5	R	287	Total 2309	C 1545	N 358	O 380	S 26	0	0

• Molecule 6 is (4S)-4-[(2S)-2-phenylbutyl]-1,3-oxazolidin-2-imine (three-letter code: T5U) (formula:  $C_{13}H_{18}N_2O$ ).



Mol	Chain	Residues	Atoms				AltConf
6	R	1	Total 16	C 13	N 2	0 1	0

• Molecule 7 is water.

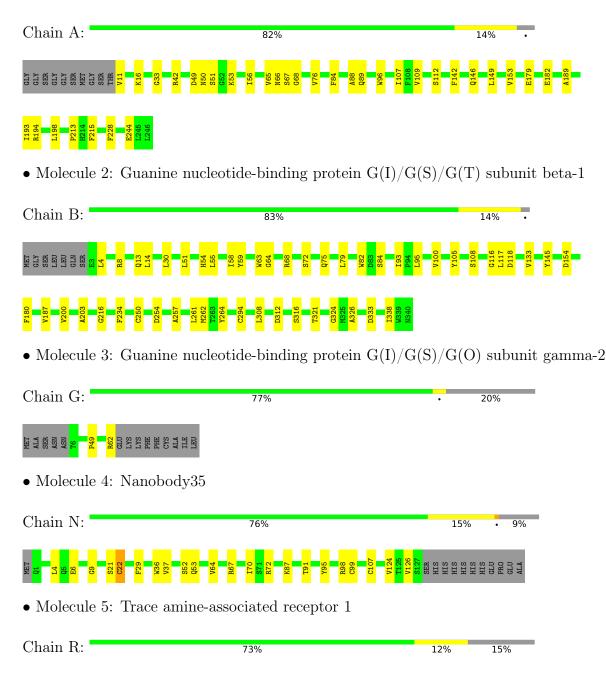
Mol	Chain	Residues	Atoms	AltConf
7	R	1	Total O 1 1	0



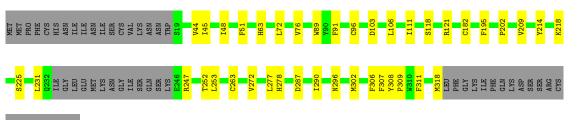
# 3 Residue-property plots (i)

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.

• Molecule 1: Guanine nucleotide-binding protein G(s) subunit alpha isoforms short







LYS LEU PHE LEU GLU LEU SER SER



# 4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	145907	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{\AA}^2)$	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor



# 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:  $\mathrm{T5U}$ 

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		
	Unam	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.35	0/1973	0.56	0/2659	
2	В	0.28	0/2644	0.53	0/3585	
3	G	0.23	0/442	0.43	0/597	
4	N	0.36	0/987	0.54	0/1337	
5	R	0.32	0/2378	0.48	0/3230	
All	All	0.32	0/8424	0.52	0/11408	

There are no bond length outliers.

There are no bond angle outliers.

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	А	1934	0	1891	21	0
2	В	2597	0	2496	31	0
3	G	436	0	448	1	0
4	N	967	0	935	12	0
5	R	2309	0	2334	26	0
6	R	16	0	0	1	0
7	R	1	0	0	0	0
All	All	8260	0	8104	85	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.

The worst 5 of 85 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)
5:R:252:THR:HG22	5:R:307:PHE:CE2	2.37	0.60
5:R:252:THR:HG22	5:R:307:PHE:HE2	1.68	0.58
1:A:76:VAL:HG21	1:A:228:PHE:HB2	1.87	0.55
5:R:89:TRP:CD2	5:R:182:CYS:SG	3.01	0.53
5:R:72:LEU:HD13	5:R:106:LEU:HB2	1.90	0.53

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 PDB entries followed by that with respect to all EM entries.

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	Perce	entiles
1	А	234/246~(95%)	229~(98%)	5(2%)	0	100	100
2	В	336/345~(97%)	325~(97%)	11 (3%)	0	100	100
3	G	55/71~(78%)	54 (98%)	1 (2%)	0	100	100
4	Ν	125/139~(90%)	121 (97%)	4(3%)	0	100	100
5	R	283/339~(84%)	275~(97%)	8(3%)	0	100	100
All	All	1033/1140~(91%)	1004 (97%)	29 (3%)	0	100	100

There are no Ramachandran outliers to report.

#### 5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.



Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	А	207/213~(97%)	206 (100%)	1 (0%)	88 96
2	В	280/287~(98%)	280 (100%)	0	100 100
3	G	46/58~(79%)	45~(98%)	1 (2%)	52 83
4	Ν	105/116~(90%)	103~(98%)	2(2%)	57 85
5	R	256/309~(83%)	253~(99%)	3~(1%)	71 92
All	All	894/983~(91%)	887~(99%)	7~(1%)	82 94

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

5 of 7 residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
4	Ν	22	CYS
5	R	225	SER
5	R	278	HIS
5	R	277	LEU
4	Ν	21	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	59	GLN
1	А	130	ASN
1	А	146	GLN
2	В	13	GLN
4	N	120	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 monosaccharides in this entry.



## 5.6 Ligand geometry (i)

1 ligand is 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	ol Type Chain Re	vpe Chain 1		Link	Bo	ond leng	$\mathbf{ths}$	В	ond ang	les
WIOI	Type	Ullalli	n Res Link		Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2
6	T5U	R	401	-	16,17,17	1.41	3 (18%)	18,22,22	2.53	3 (16%)

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
6	T5U	R	401	-	-	6/10/19/19	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	R	401	T5U	C13-N03	3.26	1.35	1.27
6	R	401	T5U	C09-C06	2.71	1.57	1.52
6	R	401	T5U	O01-C09	-2.51	1.40	1.45

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
6	R	401	T5U	O01-C13-N02	8.22	116.04	110.62
6	R	401	T5U	C06-N02-C13	-4.81	106.09	113.13
6	R	401	T5U	C09-C06-N02	4.53	103.83	99.88

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	R	401	T5U	C07-C04-C05-C06
6	R	401	T5U	C08-C04-C05-C06

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Mol	Chain	Res	Type	Atoms
6	R	401	T5U	C05-C04-C07-C10
6	R	401	T5U	C07-C04-C08-C11
6	R	401	T5U	C07-C04-C08-C12

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	R	401	T5U	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.

