



Full wwPDB NMR Structure Validation Report ⓘ

Mar 6, 2026 – 08:02 PM UTC

PDB ID : 5JS7 / pdb_00005js7
BMRB ID : 30077
Title : Structural model of a apo G-protein alpha subunit determined with NMR residual dipolar couplings and SAXS
Authors : Goricanec, D.; Stehle, R.; Grigoriu, S.; Wagner, G.; Hagn, F.
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 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
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
BMRB Restraints Analysis : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

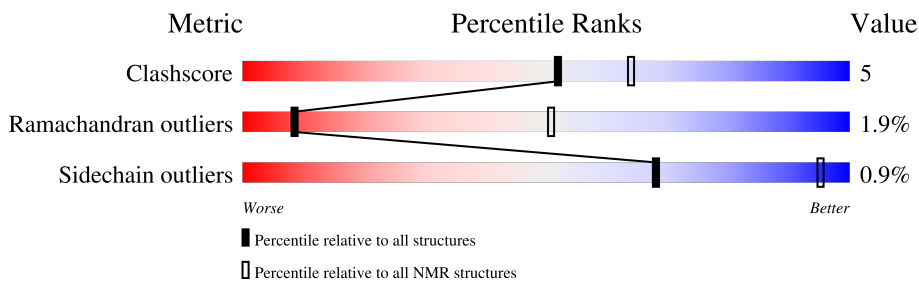
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 11%.

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	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

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	 82% 11% 6% .

2 Ensemble composition and analysis

This entry contains 10 models. Model 9 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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:57, A:63-A:177, A:184-A:347 (304)	0.63	9

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 2 single-model clusters were found.

Cluster number	Models
1	1, 4, 5, 6, 9, 10
2	2, 8
Single-model clusters	3; 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
			Total	C	H	N	O	S	
1	A	323	5174	1651	2575	438	494	16	0

There are 4 discrepancies between the modelled and reference sequences:

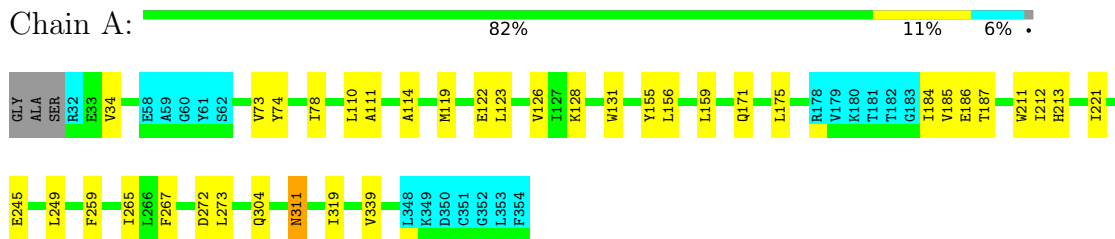
Chain	Residue	Modelled	Actual	Comment	Reference
A	29	GLY	-	expression tag	UNP P63096
A	31	SER	ALA	conflict	UNP P63096
A	219	ALA	THR	conflict	UNP P63096
A	288	GLN	PRO	conflict	UNP P63096

4 Residue-property plots [i](#)

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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 outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

