



Full wwPDB NMR Structure Validation Report ⓘ

May 4, 2019 – 08:58 AM EDT

PDB ID : 5JS8
Title : Structural Model of a Protein alpha subunit in complex with GDP obtained with SAXS and NMR residual couplings
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Deposited on : 2016-05-07

This is a Full wwPDB NMR 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/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20031633
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20031633

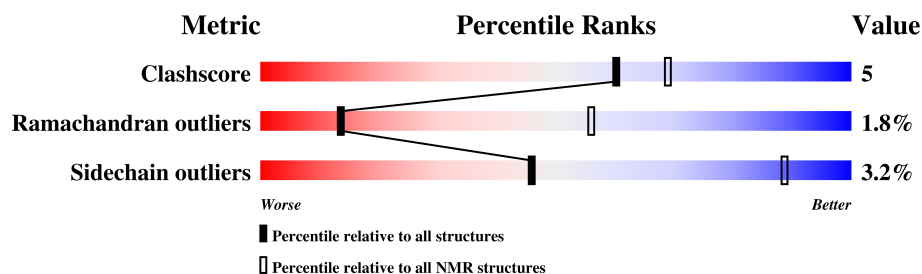
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 12%.

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)	NMR archive (#Entries)
Clashscore	136327	12091
Ramachandran outliers	132723	10835
Sidechain outliers	132532	10811

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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	A	326	

2 Ensemble composition and analysis

This entry contains 10 models. Model 1 is the overall representative, medoid model (most similar to other models).

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:33-A:52, A:191-A:354 (184)	0.11	1
2	A:53-A:190 (138)	0.14	1

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 2 clusters and 1 single-model cluster was found.

Cluster number	Models
1	4, 5, 6, 8, 9, 10
2	1, 2, 3
Single-model clusters	7

3 Entry composition

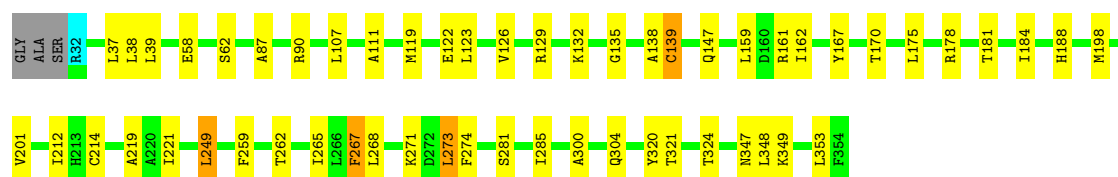
There is only 1 type of molecule in this entry. The entry contains 5174 atoms, of which 2575 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Guanine nucleotide-binding protein G(i) subunit alpha-1.

Mol	Chain	Residues	Atoms						Trace
1	A	323	Total	C	H	N	O	S	0
			5174	1651	2575	438	494	16	

There are 4 discrepancies between the modelled and reference sequences:

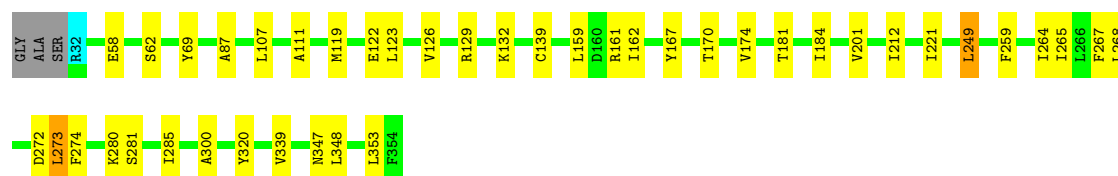
Chain	Residue	Modelled	Actual	Comment	Reference
A	29	GLY	-	expression tag	UNP P63096
A	31	SER	ALA	conflict	UNP P63096
A	219	ALA	THR	conflict	UNP P63096
A	288	GLN	PRO	conflict	UNP P63096



4.2.3 Score per residue for model 3

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

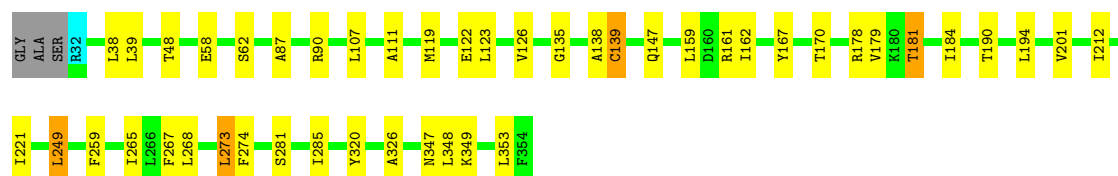
Chain A: 86% 12% ..



