



wwPDB EM Validation Summary Report ⓘ

Jul 8, 2025 – 04:49 PM JST

PDB ID : 9LMP / pdb_00009lmp
EMDB ID : EMD-63220
Title : Cryo-EM structure of antagonist-bounded inactive human GPR4
Authors : Chen, L.N.; Zhou, H.; Xi, K.; Cheng, S.Z.; Liu, Y.F.; Fu, Y.F.; Ma, X.Y.; Xu, P.; Ji, S.Y.; Wang, W.W.; Shen, D.D.; Zhang, H.B.; Shen, Q.Y.; Chai, R.; Zhang, M.; Yang, L.; Han, F.; Mao, C.Y.; Cai, X.J.; Zhang, Y.
Deposited on : 2025-01-19
Resolution : 2.65 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

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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 : 4-5-2 with Phenix2.0rc1
buster-report : 1.1.7 (2018)
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) : 2.44

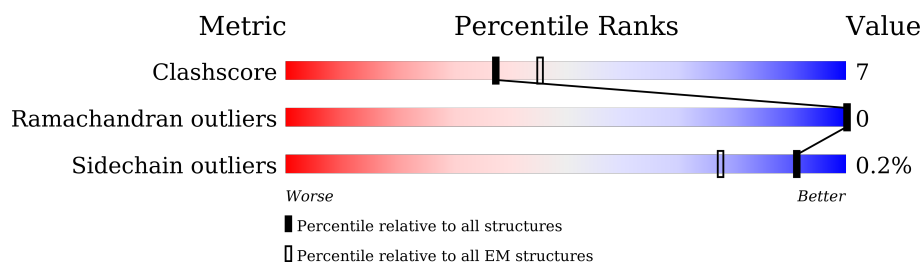
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.65 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)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	H	235	
2	L	216	
3	R	462	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6224 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 Heavy chain of anti-Bril Fab.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	H	225	Total	C	N	O	S	0	0
			1686	1072	280	329	5		

- Molecule 2 is a protein called Light chain of anti-Bril Fab.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L	212	Total	C	N	O	S	0	0
			1632	1025	272	330	5		

- Molecule 3 is a protein called G-protein coupled receptor 4,Soluble cytochrome b562.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	R	371	Total	C	N	O	S	0	0
			2875	1873	485	503	14		

There are 21 discrepancies between the modelled and reference sequences:

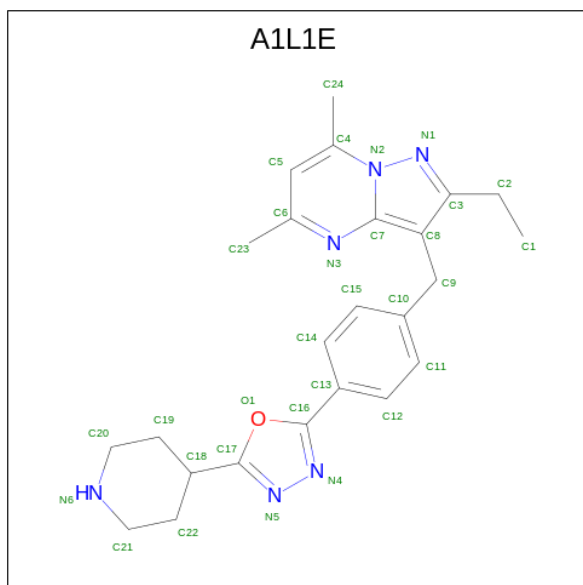
Chain	Residue	Modelled	Actual	Comment	Reference
R	209	ASP	-	linker	UNP P46093
R	210	LYS	-	linker	UNP P46093
R	211	ARG	-	linker	UNP P46093
R	212	LYS	-	linker	UNP P46093
R	219	TRP	MET	conflict	UNP P0ABE7
R	?	-	PRO	deletion	UNP P0ABE7
R	?	-	PRO	deletion	UNP P0ABE7
R	?	-	LYS	deletion	UNP P0ABE7
R	?	-	LEU	deletion	UNP P0ABE7
R	?	-	GLU	deletion	UNP P0ABE7
R	309	ILE	HIS	conflict	UNP P0ABE7
R	313	LEU	-	linker	UNP P0ABE7
R	314	GLU	-	linker	UNP P0ABE7
R	315	TYR	-	linker	UNP P0ABE7
R	316	LEU	-	linker	UNP P0ABE7

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Chain	Residue	Modelled	Actual	Comment	Reference
R	317	ASP	-	linker	UNP P0ABE7
R	318	GLY	-	linker	UNP P0ABE7
R	319	LEU	-	linker	UNP P0ABE7
R	320	GLU	-	linker	UNP P0ABE7
R	321	ARG	-	linker	UNP P0ABE7
R	322	ILE	-	linker	UNP P0ABE7

- Molecule 4 is NE52-QQ57 (CCD ID: A1L1E) (formula: C₂₄H₂₈N₆O) (labeled as "Ligand of Interest" by depositor).