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

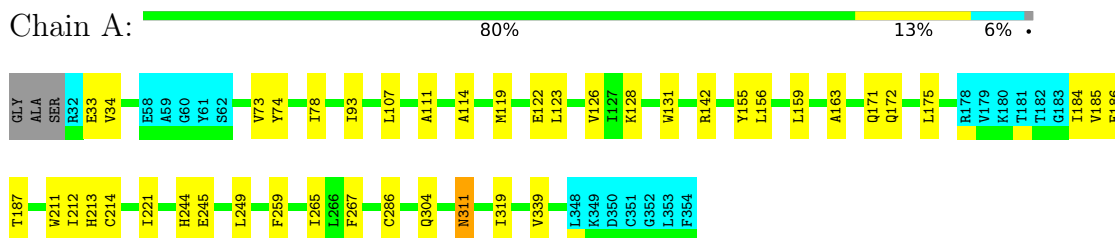


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

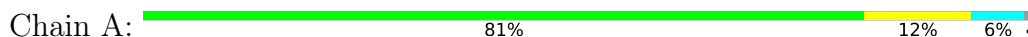
4.2.1 Score per residue for model 1

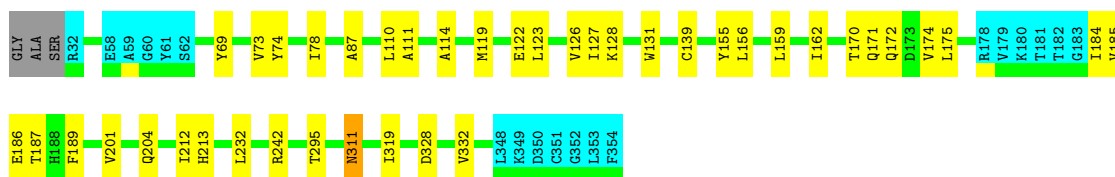
- Molecule 1: Guanine nucleotide-binding protein G(i) subunit alpha-1



4.2.2 Score per residue for model 2

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

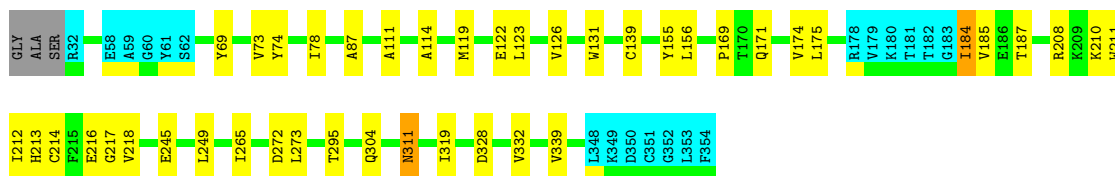




4.2.3 Score per residue for model 3

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

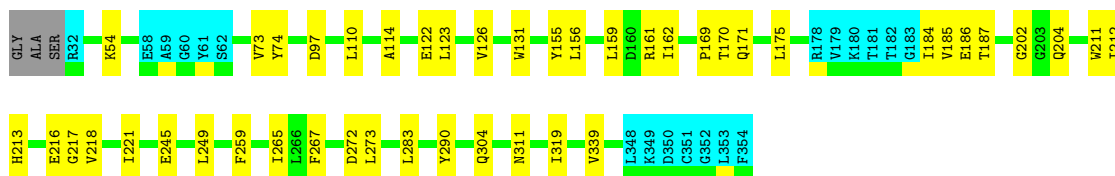
Chain A: 80% 13% 6%



4.2.4 Score per residue for model 4

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

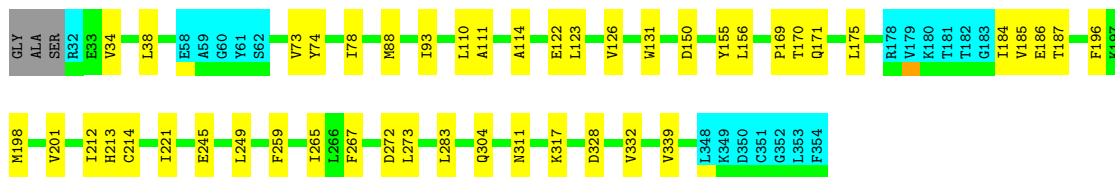
Chain A: 79% 14% 6%



4.2.5 Score per residue for model 5

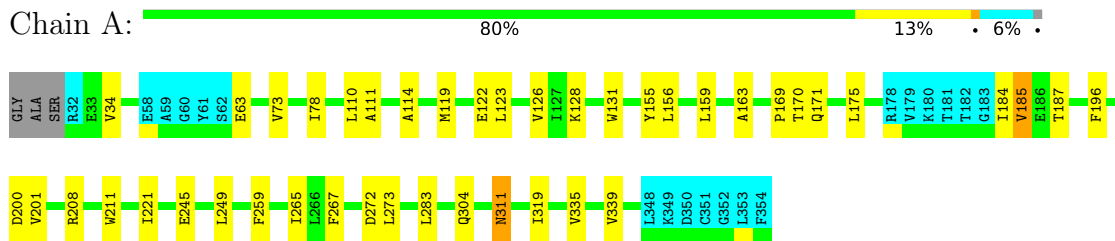
- Molecule 1: Guanine nucleotide-binding protein G(i) subunit alpha-1

