



## wwPDB EM Validation Summary Report ⓘ

Jul 9, 2025 – 12:11 PM JST

PDB ID : 9J31 / pdb\_00009j31  
EMDB ID : EMD-61104  
Title : cryo-EM structure of zebrafish GPR4-Gs complex at pH 8.5  
Authors : Ma, Y.T.; Tang, M.Y.; Song, G.J.; Ru, H.  
Deposited on : 2024-08-07  
Resolution : 3.05 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : **FAILED**  
MolProbity : 4-5-2 with Phenix2.0rc1  
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

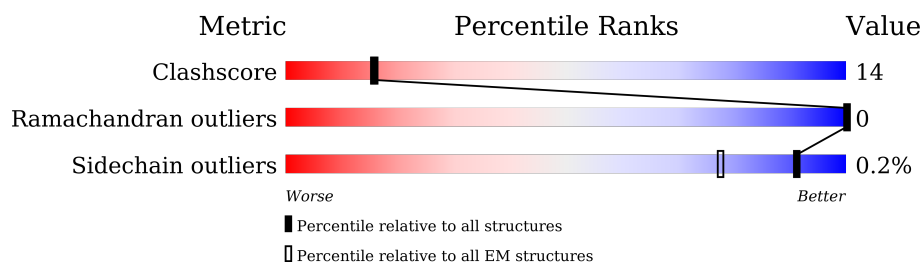
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.05 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  $\geq 3$ , 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	B	366	63% 30% 7%
2	D	295	49% 28% 22%
3	A	246	71% 25% .
4	R	642	28% 16% 56%
5	G	70	60% 23% 17%

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8994 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 Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	341	Total	C	N	O	S	0	0
			2616	1612	470	513	21		

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	341	GLY	-	expression tag	UNP P62873
B	342	SER	-	expression tag	UNP P62873
B	343	SER	-	expression tag	UNP P62873
B	344	GLY	-	expression tag	UNP P62873
B	345	GLY	-	expression tag	UNP P62873
B	346	GLY	-	expression tag	UNP P62873
B	347	GLY	-	expression tag	UNP P62873
B	348	SER	-	expression tag	UNP P62873
B	349	GLY	-	expression tag	UNP P62873
B	350	GLY	-	expression tag	UNP P62873
B	351	GLY	-	expression tag	UNP P62873
B	352	GLY	-	expression tag	UNP P62873
B	353	SER	-	expression tag	UNP P62873
B	354	SER	-	expression tag	UNP P62873
B	355	GLY	-	expression tag	UNP P62873
B	356	VAL	-	expression tag	UNP P62873
B	357	SER	-	expression tag	UNP P62873
B	358	GLY	-	expression tag	UNP P62873
B	359	TRP	-	expression tag	UNP P62873
B	360	ARG	-	expression tag	UNP P62873
B	361	LEU	-	expression tag	UNP P62873
B	362	PHE	-	expression tag	UNP P62873
B	363	LYS	-	expression tag	UNP P62873
B	364	LYS	-	expression tag	UNP P62873
B	365	ILE	-	expression tag	UNP P62873
B	366	SER	-	expression tag	UNP P62873

- Molecule 2 is a protein called scfv16.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	230	Total	C	N	O	S	0	0
			1764	1119	293	342	10		

- Molecule 3 is a protein called Guanine nucleotide-binding protein G(s) subunit alpha isoforms short.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	235	Total	C	N	O	S	0	0
			1938	1223	350	357	8		