Mol	Chain	Residues	Atoms				AltConf
4	R	1	Total	C	N	O	0
			31	24	6	1	

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.

- Molecule 1: Heavy chain of anti-Bril Fab

Chain H: 



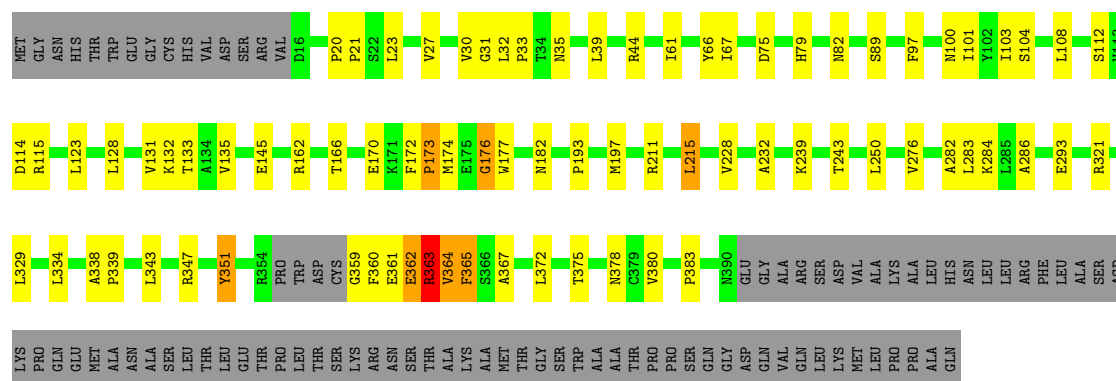
- Molecule 2: Light chain of anti-Bril Fab

Chain L: 



- Molecule 3: G-protein coupled receptor 4, Soluble cytochrome b562

Chain R: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	469564	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	52	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k 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: A1L1E

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	H	1.31	3/1734 (0.2%)	1.29	16/2369 (0.7%)
2	L	1.24	4/1667 (0.2%)	1.31	16/2264 (0.7%)
3	R	0.63	11/2946 (0.4%)	0.85	13/4012 (0.3%)
All	All	1.03	18/6347 (0.3%)	1.11	45/8645 (0.5%)

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
3	R	0	2

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	R	351	TYR	CA-C	-11.31	1.36	1.52
2	L	200	HIS	CB-CG	-10.29	1.35	1.50
3	R	367	ALA	CA-C	-9.51	1.39	1.52
3	R	321	ARG	C-N	8.77	1.45	1.33
3	R	365	PHE	C-N	8.63	1.44	1.33

The worst 5 of 45 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	R	367	ALA	N-CA-C	-14.01	96.64	113.88
3	R	362	GLU	N-CA-C	-12.90	96.00	112.90
3	R	215	LEU	O-C-N	-9.74	109.01	122.46
3	R	89	SER	CA-C-N	9.38	136.37	120.71
3	R	89	SER	C-N-CA	9.38	136.37	120.71

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	R	215	LEU	Mainchain
3	R	365	PHE	Mainchain

5.2 Too-close contacts

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	H	1686	0	1630	23	0
2	L	1632	0	1595	26	0
3	R	2875	0	2787	70	0
4	R	31	0	0	0	0
All	All	6224	0	6012	89	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 7.

The worst 5 of 89 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:H:198:VAL:CG1	1:H:202:SER:OG	2.07	1.02
1:H:198:VAL:HG12	1:H:202:SER:OG	1.61	1.00
2:L:97:LEU:CD2	3:R:239:LYS:HZ3	1.80	0.95
3:R:372:LEU:O	3:R:375:THR:HG22	1.69	0.93
2:L:97:LEU:CD2	3:R:239:LYS:NZ	2.36	0.89

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 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	Percentiles	
1	H	223/235 (95%)	219 (98%)	4 (2%)	0	100	100
2	L	210/216 (97%)	204 (97%)	6 (3%)	0	100	100
3	R	367/462 (79%)	356 (97%)	11 (3%)	0	100	100
All	All	800/913 (88%)	779 (97%)	21 (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 PDB entries followed by that with respect to all EM entries.