4.2.4 Score per residue for model 4

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

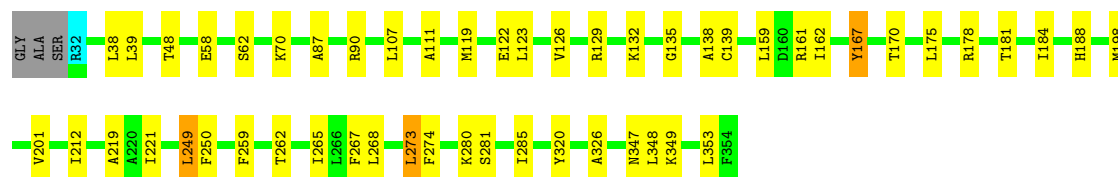
Chain A: 85% 13% ..



4.2.5 Score per residue for model 5

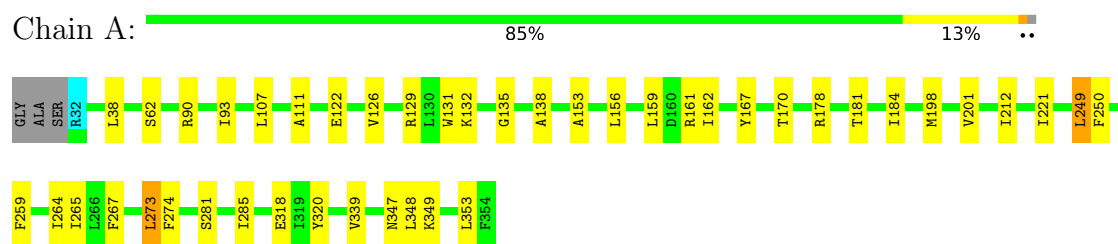
- Molecule 1: Guanine nucleotide-binding protein G(i) subunit alpha-1

Chain A: 83% 15% ..