Chain A: 79% 14% 6%



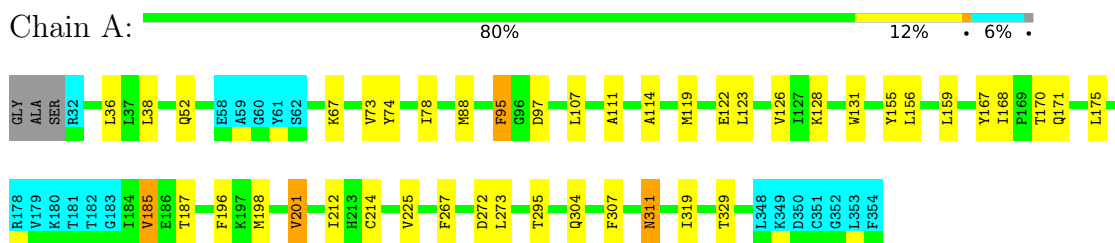
4.2.6 Score per residue for model 6

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



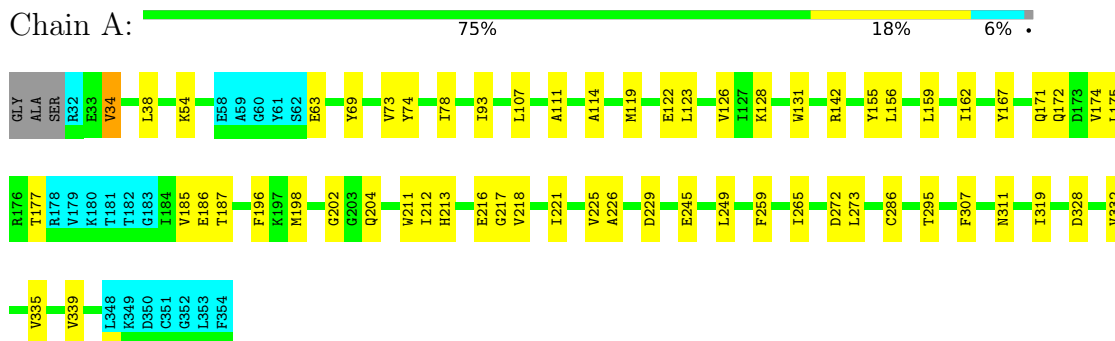
4.2.7 Score per residue for model 7

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



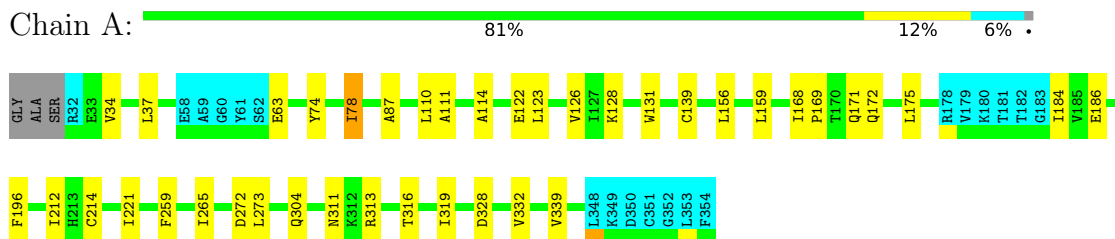
4.2.8 Score per residue for model 8

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



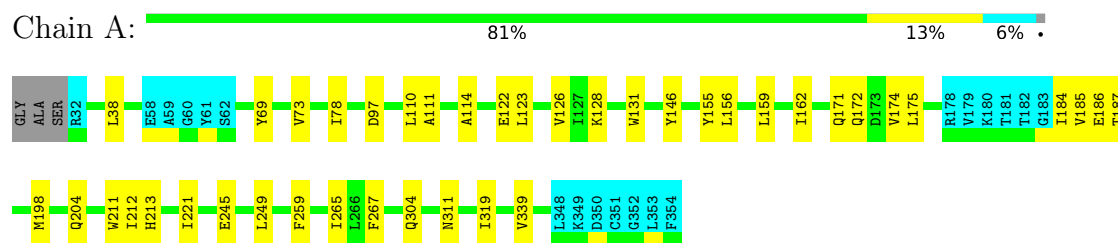
4.2.9 Score per residue for model 9 (medoid)

