



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:26 PM UTC

PDB ID : 6N9G / pdb_00006n9g
Title : Crystal Structure of RGS7-Gbeta5 dimer
Authors : Patil, D.N.; Rangarajan, E.; Izard, T.; Martemyanov, K.A.
Deposited on : 2018-12-03
Resolution : 2.13 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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/XrayValidationReportHelp>

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:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

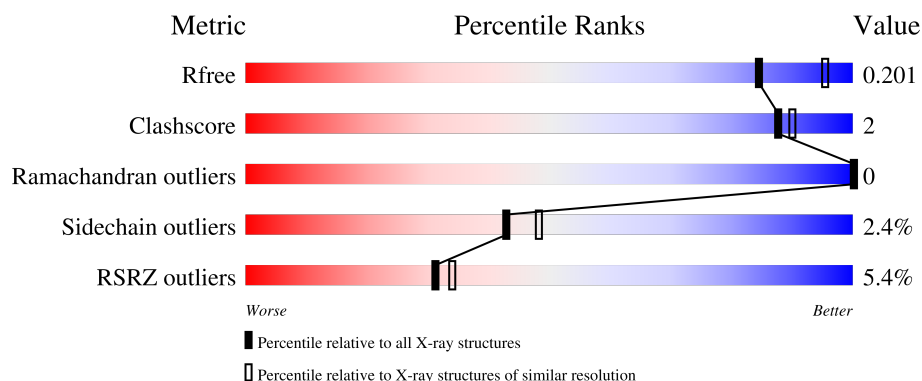
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.13 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	8290 (2.14-2.10)
Clashscore	190562	8817 (2.14-2.10)
Ramachandran outliers	187476	8738 (2.14-2.10)
Sidechain outliers	187428	8739 (2.14-2.10)
RSRZ outliers	180081	8294 (2.14-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	469	3% 82% 15%
1	B	469	7% 79% 6% 14%
2	C	353	6% 91% 7% ..
2	D	353	4% 91% 8% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12530 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Regulator of G-protein signaling 7.

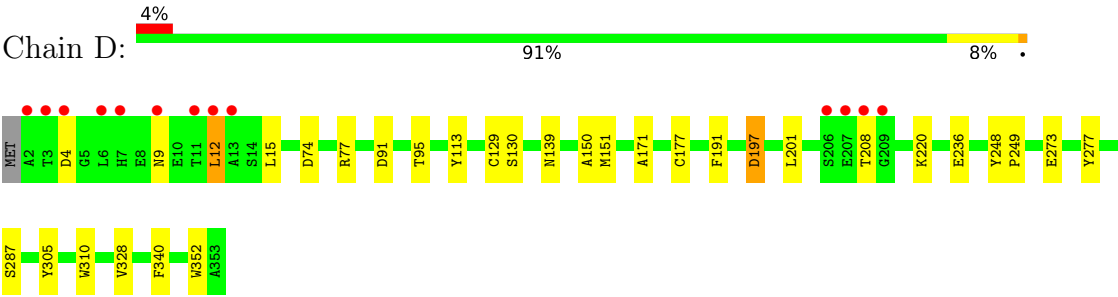
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	400	Total	C	N	O	S	0	1	0
			3327	2127	566	622	12			
1	B	401	Total	C	N	O	S	0	0	0
			3325	2127	564	622	12			

- Molecule 2 is a protein called Guanine nucleotide-binding protein subunit beta-5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	351	Total	C	N	O	S	0	0	0
			2697	1675	470	529	23			
2	D	352	Total	C	N	O	S	0	0	0
			2702	1678	471	530	23			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	175	Total	O	0	0
			175	175		
3	B	73	Total	O	0	0
			73	73		
3	C	55	Total	O	0	0
			55	55		
3	D	176	Total	O	0	0
			176	176		



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	69.32Å 162.76Å 95.30Å 90.00° 98.36° 90.00°	Depositor
Resolution (Å)	37.53 – 2.13 37.53 – 2.13	Depositor EDS
% Data completeness (in resolution range)	46.6 (37.53-2.13) 46.6 (37.53-2.13)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.58 (at 2.12Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.174 , 0.217 0.176 , 0.201	Depositor DCC
R_{free} test set	109045 reflections (49.58%)	wwPDB-VP
Wilson B-factor (Å ²)	47.3	Xtriage
Anisotropy	0.063	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 54.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12530	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.12% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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	A	0.10	0/3415	0.30	0/4621
1	B	0.11	0/3413	0.30	0/4619
2	C	0.10	0/2751	0.32	0/3718
2	D	0.11	0/2756	0.34	0/3725
All	All	0.11	0/12335	0.31	0/16683

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	A	3327	0	3252	10	0
1	B	3325	0	3252	10	0
2	C	2697	0	2594	16	0
2	D	2702	0	2599	15	0
3	A	175	0	0	2	0
3	B	73	0	0	0	0
3	C	55	0	0	0	0
3	D	176	0	0	0	0
All	All	12530	0	11697	47	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 2.

All (47) 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:47:LYS:HG3	1:B:52:LYS:HB3	1.68	0.75
1:B:137:MET:HE1	1:B:172:GLU:HA	1.81	0.61
1:B:279:VAL:HG21	2:C:270:ALA:HB2	1.88	0.56
1:B:369:LEU:HD11	1:B:377:VAL:HG13	1.91	0.53
1:A:271[B]:ARG:NH1	3:A:501:HOH:O	2.43	0.52
1:A:258:LEU:HD13	2:D:15:LEU:HB2	1.91	0.51
1:B:373:PRO:HD3	2:C:166:MET:HE3	1.94	0.49
1:A:363:TRP:HZ2	2:D:208:THR:HG22	1.76	0.49
2:D:171:ALA:HB2	2:D:201:LEU:HD23	1.95	0.48
2:C:307:ILE:HB	2:C:321:LEU:HB2	1.94	0.48
2:C:177:CYS:HB2	2:C:191:PHE:HB2	1.95	0.48
2:C:284:PHE:CD1	2:C:304:ASP:HB3	2.50	0.47
2:D:129:CYS:HB3	2:D:150:ALA:HB3	1.97	0.47
2:C:129:CYS:HB3	2:C:150:ALA:HB3	1.97	0.47
2:C:138:LYS:HD2	2:C:145:LYS:HZ1	1.80	0.46
2:C:248:TYR:CD1	2:C:249:PRO:HD2	2.50	0.46
2:C:171:ALA:HB2	2:C:201:LEU:HD23	1.98	0.46
2:C:137:ASP:N	2:C:137:ASP:OD1	2.50	0.45
2:D:197:ASP:OD1	2:D:197:ASP:N	2.48	0.45
2:D:287:SER:OG	2:D:328:VAL:O	2.25	0.45
2:C:145:LYS:HE3	2:C:145:LYS:HB3	1.91	0.45
2:C:324:HIS:CE1	2:C:350:ARG:HD2	2.51	0.44
2:D:248:TYR:CD2	2:D:249:PRO:HD2	2.52	0.44
2:D:9:ASN:HA	2:D:12:LEU:HB2	1.99	0.43
2:C:138:LYS:HD2	2:C:145:LYS:NZ	2.33	0.43
1:B:45:THR:HG23	1:B:54:PRO:HA	2.00	0.43
1:A:299:PRO:HA	1:A:300:PRO:HD3	1.91	0.42
2:D:151:MET:HE2	2:D:151:MET:HB3	1.92	0.42
1:B:80:HIS:O	1:B:83:THR:HG22	2.20	0.42
1:B:405:ASP:O	1:B:409:GLN:HG2	2.20	0.42
2:D:220:LYS:HG2	2:D:236:GLU:HB2	2.00	0.42
1:A:80:HIS:O	1:A:83:THR:HG22	2.20	0.42
1:A:252:PRO:HA	1:A:253:PRO:HD3	1.92	0.41
1:B:368:ASP:O	1:B:372:ARG:HG2	2.20	0.41
1:A:368:ASP:O	1:A:372:ARG:HG2	2.20	0.41
2:C:305:TYR:N	2:C:305:TYR:CD1	2.89	0.41
2:D:74:ASP:OD2	2:D:77:ARG:HD2	2.20	0.41
2:D:177:CYS:HB2	2:D:191:PHE:HB2	2.02	0.41
2:D:277:TYR:HB3	2:D:310:TRP:CD2	2.55	0.41
1:A:45:THR:HG23	1:A:54:PRO:HA	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:340:PHE:CE2	2:C:352:TRP:HB2	2.55	0.41
2:D:91:ASP:O	2:D:95:THR:N	2.54	0.41
1:A:437:ARG:NH1	3:A:504:HOH:O	2.53	0.41
2:D:340:PHE:CE2	2:D:352:TRP:HB2	2.56	0.41
1:B:330:TRP:O	1:B:435:TYR:OH	2.32	0.41
2:C:197:ASP:OD1	2:C:197:ASP:N	2.54	0.41
1:A:267:ILE:HD13	1:A:267:ILE:HA	1.96	0.40

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 X-ray entries followed by that with respect to entries of similar resolution.

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	A	397/469 (85%)	387 (98%)	10 (2%)	0	100	100
1	B	397/469 (85%)	385 (97%)	12 (3%)	0	100	100
2	C	349/353 (99%)	331 (95%)	18 (5%)	0	100	100
2	D	350/353 (99%)	333 (95%)	17 (5%)	0	100	100
All	All	1493/1644 (91%)	1436 (96%)	57 (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 X-ray entries followed by that with respect to entries of similar resolution.

