



## wwPDB EM Validation Summary Report ⓘ

Oct 21, 2024 – 10:18 PM JST

PDB ID : 8ZCJ  
EMDB ID : EMD-39931  
Title : Cryo-EM structure of the pasireotide-bound SSTR5-Gi complex  
Authors : Li, Y.G.; Meng, X.Y.; Yang, X.R.; Ling, S.L.; Shi, P.; Tian, C.L.; Yang, F.  
Deposited on : 2024-04-29  
Resolution : 3.09 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**  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
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) : 2.39

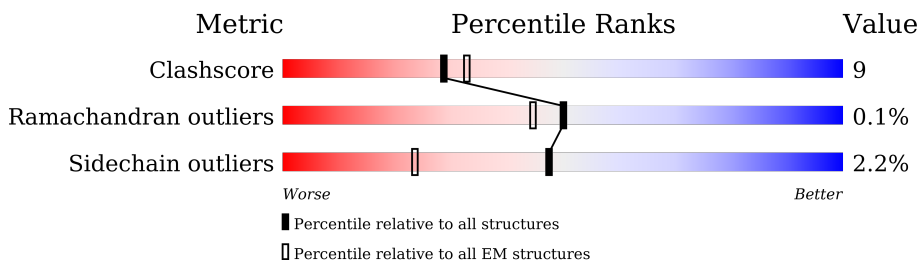
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.09 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	354	
2	C	377	
3	D	71	
4	E	304	
5	G	570	
6	A	6	

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 7808 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) subunit alpha-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	222	Total	C	N	O	S	0	0
			1556	985	264	297	10		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	203	ALA	GLY	conflict	UNP P63096
B	326	SER	ALA	conflict	UNP P63096

- 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	C	341	Total	C	N	O	S	0	0
			2369	1471	430	457	11		

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-10	MET	-	initiating methionine	UNP P54311
C	-9	HIS	-	expression tag	UNP P54311
C	-8	HIS	-	expression tag	UNP P54311
C	-7	HIS	-	expression tag	UNP P54311
C	-6	HIS	-	expression tag	UNP P54311
C	-5	HIS	-	expression tag	UNP P54311
C	-4	HIS	-	expression tag	UNP P54311
C	-3	GLY	-	expression tag	UNP P54311
C	-2	SER	-	expression tag	UNP P54311
C	-1	LEU	-	expression tag	UNP P54311
C	0	LEU	-	expression tag	UNP P54311
C	1	GLN	-	expression tag	UNP P54311
C	341	GLY	-	expression tag	UNP P54311
C	342	SER	-	expression tag	UNP P54311

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Chain	Residue	Modelled	Actual	Comment	Reference
C	343	SER	-	expression tag	UNP P54311
C	344	GLY	-	expression tag	UNP P54311
C	345	GLY	-	expression tag	UNP P54311
C	346	GLY	-	expression tag	UNP P54311
C	347	GLY	-	expression tag	UNP P54311
C	348	SER	-	expression tag	UNP P54311
C	349	GLY	-	expression tag	UNP P54311
C	350	GLY	-	expression tag	UNP P54311
C	351	GLY	-	expression tag	UNP P54311
C	352	GLY	-	expression tag	UNP P54311
C	353	SER	-	expression tag	UNP P54311
C	354	SER	-	expression tag	UNP P54311
C	355	GLY	-	expression tag	UNP P54311
C	356	VAL	-	expression tag	UNP P54311
C	357	SER	-	expression tag	UNP P54311
C	358	GLY	-	expression tag	UNP P54311
C	359	TRP	-	expression tag	UNP P54311
C	360	ARG	-	expression tag	UNP P54311
C	361	LEU	-	expression tag	UNP P54311
C	362	PHE	-	expression tag	UNP P54311
C	363	LYS	-	expression tag	UNP P54311
C	364	LYS	-	expression tag	UNP P54311
C	365	ILE	-	expression tag	UNP P54311
C	366	SER	-	expression tag	UNP P54311

- 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	D	50	Total	C	N	O	0	0
			296	187	53	56		

- Molecule 4 is a protein called ScFv16.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	233	Total	C	N	O	S	0	0
			1705	1080	281	336	8		