There are 45 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP P63092
A	2	SER	-	expression tag	UNP P63092
A	3	ALA	-	expression tag	UNP P63092
A	4	THR	-	expression tag	UNP P63092
A	5	VAL	-	expression tag	UNP P63092
A	6	SER	-	expression tag	UNP P63092
A	7	ALA	-	expression tag	UNP P63092
A	8	GLU	-	expression tag	UNP P63092
A	9	ASP	-	expression tag	UNP P63092
A	10	LYS	-	expression tag	UNP P63092
A	11	ALA	-	expression tag	UNP P63092
A	12	ALA	-	expression tag	UNP P63092
A	13	ALA	-	expression tag	UNP P63092
A	14	GLU	-	expression tag	UNP P63092
A	15	ARG	-	expression tag	UNP P63092
A	16	SER	-	expression tag	UNP P63092
A	17	LYS	-	expression tag	UNP P63092
A	18	MET	-	expression tag	UNP P63092
A	42	ASP	GLY	engineered mutation	UNP P63092
A	43	ASN	GLU	engineered mutation	UNP P63092
A	56	TYR	LEU	engineered mutation	UNP P63092
A	58	GLY	-	linker	UNP P63092
A	59	GLY	-	linker	UNP P63092
A	191	SER	-	linker	UNP P63092
A	192	GLY	-	linker	UNP P63092
A	193	GLY	-	linker	UNP P63092
A	194	SER	-	linker	UNP P63092
A	195	GLY	-	linker	UNP P63092
A	196	GLY	-	linker	UNP P63092

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Chain	Residue	Modelled	Actual	Comment	Reference
A	197	THR	-	linker	UNP P63092
A	242	ASP	ALA	engineered mutation	UNP P63092
A	245	ASP	SER	engineered mutation	UNP P63092
A	?	-	ASN	deletion	UNP P63092
A	?	-	MET	deletion	UNP P63092
A	?	-	VAL	deletion	UNP P63092
A	?	-	ILE	deletion	UNP P63092
A	?	-	ARG	deletion	UNP P63092
A	?	-	GLU	deletion	UNP P63092
A	?	-	ASP	deletion	UNP P63092
A	?	-	ASN	deletion	UNP P63092
A	?	-	GLN	deletion	UNP P63092
A	?	-	THR	deletion	UNP P63092
A	255	ASP	LEU	engineered mutation	UNP P63092
A	355	ALA	ILE	engineered mutation	UNP P63092
A	358	ILE	VAL	engineered mutation	UNP P63092

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	R	280	Total	C	N	O	S	0	0
			2232	1482	364	369	17		

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	-128	MET	-	initiating methionine	UNP P0ABE7
R	-127	LYS	-	expression tag	UNP P0ABE7
R	-126	THR	-	expression tag	UNP P0ABE7
R	-125	ILE	-	expression tag	UNP P0ABE7
R	-124	ILE	-	expression tag	UNP P0ABE7
R	-123	ALA	-	expression tag	UNP P0ABE7
R	-122	LEU	-	expression tag	UNP P0ABE7
R	-121	SER	-	expression tag	UNP P0ABE7
R	-120	TYR	-	expression tag	UNP P0ABE7
R	-119	ILE	-	expression tag	UNP P0ABE7
R	-118	PHE	-	expression tag	UNP P0ABE7
R	-117	CYS	-	expression tag	UNP P0ABE7
R	-116	LEU	-	expression tag	UNP P0ABE7
R	-115	VAL	-	expression tag	UNP P0ABE7
R	-114	PHE	-	expression tag	UNP P0ABE7
R	-113	ALA	-	expression tag	UNP P0ABE7

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Chain	Residue	Modelled	Actual	Comment	Reference
R	-112	ASP	-	expression tag	UNP P0ABE7
R	-111	TYR	-	expression tag	UNP P0ABE7
R	-110	LYS	-	expression tag	UNP P0ABE7
R	-109	ASP	-	expression tag	UNP P0ABE7
R	-108	ASP	-	expression tag	UNP P0ABE7
R	-107	ASP	-	expression tag	UNP P0ABE7
R	-106	ASP	-	expression tag	UNP P0ABE7
R	-98	TRP	MET	engineered mutation	UNP P0ABE7
R	-3	ILE	HIS	engineered mutation	UNP P0ABE7
R	1	LEU	ARG	engineered mutation	UNP P0ABE7

- Molecule 5 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	58	Total	C	N	O	S	0	0
			444	277	79	85	3		

There are 3 discrepancies between the modelled and reference sequences:

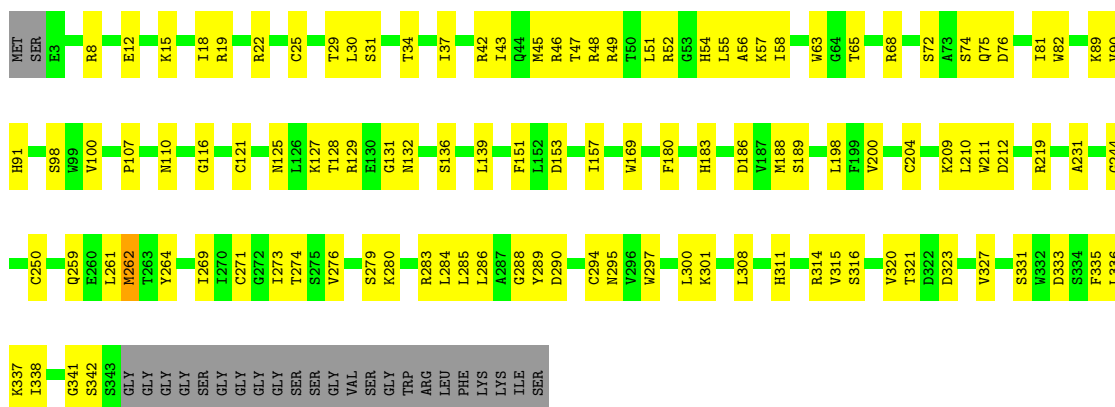
Chain	Residue	Modelled	Actual	Comment	Reference
G	68	GLY	-	expression tag	UNP P59768
G	69	SER	-	expression tag	UNP P59768
G	70	ALA	-	expression tag	UNP P59768

### 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: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1

Chain B: 





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	314824	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	52	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	B	0.15	0/2663	0.37	0/3610
2	D	0.13	0/1808	0.37	0/2452
3	A	0.14	0/1977	0.33	0/2660
4	R	0.16	0/2290	0.42	0/3119
5	G	0.16	0/450	0.36	0/608
All	All	0.15	0/9188	0.38	0/12449

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	B	2616	0	2518	86	0
2	D	1764	0	1697	62	0
3	A	1938	0	1907	50	0
4	R	2232	0	2290	73	0
5	G	444	0	454	12	0
All	All	8994	0	8866	255	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 14.

The worst 5 of 255 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:B:54:HIS:HE2	1:B:72:SER:HG	1.15	0.90
1:B:301:LYS:HE3	1:B:301:LYS:HA	1.58	0.85
4:R:77:THR:HG23	4:R:101:PHE:HB2	1.61	0.82
2:D:129:THR:HG23	2:D:156:THR:HA	1.60	0.81
4:R:262:ASN:HD21	4:R:265:ASP:HB3	1.50	0.76

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	Percentiles	
1	B	339/366 (93%)	329 (97%)	10 (3%)	0	100	100
2	D	226/295 (77%)	214 (95%)	12 (5%)	0	100	100
3	A	231/246 (94%)	222 (96%)	9 (4%)	0	100	100
4	R	274/642 (43%)	262 (96%)	12 (4%)	0	100	100
5	G	56/70 (80%)	55 (98%)	1 (2%)	0	100	100
All	All	1126/1619 (70%)	1082 (96%)	44 (4%)	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 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	B	283/298 (95%)	282 (100%)	1 (0%)	89	93

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D	194/237 (82%)	194 (100%)	0	100	100
3	A	208/213 (98%)	208 (100%)	0	100	100
4	R	240/551 (44%)	239 (100%)	1 (0%)	89	93
5	G	47/56 (84%)	47 (100%)	0	100	100
All	All	972/1355 (72%)	970 (100%)	2 (0%)	91	95

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	262	MET
4	R	240	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
4	R	108	ASN
4	R	219	ASN
1	B	183	HIS
1	B	266	HIS
2	D	207	ASN

### 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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 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.