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	A	364/425 (86%)	361 (99%)	3 (1%)	73	80
1	B	364/425 (86%)	352 (97%)	12 (3%)	33	36
2	C	294/295 (100%)	285 (97%)	9 (3%)	35	38
2	D	294/295 (100%)	286 (97%)	8 (3%)	39	44
All	All	1316/1440 (91%)	1284 (98%)	32 (2%)	43	48

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	83	THR
1	A	144	GLU
1	A	426	ILE
1	B	22	LEU
1	B	29	ASP
1	B	41	ILE
1	B	52	LYS
1	B	53	ILE
1	B	64	GLN
1	B	69	ASN
1	B	136	THR
1	B	144	GLU
1	B	189	LEU
1	B	254	THR
1	B	429	LEU
2	C	113	TYR
2	C	138	LYS
2	C	140	GLU
2	C	141	ASN
2	C	197	ASP
2	C	273	GLU
2	C	305	TYR
2	C	318	VAL
2	C	319	SER
2	D	4	ASP
2	D	12	LEU
2	D	113	TYR
2	D	130	SER
2	D	139	ASN
2	D	197	ASP
2	D	273	GLU
2	D	305	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	64	GLN
1	A	69	ASN
1	B	69	ASN
1	B	346	GLN
1	B	382	GLN
1	B	409	GLN
2	C	141	ASN
2	C	243	ASN
2	D	39	HIS
2	D	189	GLN

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 ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	400/469 (85%)	0.05	13 (3%)	49 52	24, 54, 90, 127	1 (0%)
1	B	401/469 (85%)	0.71	34 (8%)	16 18	40, 82, 133, 174	0
2	C	351/353 (99%)	0.37	21 (5%)	27 30	42, 65, 119, 202	0
2	D	352/353 (99%)	-0.22	13 (3%)	45 48	25, 42, 89, 139	0
All	All	1504/1644 (91%)	0.24	81 (5%)	31 34	24, 61, 117, 202	1 (0%)

All (81) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	50	LEU	6.0
1	A	254	THR	5.3
2	D	2	ALA	5.2
2	C	136	PHE	4.8
1	B	49	PHE	4.6
1	B	258	LEU	4.4
2	D	208	THR	4.2
1	A	450	ALA	4.1
2	D	3	THR	4.0
2	C	6	LEU	3.9
1	B	450	ALA	3.9
1	B	107	PHE	3.7
1	B	53	ILE	3.7
1	B	57	PHE	3.6
1	B	43	ILE	3.6
1	A	355	PHE	3.5
1	B	42	PRO	3.5
2	C	208	THR	3.5
2	D	12	LEU	3.4
1	A	18	SER	3.3
1	A	252	PRO	3.3

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Mol	Chain	Res	Type	RSRZ
2	C	143	ALA	3.2
1	B	355	PHE	3.2
2	C	206	SER	3.1
2	C	3	THR	3.0
1	B	70	LEU	3.0
1	A	255	GLU	2.9
2	D	207	GLU	2.9
2	D	209	GLY	2.9
1	B	252	PRO	2.9
1	B	19	PRO	2.9
2	D	206	SER	2.9
2	C	7	HIS	2.9
2	D	9	ASN	2.9
2	D	7	HIS	2.8
2	C	284	PHE	2.8
2	C	15	LEU	2.8
1	B	44	ARG	2.7
1	A	258	LEU	2.7
2	D	11	THR	2.7
2	C	9	ASN	2.6
1	B	319	SER	2.6
1	B	64	GLN	2.5
1	B	21	MET	2.5
2	C	209	GLY	2.5
1	A	19	PRO	2.5
2	D	13	ALA	2.5
1	B	46	VAL	2.5
1	A	253	PRO	2.4
1	B	253	PRO	2.4
1	B	439	ILE	2.4
1	B	251	LYS	2.4
2	C	11	THR	2.3
2	C	205	PRO	2.3
2	C	144	ALA	2.3
2	C	12	LEU	2.3
2	D	6	LEU	2.3
2	C	207	GLU	2.3
1	B	41	ILE	2.2
1	B	67	ILE	2.2
1	B	84	LEU	2.2
1	B	265	TRP	2.2
1	B	254	THR	2.2

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Mol	Chain	Res	Type	RSRZ
2	C	217	CYS	2.1
2	C	141	ASN	2.1
2	C	4	ASP	2.1
1	B	91	PHE	2.1
2	C	137	ASP	2.1
1	A	166	PHE	2.1
1	B	51	SER	2.1
1	B	292	GLU	2.1
1	B	105	GLY	2.1
1	B	52	LYS	2.1
1	B	218	SER	2.1
1	A	398	ASN	2.0
1	B	114	TYR	2.0
1	B	62	ILE	2.0
1	A	218	SER	2.0
1	A	401	SER	2.0
2	C	17	SER	2.0
2	D	4	ASP	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.