- 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	structure calculation	
Xplor-NIH	refinement	

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)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	488
Number of shifts mapped to atoms	488
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	11%

6 Model quality i

6.1 Standard geometry i

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 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 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	2452	2426	2426	26±4
All	All	24520	24260	24260	265

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:175:LEU:HD22	1:A:185:VAL:HG13	0.83	1.48	5	7
1:A:114:ALA:HB2	1:A:123:LEU:HD21	0.70	1.63	4	8
1:A:171:GLN:CB	1:A:187:THR:HG23	0.69	2.18	3	9
1:A:221:ILE:HD11	1:A:259:PHE:CD1	0.68	2.24	4	7
1:A:171:GLN:HB3	1:A:187:THR:HG23	0.67	1.66	10	9
1:A:114:ALA:HB2	1:A:123:LEU:CD2	0.66	2.20	7	8
1:A:272:ASP:OD1	1:A:273:LEU:HD12	0.63	1.92	8	7
1:A:212:ILE:HD12	1:A:213:HIS:N	0.62	2.08	3	7
1:A:311:ASN:HB2	1:A:319:ILE:HD11	0.60	1.74	8	9
1:A:221:ILE:HD11	1:A:259:PHE:CE1	0.59	2.32	5	5
1:A:78:ILE:HG21	1:A:111:ALA:HB1	0.58	1.74	3	8
1:A:216:GLU:O	1:A:218:VAL:HG23	0.58	1.97	3	3
1:A:175:LEU:HD11	1:A:186:GLU:O	0.58	1.99	10	5
1:A:107:LEU:O	1:A:111:ALA:HB2	0.55	2.00	8	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:175:LEU:HD13	1:A:185:VAL:HG13	0.55	1.77	10	3
1:A:328:ASP:O	1:A:332:VAL:HG23	0.55	2.02	5	5
1:A:67:LYS:HE3	1:A:168:ILE:HD12	0.55	1.79	7	1
1:A:119:MET:SD	1:A:123:LEU:HD23	0.53	2.44	8	4
1:A:225:VAL:HG11	1:A:307:PHE:CZ	0.53	2.37	7	2
1:A:73:VAL:HG13	1:A:155:TYR:CE1	0.53	2.38	1	9
1:A:175:LEU:HD21	1:A:186:GLU:O	0.53	2.04	1	5
1:A:175:LEU:HD22	1:A:185:VAL:CG1	0.53	2.30	7	2
1:A:245:GLU:O	1:A:249:LEU:HD13	0.53	2.04	5	1
1:A:184:ILE:HG23	1:A:201:VAL:HG12	0.52	1.79	2	1
1:A:184:ILE:HD13	1:A:214:CYS:SG	0.52	2.44	3	3
1:A:122:GLU:O	1:A:126:VAL:HG23	0.52	2.04	2	10
1:A:128:LYS:CG	1:A:159:LEU:HD23	0.52	2.34	8	6
1:A:167:TYR:O	1:A:168:ILE:HD13	0.51	2.05	7	1
1:A:131:TRP:CE3	1:A:156:LEU:HD13	0.51	2.40	4	10
1:A:265:ILE:HD13	1:A:339:VAL:HG13	0.51	1.81	5	7
1:A:244:HIS:CD2	1:A:286:CYS:HG	0.51	2.23	1	1
1:A:93:ILE:HD11	1:A:142:ARG:HH21	0.51	1.65	1	2
1:A:175:LEU:HD11	1:A:187:THR:OG1	0.51	2.06	5	4
1:A:185:VAL:HG23	1:A:200:ASP:HB3	0.51	1.82	6	1
1:A:69:TYR:CG	1:A:174:VAL:HG13	0.50	2.42	8	4
1:A:74:TYR:HB3	1:A:114:ALA:HB1	0.50	1.82	7	8
1:A:110:LEU:HD11	1:A:122:GLU:CD	0.49	2.32	6	6
1:A:265:ILE:HD13	1:A:339:VAL:CG1	0.49	2.37	6	7
1:A:34:VAL:HG11	1:A:196:PHE:CE2	0.48	2.44	9	4
1:A:159:LEU:HD12	1:A:162:ILE:HD11	0.48	1.86	2	3
1:A:232:LEU:HD13	1:A:242:ARG:NH1	0.48	2.24	2	1
1:A:211:TRP:CH2	1:A:249:LEU:HD23	0.47	2.44	3	6
1:A:88:MET:HE2	1:A:93:ILE:O	0.47	2.09	5	1
1:A:119:MET:CE	1:A:163:ALA:HB2	0.47	2.39	6	1
1:A:175:LEU:HD13	1:A:185:VAL:HG12	0.47	1.86	5	1
1:A:175:LEU:HD13	1:A:185:VAL:CG1	0.46	2.40	5	4
1:A:38:LEU:HD11	1:A:198:MET:SD	0.46	2.51	5	4
1:A:128:LYS:HG2	1:A:159:LEU:HD23	0.46	1.87	7	3
1:A:78:ILE:CD1	1:A:127:ILE:HD11	0.46	2.41	2	1
1:A:184:ILE:HD12	1:A:201:VAL:HG12	0.45	1.87	2	1
1:A:245:GLU:O	1:A:249:LEU:HD12	0.45	2.12	10	6
1:A:212:ILE:HD12	1:A:212:ILE:C	0.45	2.37	5	4
1:A:88:MET:HE1	1:A:95:PHE:HA	0.45	1.89	7	1
1:A:162:ILE:HG22	1:A:167:TYR:CZ	0.44	2.48	8	1
1:A:54:LYS:HZ1	1:A:161:ARG:NH1	0.44	2.10	4	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:184:ILE:HD12	1:A:214:CYS:SG	0.44	2.53	5	1
1:A:175:LEU:CD2	1:A:185:VAL:HG13	0.44	2.35	7	1
1:A:37:LEU:HD13	1:A:214:CYS:HB3	0.43	1.91	9	1
1:A:36:LEU:HD11	1:A:196:PHE:CD2	0.43	2.49	7	1
1:A:128:LYS:HG3	1:A:159:LEU:HD23	0.43	1.91	8	1
1:A:313:ARG:HH21	1:A:316:THR:HG21	0.43	1.73	9	1
1:A:87:ALA:HB3	1:A:139:CYS:SG	0.43	2.54	9	3
1:A:226:ALA:HB3	1:A:229:ASP:CG	0.43	2.38	8	1
1:A:208:ARG:HD3	1:A:249:LEU:HD21	0.43	1.89	6	2
1:A:313:ARG:NH2	1:A:316:THR:HG21	0.43	2.28	9	1
1:A:63:GLU:HG3	1:A:168:ILE:HG21	0.42	1.91	9	1
1:A:175:LEU:HD22	1:A:185:VAL:HB	0.42	1.92	6	2
1:A:174:VAL:O	1:A:177:THR:HG23	0.42	2.15	8	1
1:A:119:MET:HE3	1:A:159:LEU:HD11	0.42	1.92	8	1
1:A:119:MET:SD	1:A:163:ALA:HB2	0.42	2.54	1	1
1:A:52:GLN:OE1	1:A:329:THR:HG23	0.41	2.15	7	1
1:A:201:VAL:HG12	1:A:214:CYS:SG	0.41	2.56	7	1
1:A:167:TYR:C	1:A:168:ILE:HD13	0.41	2.41	7	1
1:A:335:VAL:O	1:A:339:VAL:HG23	0.41	2.15	8	2