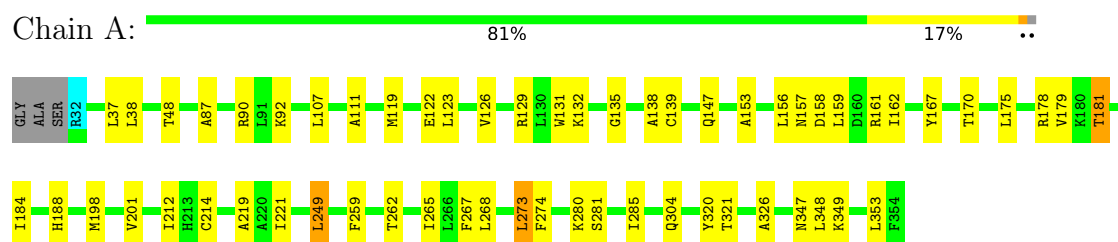
4.2.6 Score per residue for model 6

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



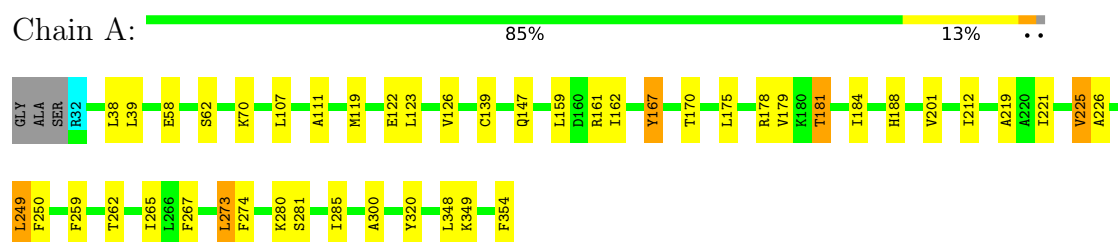
4.2.7 Score per residue for model 7

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



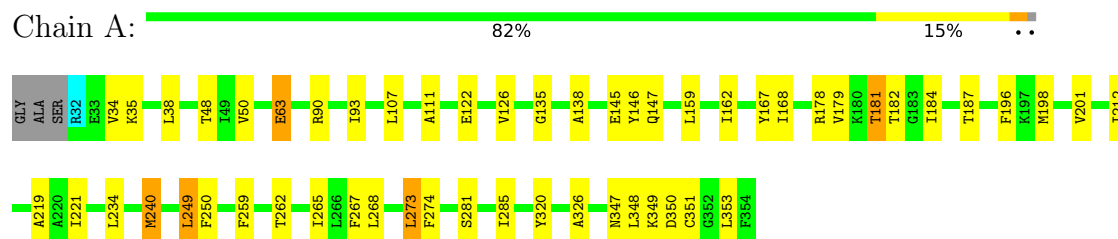
4.2.8 Score per residue for model 8

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



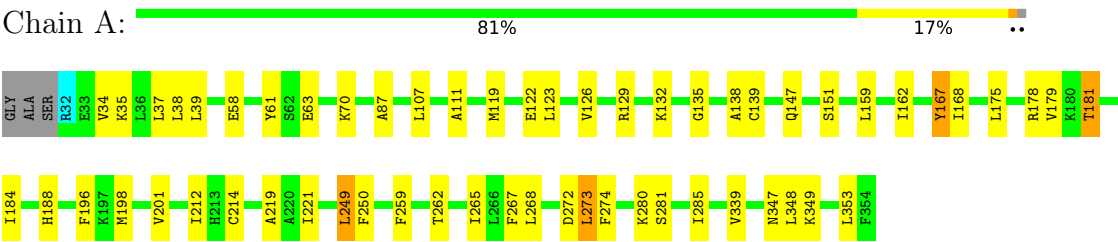
4.2.9 Score per residue for model 9

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



4.2.10 Score per residue for model 10

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



5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing*.

Of the 50 calculated structures, 10 were deposited, based on the following criterion: *structures with the least restraint violations*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
Xplor-NIH	refinement	
Xplor-NIH	structure calculation	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	5js8_cs.cif
Number of chemical shift lists	1
Total number of shifts	486
Number of shifts mapped to atoms	486
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	12%

No validations of the models with respect to experimental NMR restraints is performed at this time.

6 Model quality [i](#)

6.1 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 (average) 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	0.66±0.00	0±0/2634 (0.0±0.0%)	0.83±0.01	1±1/3545 (0.0±0.0%)
All	All	0.66	0/26340 (0.0%)	0.83	8/35450 (0.0%)

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	Planarity
1	A	0.0±0.0	0.6±0.8
All	All	0	6

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	90	ARG	NE-CZ-NH1	5.21	122.91	120.30	5	7
1	A	271	LYS	CB-CA-C	-5.01	100.38	110.40	2	1

There are no chirality outliers.

All unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	153	ALA	Mainchain	2
1	A	225	VAL	Mainchain,Peptide	1
1	A	157	ASN	Peptide	1
1	A	151	SER	Mainchain	1

6.2 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 each 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 averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	2588	2562	2562	26±2
All	All	25880	25620	25620	263