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	H	186/196 (95%)	186 (100%)	0	100	100
2	L	188/191 (98%)	188 (100%)	0	100	100
3	R	287/390 (74%)	286 (100%)	1 (0%)	91	96
All	All	661/777 (85%)	660 (100%)	1 (0%)	91	97

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	R	363	ARG

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

Mol	Chain	Res	Type
1	H	85	GLN
1	H	213	ASN
3	R	155	HIS
3	R	287	ASN
3	R	369	HIS

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 ⓘ

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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	A1L1E	R	501	-	25,35,35	1.04	2 (8%)	29,50,50	1.13	1 (3%)

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
4	A1L1E	R	501	-	-	2/8/22/22	0/5/5/5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	R	501	A1L1E	C24-C4	2.53	1.53	1.50
4	R	501	A1L1E	C7-N3	2.45	1.39	1.35

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	R	501	A1L1E	C5-C6-N3	-2.26	119.89	122.57

There are no chirality outliers.

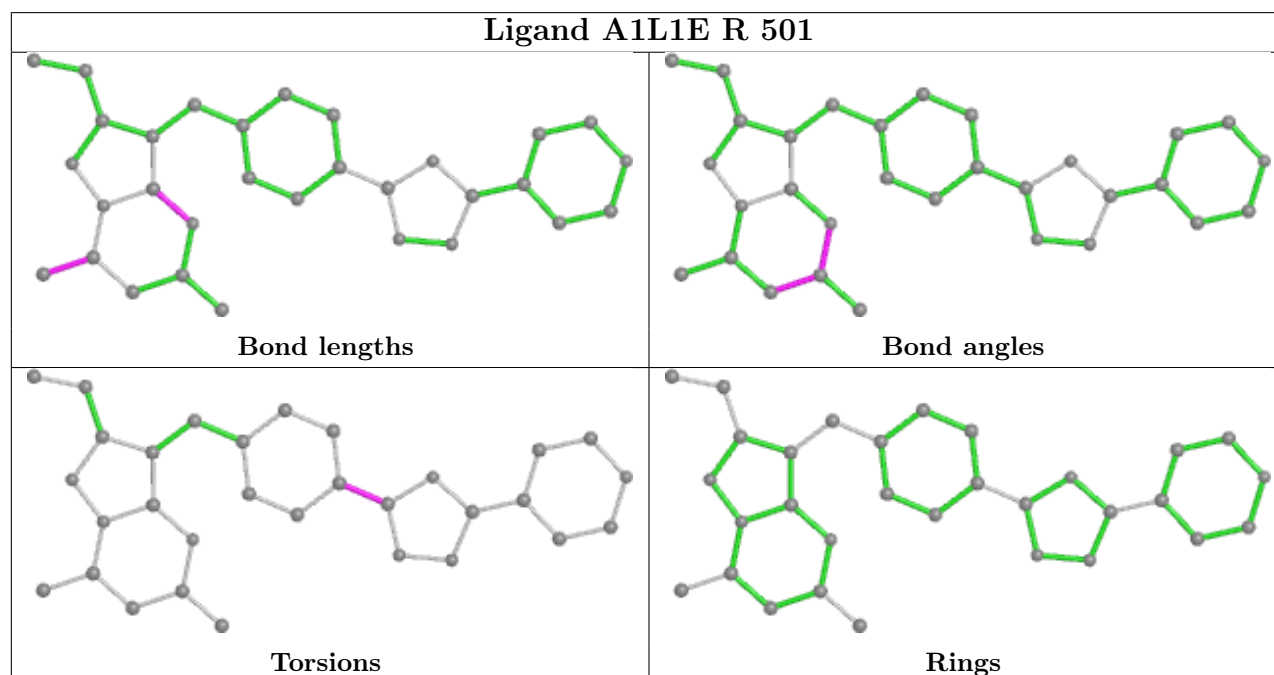
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	R	501	A1L1E	C12-C13-C16-N4
4	R	501	A1L1E	C14-C13-C16-N4

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 all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.