6.3 Torsion angles [i](#)

6.3.1 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 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	304/326 (93%)	282±2 (93±1%)	16±3 (5±1%)	6±2 (2±1%)	8	51
All	All	3040/3260 (93%)	2822 (93%)	160 (5%)	58 (2%)	8	51

All 22 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	304	GLN	8
1	A	311	ASN	6
1	A	169	PRO	5

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Mol	Chain	Res	Type	Models (Total)
1	A	204	GLN	4
1	A	295	THR	4
1	A	184	ILE	4
1	A	217	GLY	3
1	A	97	ASP	3
1	A	283	LEU	3
1	A	201	VAL	3
1	A	34	VAL	2
1	A	202	GLY	2
1	A	63	GLU	2
1	A	33	GLU	1
1	A	290	TYR	1
1	A	317	LYS	1
1	A	185	VAL	1
1	A	286	CYS	1
1	A	171	GLN	1
1	A	175	LEU	1
1	A	186	GLU	1
1	A	146	TYR	1

6.3.2 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 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	265/281 (94%)	263±1 (99±0%)	2±1 (1±0%)	68 95
All	All	2650/2810 (94%)	2626 (99%)	24 (1%)	68 95

All 9 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	267	PHE	6
1	A	172	GLN	5
1	A	170	THR	5
1	A	78	ILE	2
1	A	212	ILE	2
1	A	210	LYS	1

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Mol	Chain	Res	Type	Models (Total)
1	A	185	VAL	1
1	A	95	PHE	1
1	A	54	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 oligosaccharides 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 i

The completeness of assignment taking into account all chemical shift lists is 11% for the well-defined parts and 11% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *gnai1-apo-bmrb.dat*

7.1.1 Bookkeeping i

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	488
Number of shifts mapped to atoms	488
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 i

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
¹³ C _α	0	—	None (insufficient data)
¹³ C _β	0	—	None (insufficient data)
¹³ C'	0	—	None (insufficient data)
¹⁵ N	241	-0.10 \pm 0.24	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments i

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 11%, i.e. 458 atoms were assigned a chemical shift out of a possible 4222. 0 out of 40 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	452/1527 (30%)	226/618 (37%)	0/608 (0%)	226/301 (75%)
Sidechain	0/2329 (0%)	0/1507 (0%)	0/730 (0%)	0/92 (0%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	6/366 (2%)	3/180 (2%)	0/177 (0%)	3/9 (33%)
Overall	458/4222 (11%)	229/2305 (10%)	0/1515 (0%)	229/402 (57%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 11%, i.e. 488 atoms were assigned a chemical shift out of a possible 4476. 0 out of 43 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	482/1625 (30%)	241/659 (37%)	0/646 (0%)	241/320 (75%)
Sidechain	0/2466 (0%)	0/1595 (0%)	0/771 (0%)	0/100 (0%)
Aromatic	6/385 (2%)	3/189 (2%)	0/187 (0%)	3/9 (33%)
Overall	488/4476 (11%)	244/2443 (10%)	0/1604 (0%)	244/429 (57%)

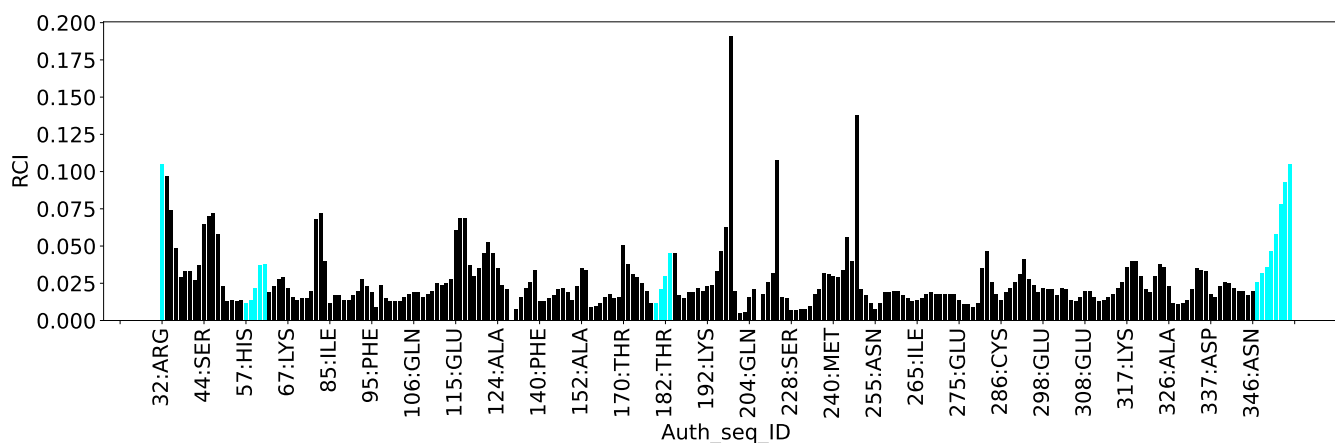
7.1.4 Statistically unusual chemical shifts [i](#)

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. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:



8 NMR restraints analysis

No restraints data found

9 Distance violation analysis

No distance restraints data found

10 Dihedral-angle violation analysis

No dihedral-angle restraints found