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.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:159:LEU:HD12	1:A:162:ILE:HD11	0.90	1.43	8	10
1:A:221:ILE:HD11	1:A:259:PHE:CE1	0.66	2.26	2	10
1:A:37:LEU:HD21	1:A:39:LEU:HD21	0.63	1.70	1	3
1:A:281:SER:OG	1:A:285:ILE:HD12	0.62	1.94	5	10
1:A:219:ALA:O	1:A:262:THR:HG23	0.62	1.94	8	7
1:A:63:GLU:HG3	1:A:168:ILE:HD13	0.60	1.74	9	2
1:A:38:LEU:HD11	1:A:198:MET:SD	0.59	2.38	1	7
1:A:221:ILE:HD11	1:A:259:PHE:CD1	0.59	2.33	3	10
1:A:273:LEU:HD13	1:A:273:LEU:H	0.59	1.58	4	3
1:A:273:LEU:HD22	1:A:274:PHE:N	0.58	2.14	6	10
1:A:273:LEU:H	1:A:273:LEU:HD13	0.58	1.57	6	7
1:A:184:ILE:HD12	1:A:201:VAL:HG12	0.57	1.75	4	10
1:A:119:MET:SD	1:A:123:LEU:HD23	0.54	2.43	7	8
1:A:63:GLU:CG	1:A:168:ILE:HD13	0.54	2.32	9	1
1:A:265:ILE:HG23	1:A:320:TYR:O	0.53	2.03	3	8
1:A:135:GLY:O	1:A:138:ALA:HB3	0.53	2.03	9	8
1:A:122:GLU:O	1:A:126:VAL:HG23	0.53	2.04	4	10
1:A:161:ARG:NH1	1:A:170:THR:HG23	0.53	2.18	7	8
1:A:265:ILE:HD13	1:A:339:VAL:CG1	0.52	2.34	6	2
1:A:69:TYR:CD2	1:A:174:VAL:HG13	0.52	2.40	3	1
1:A:190:THR:HG23	1:A:194:LEU:O	0.52	2.04	4	1
1:A:34:VAL:O	1:A:219:ALA:HB2	0.52	2.04	9	1
1:A:37:LEU:CD2	1:A:39:LEU:HD21	0.51	2.36	1	2
1:A:126:VAL:HG22	1:A:129:ARG:NH2	0.51	2.21	7	7
1:A:274:PHE:CE2	1:A:300:ALA:HB2	0.50	2.41	2	3
1:A:347:ASN:C	1:A:348:LEU:HD23	0.50	2.27	10	9
1:A:249:LEU:HD13	1:A:250:PHE:N	0.50	2.21	6	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:131:TRP:CE3	1:A:156:LEU:HD13	0.49	2.43	7	2
1:A:34:VAL:HG11	1:A:196:PHE:CE2	0.49	2.43	9	2
1:A:107:LEU:O	1:A:111:ALA:HB2	0.48	2.09	8	10
1:A:273:LEU:N	1:A:273:LEU:HD13	0.48	2.24	4	3
1:A:221:ILE:HD12	1:A:264:ILE:CD1	0.48	2.39	3	2
1:A:265:ILE:HD13	1:A:339:VAL:HG13	0.47	1.86	6	3
1:A:348:LEU:HD23	1:A:348:LEU:N	0.47	2.25	9	5
1:A:179:VAL:O	1:A:181:THR:HG22	0.47	2.10	8	5
1:A:348:LEU:N	1:A:348:LEU:HD23	0.46	2.25	2	5
1:A:70:LYS:HZ2	1:A:167:TYR:HD2	0.46	1.53	8	3
1:A:304:GLN:HG3	1:A:321:THR:HG21	0.46	1.88	7	2
1:A:249:LEU:HD22	1:A:249:LEU:C	0.46	2.31	7	8
1:A:87:ALA:HB3	1:A:139:CYS:SG	0.46	2.51	3	7
1:A:249:LEU:C	1:A:249:LEU:HD22	0.45	2.31	2	2
1:A:175:LEU:HD11	1:A:188:HIS:CE1	0.45	2.47	1	6
1:A:285:ILE:HG22	1:A:285:ILE:O	0.44	2.13	4	5
1:A:182:THR:O	1:A:182:THR:HG23	0.44	2.12	9	1
1:A:285:ILE:O	1:A:285:ILE:HG22	0.44	2.13	1	5
1:A:37:LEU:HD13	1:A:214:CYS:HB3	0.44	1.90	7	3
1:A:267:PHE:CE2	1:A:324:THR:HG21	0.43	2.48	2	1
1:A:38:LEU:O	1:A:39:LEU:HD23	0.43	2.13	8	2
1:A:318:GLU:HG3	1:A:320:TYR:H	0.43	1.73	6	1
1:A:48:THR:CG2	1:A:326:ALA:HB1	0.43	2.44	5	4
1:A:69:TYR:CG	1:A:174:VAL:HG13	0.43	2.48	3	1
1:A:39:LEU:HD12	1:A:221:ILE:HG21	0.42	1.91	5	1
1:A:162:ILE:HG22	1:A:167:TYR:CZ	0.42	2.49	8	1
1:A:249:LEU:HD13	1:A:250:PHE:H	0.42	1.75	6	3
1:A:34:VAL:HG21	1:A:196:PHE:CE2	0.42	2.50	1	1
1:A:50:VAL:HG13	1:A:187:THR:OG1	0.41	2.15	9	1
1:A:159:LEU:CD1	1:A:162:ILE:HD11	0.41	2.43	2	1
1:A:273:LEU:HD13	1:A:273:LEU:N	0.41	2.29	10	1
1:A:272:ASP:OD1	1:A:273:LEU:HD13	0.40	2.17	3	2
1:A:234:LEU:HD12	1:A:240:MET:HG2	0.40	1.94	9	1