- Molecule 5 is a protein called Beta-2 adrenergic receptor,Somatostatin receptor type 5,lgbit (fusion protein).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	275	Total	C	N	O	S	0	0
			1818	1174	308	324	12		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	-47	MET	-	initiating methionine	UNP P07550
G	-46	LYS	-	expression tag	UNP P07550
G	-45	THR	-	expression tag	UNP P07550
G	-44	ILE	-	expression tag	UNP P07550
G	-43	ILE	-	expression tag	UNP P07550
G	-42	ALA	-	expression tag	UNP P07550
G	-41	LEU	-	expression tag	UNP P07550
G	-40	SER	-	expression tag	UNP P07550
G	-39	TYR	-	expression tag	UNP P07550
G	-38	ILE	-	expression tag	UNP P07550
G	-37	PHE	-	expression tag	UNP P07550
G	-36	CYS	-	expression tag	UNP P07550
G	-35	LEU	-	expression tag	UNP P07550
G	-34	VAL	-	expression tag	UNP P07550
G	-33	PHE	-	expression tag	UNP P07550
G	-32	ALA	-	expression tag	UNP P07550
G	-31	ASP	-	expression tag	UNP P07550
G	-30	TYR	-	expression tag	UNP P07550
G	-29	LYS	-	expression tag	UNP P07550
G	-28	ASP	-	expression tag	UNP P07550
G	-27	ASP	-	expression tag	UNP P07550
G	-26	ASP	-	expression tag	UNP P07550
G	-25	ASP	-	expression tag	UNP P07550
G	-24	LYS	-	expression tag	UNP P07550

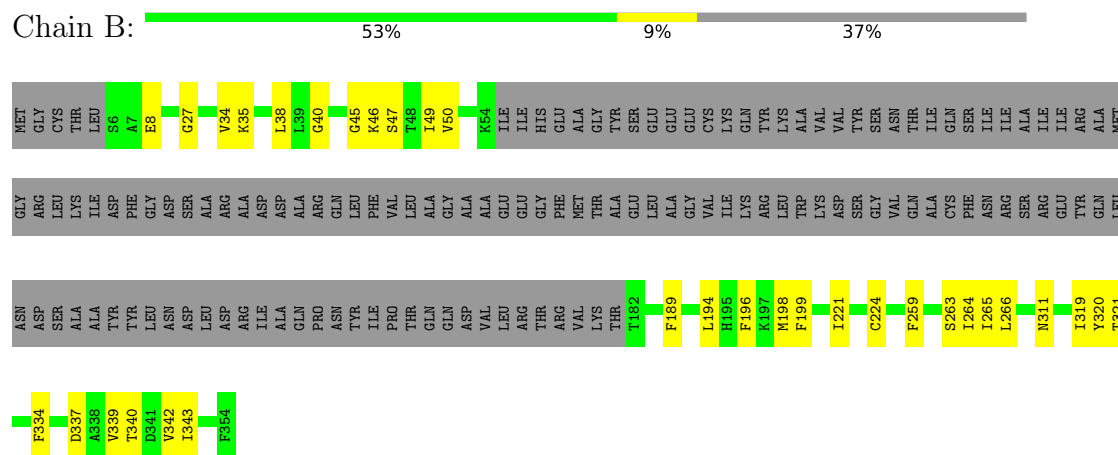
- Molecule 6 is a protein called 004-DTR-LYS-TYR-PHA-HYP.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	A	6	Total	C	N	O	0	0
			64	48	8	8		

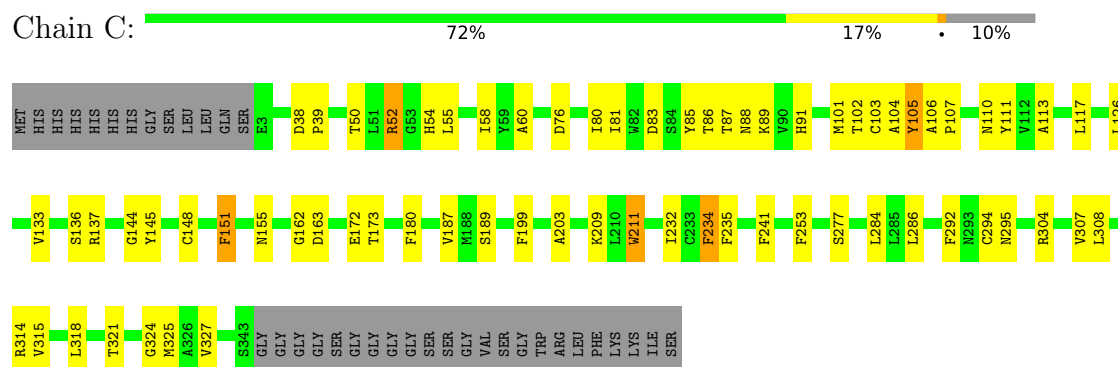
### 3 Residue-property plots [i](#)

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.

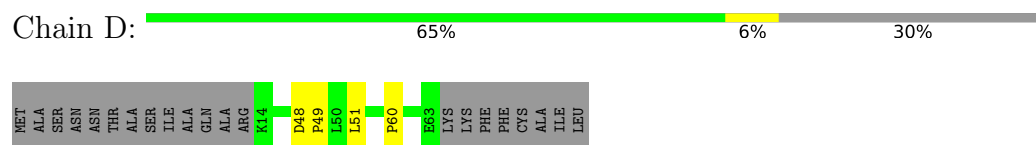
- Molecule 1: Guanine nucleotide-binding protein G(i) subunit alpha-1



- Molecule 2: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1



- Molecule 3: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2



- Molecule 4: ScFv16





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1227503	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 ( $e^-/\text{\AA}^2$ )	55	Depositor
Minimum defocus (nm)	1400	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: HYP, PHA, DTR, 004

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	0.32	0/1579	0.54	0/2148
2	C	0.29	0/2416	0.57	0/3306
3	D	0.25	0/302	0.45	0/422
4	E	0.28	0/1747	0.55	0/2381
5	G	0.28	0/1856	0.52	0/2562
6	A	2.15	1/21 (4.8%)	1.70	0/26
All	All	0.31	1/7921 (0.0%)	0.55	0/10845

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	3	LYS	C-N	7.41	1.51	1.34

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	1556	0	1365	30	0
2	C	2369	0	2017	46	0
3	D	296	0	204	3	0
4	E	1705	0	1562	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	G	1818	0	1619	38	0
6	A	64	0	54	2	0
All	All	7808	0	6821	135	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 9.

The worst 5 of 135 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:G:147:SER:O	5:G:151:ARG:N	2.26	0.68
5:G:89:TYR:HB2	5:G:122:ASN:HB3	1.78	0.65
5:G:74:VAL:HG21	5:G:151:ARG:HD3	1.83	0.61
5:G:81:ASN:ND2	5:G:160:SER:OG	2.34	0.61
5:G:127:VAL:HG12	5:G:213:PRO:HB2	1.83	0.60

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	218/354 (62%)	210 (96%)	8 (4%)	0	100	100
2	C	339/377 (90%)	318 (94%)	21 (6%)	0	100	100
3	D	48/71 (68%)	45 (94%)	3 (6%)	0	100	100
4	E	229/304 (75%)	221 (96%)	8 (4%)	0	100	100
5	G	273/570 (48%)	253 (93%)	19 (7%)	1 (0%)	30	63
6	A	2/6 (33%)	2 (100%)	0	0	100	100
All	All	1109/1682 (66%)	1049 (95%)	59 (5%)	1 (0%)	50	79

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	G	193	PRO

### 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	139/306 (45%)	139 (100%)	0	100	100
2	C	202/308 (66%)	196 (97%)	6 (3%)	36	64
3	D	14/58 (24%)	14 (100%)	0	100	100
4	E	174/247 (70%)	172 (99%)	2 (1%)	70	84
5	G	150/471 (32%)	143 (95%)	7 (5%)	22	52
6	A	2/2 (100%)	2 (100%)	0	100	100
All	All	681/1392 (49%)	666 (98%)	15 (2%)	47	71

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	E	239	PHE
5	G	286	TYR
5	G	68	PHE
5	G	304	TYR
5	G	221	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
5	G	99	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

4 non-standard protein/DNA/RNA residues 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$
6	PHA	A	5	6	10,11,11	0.54	0	10,13,13	1.37	1 (10%)
6	HYP	A	6	6	6,8,9	4.16	3 (50%)	5,10,12	1.07	0
6	DTR	A	2	6	13,15,16	1.12	1 (7%)	13,20,22	1.22	1 (7%)
6	004	A	1	6	9,10,11	0.74	0	9,12,14	0.99	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
6	PHA	A	5	6	-	0/5/6/6	0/1/1/1
6	HYP	A	6	6	-	0/0/11/13	0/1/1/1
6	DTR	A	2	6	-	1/4/6/8	0/2/2/2
6	004	A	1	6	-	0/4/6/8	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	6	HYP	CB-CA	-8.91	1.34	1.54
6	A	6	HYP	CD-N	-4.16	1.32	1.47
6	A	6	HYP	OD1-CG	-2.42	1.36	1.43
6	A	2	DTR	CD2-CE2	-2.37	1.36	1.42

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	2	DTR	CG-CB-CA	-3.39	109.28	114.53
6	A	5	PHA	CG-CB-CA	-3.28	107.47	114.10

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	2	DTR	CA-CB-CG-CD1

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	5	PHA	2	0

## 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.