6.3 Torsion angles ⓘ

6.3.1 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 NMR 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	A	321/326 (98%)	282±2 (88±1%)	34±2 (10±0%)	6±2 (2±1%)	13	56
All	All	3210/3260 (98%)	2817 (88%)	336 (10%)	57 (2%)	13	56

All 17 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	181	THR	10
1	A	178	ARG	9
1	A	349	LYS	9
1	A	268	LEU	8
1	A	62	SER	7
1	A	35	LYS	2
1	A	93	ILE	2
1	A	63	GLU	1
1	A	350	ASP	1
1	A	147	GLN	1
1	A	226	ALA	1
1	A	351	CYS	1
1	A	225	VAL	1
1	A	146	TYR	1
1	A	61	TYR	1
1	A	158	ASP	1
1	A	145	GLU	1

6.3.2 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 NMR 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	A	279/281 (99%)	270±1 (97±0%)	9±1 (3±0%)	46	89
All	All	2790/2810 (99%)	2700 (97%)	90 (3%)	46	89

All 14 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	212	ILE	10
1	A	267	PHE	10
1	A	273	LEU	10
1	A	249	LEU	10
1	A	167	TYR	10
1	A	353	LEU	8
1	A	132	LYS	7
1	A	58	GLU	7
1	A	280	LYS	6
1	A	147	GLN	6
1	A	139	CYS	3
1	A	240	MET	1
1	A	354	PHE	1
1	A	92	LYS	1

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 12% for the well-defined parts and 12% for the entire structure.

7.1 Chemical shift list 1

File name: 5js8_cs.cif

Chemical shift list name: *gnai1-GDP-bmrB.dat*

7.1.1 Bookkeeping

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	486
Number of shifts mapped to atoms	486
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	0	—	None (insufficient data)
$^{13}\text{C}_\beta$	0	—	None (insufficient data)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	240	-0.24 ± 0.39	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 12%, i.e. 487 atoms were assigned a chemical shift out of a possible 4027. 0 out of 43 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	478/1604 (30%)	239/641 (37%)	0/644 (0%)	239/319 (75%)
Sidechain	0/2070 (0%)	0/1206 (0%)	0/767 (0%)	0/97 (0%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	9/353 (3%)	6/189 (3%)	0/155 (0%)	3/9 (33%)
Overall	487/4027 (12%)	245/2036 (12%)	0/1566 (0%)	242/425 (57%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 12%, i.e. 489 atoms were assigned a chemical shift out of a possible 4050. 0 out of 43 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	480/1609 (30%)	240/643 (37%)	0/646 (0%)	240/320 (75%)
Sidechain	0/2088 (0%)	0/1217 (0%)	0/771 (0%)	0/100 (0%)
Aromatic	9/353 (3%)	6/189 (3%)	0/155 (0%)	3/9 (33%)
Overall	489/4050 (12%)	246/2049 (12%)	0/1572 (0%)	243/429 (57%)

7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots [i](#)

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.

Random coil index (RCI) for chain A:

