



Full wwPDB NMR Structure Validation Report ⓘ

Apr 27, 2016 – 04:39 AM BST

PDB ID : 2OWI
Title : Solution structure of the RGS domain from human RGS18
Authors : Higman, V.A.; Leidert, M.; Bray, J.; Elkins, J.; Soundararajan, M.; Doyle, D.A.; Gileadi, C.; Phillips, C.; Schoch, G.; Yang, X.; Brockmann, C.; Schmieder, P.; Diehl, A.; Sundstrom, M.; Arrowsmith, C.; Weigelt, J.; Edwards, A.; Oschkinat, H.; Ball, L.J.; Structural Genomics Consortium (SGC)
Deposited on : 2007-02-16

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
<http://wwpdb.org/validation/2016/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
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20027457
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

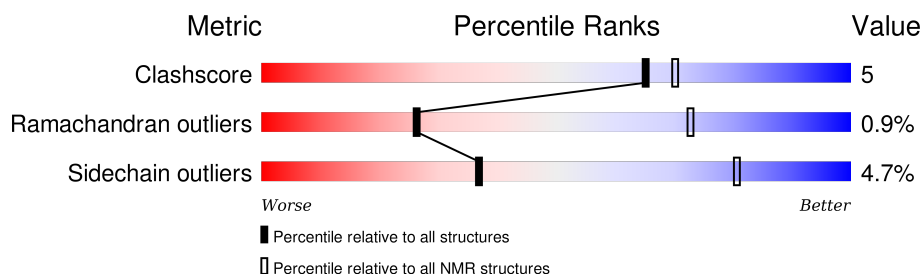
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

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	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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	151	

2 Ensemble composition and analysis

This entry contains 20 models. Model 13 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:3-A:130 (128)	0.70	13

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 6 clusters and 1 single-model cluster was found.

Cluster number	Models
1	1, 5, 11, 14
2	7, 12, 13, 15
3	3, 9, 10, 20
4	2, 4, 6
5	16, 19
6	17, 18
Single-model clusters	8

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2183 atoms, of which 1079 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Regulator of G-protein signaling 18.

Mol	Chain	Residues	Atoms						Trace
1	A	134	Total	C	H	N	O	S	0
			2183	706	1079	181	213	4	

There are 2 discrepancies between the modelled and reference sequences:

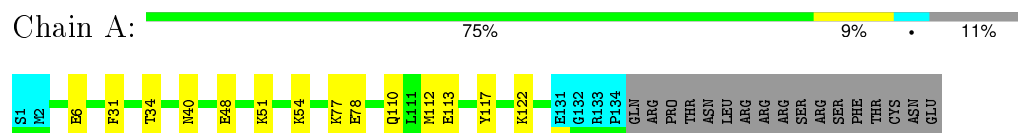
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	SER	-	CLONING ARTIFACT	UNP Q9NS28
A	2	MET	-	CLONING ARTIFACT	UNP Q9NS28

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

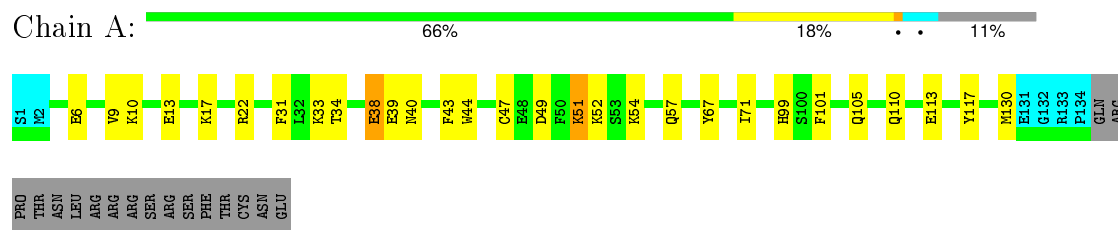
These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain 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: Regulator of G-protein signaling 18



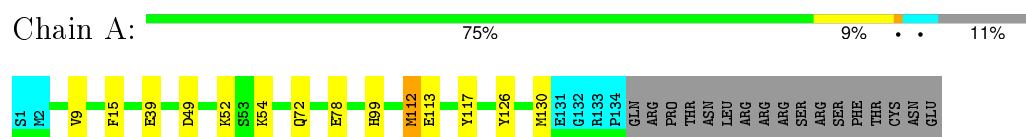
4.2.3 Score per residue for model 3

- Molecule 1: Regulator of G-protein signaling 18



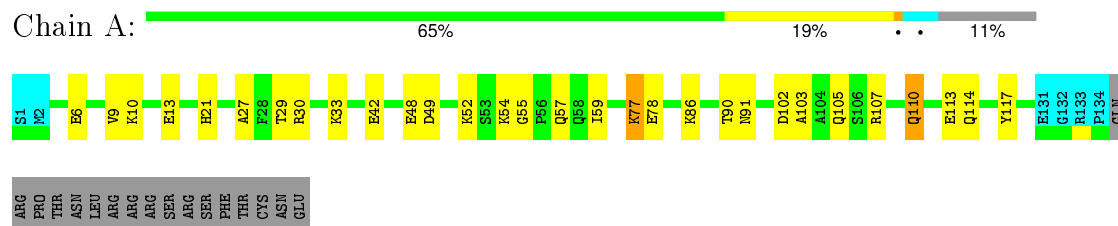
4.2.4 Score per residue for model 4

- Molecule 1: Regulator of G-protein signaling 18



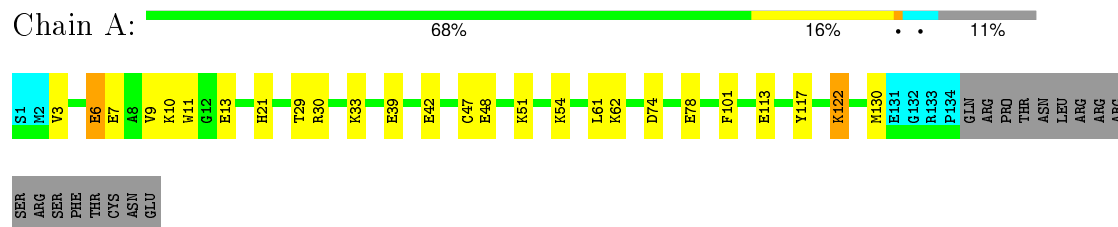
4.2.5 Score per residue for model 5

- Molecule 1: Regulator of G-protein signaling 18



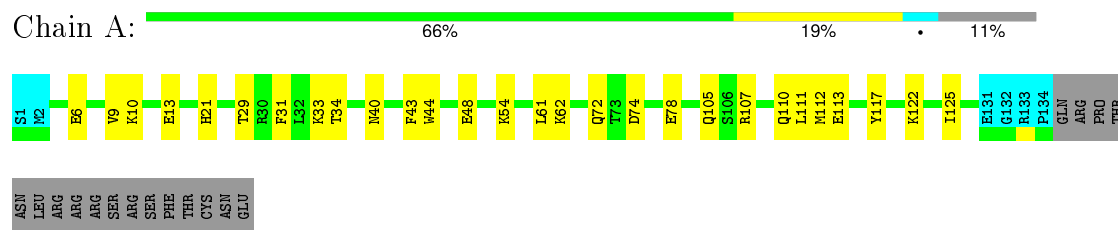
4.2.6 Score per residue for model 6

- Molecule 1: Regulator of G-protein signaling 18



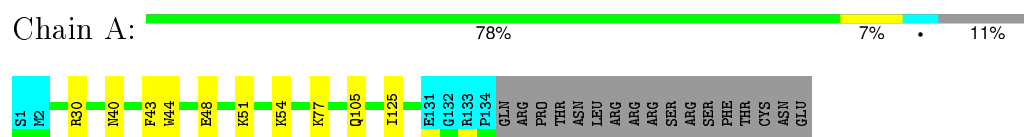
4.2.7 Score per residue for model 7

- Molecule 1: Regulator of G-protein signaling 18



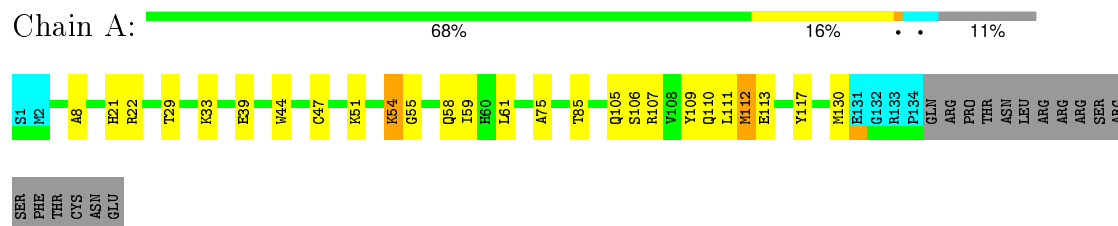
4.2.8 Score per residue for model 8

- Molecule 1: Regulator of G-protein signaling 18



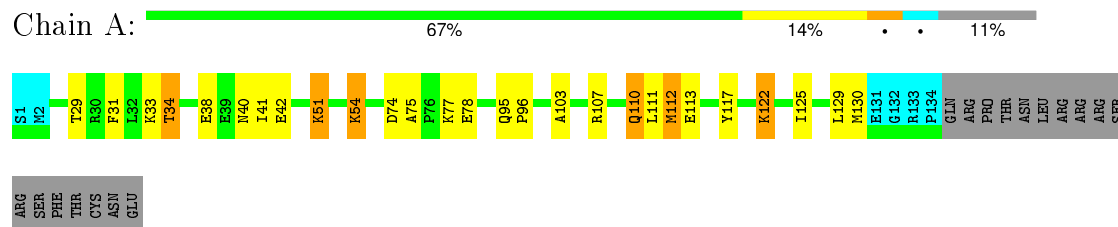
4.2.9 Score per residue for model 9

- Molecule 1: Regulator of G-protein signaling 18



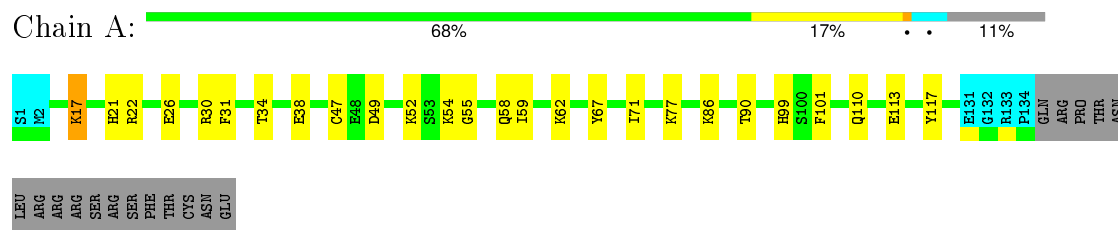
4.2.10 Score per residue for model 10

- Molecule 1: Regulator of G-protein signaling 18



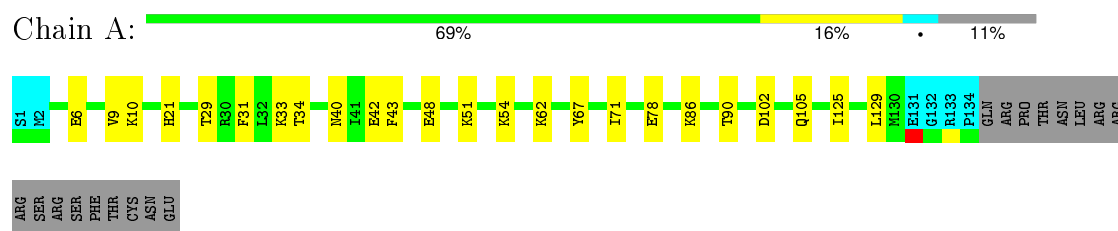
4.2.11 Score per residue for model 11

- Molecule 1: Regulator of G-protein signaling 18



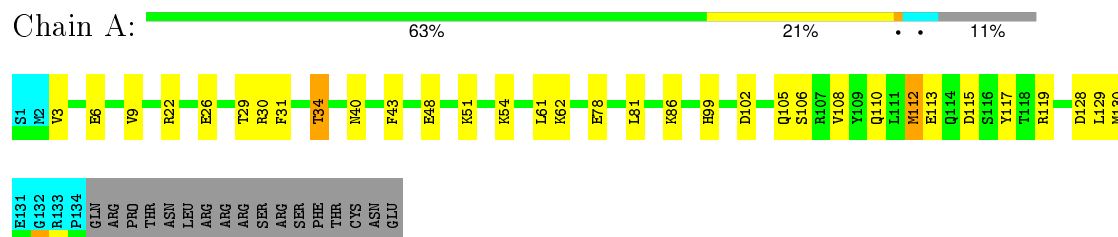
4.2.12 Score per residue for model 12

- Molecule 1: Regulator of G-protein signaling 18



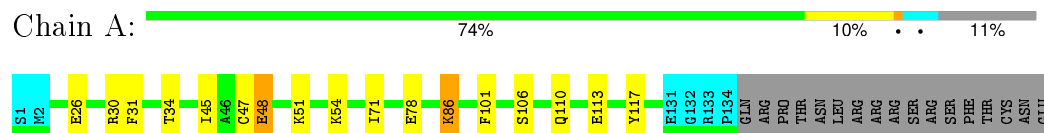
4.2.13 Score per residue for model 13 (medoid)

- Molecule 1: Regulator of G-protein signaling 18



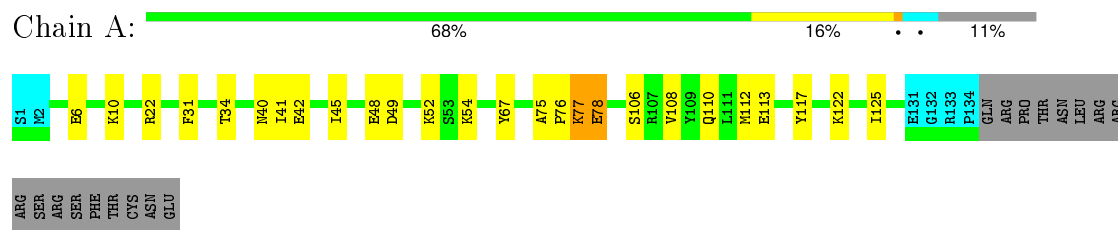
4.2.14 Score per residue for model 14

- Molecule 1: Regulator of G-protein signaling 18



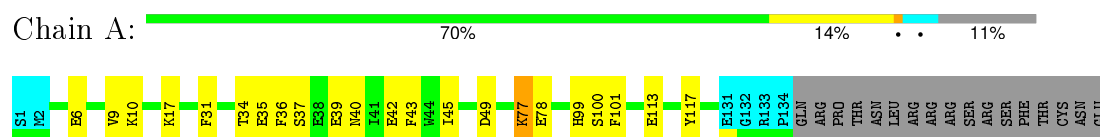
4.2.15 Score per residue for model 15

- Molecule 1: Regulator of G-protein signaling 18



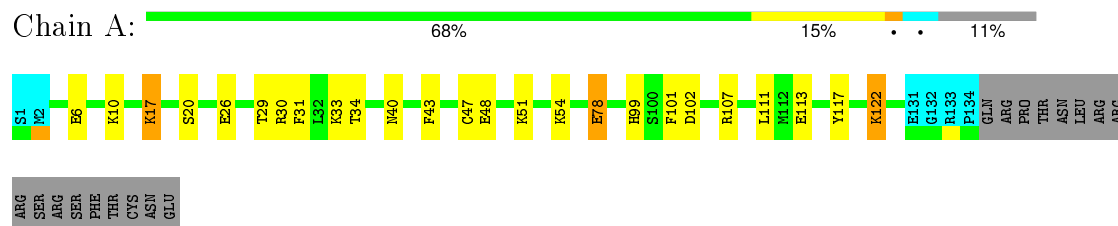
4.2.16 Score per residue for model 16

- Molecule 1: Regulator of G-protein signaling 18



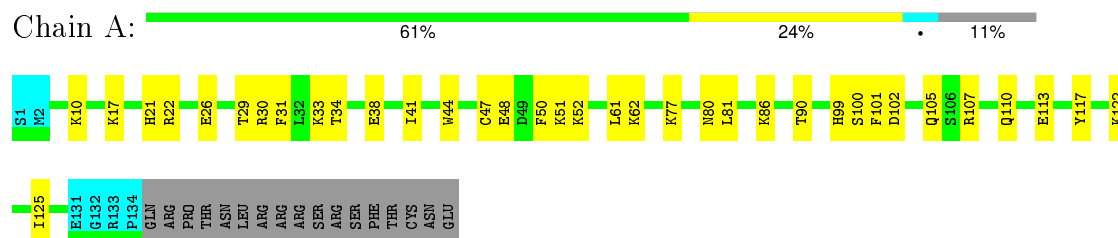
4.2.17 Score per residue for model 17

- Molecule 1: Regulator of G-protein signaling 18



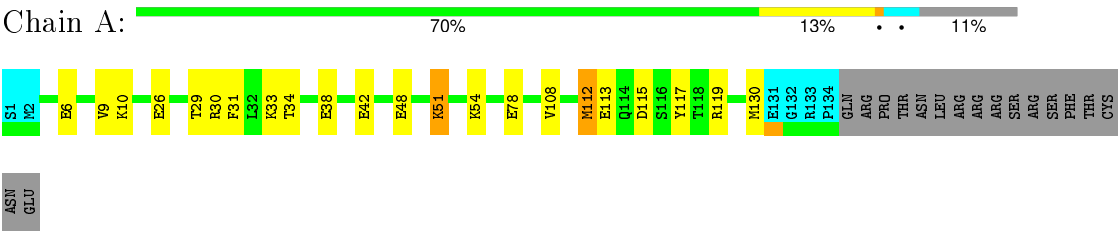
4.2.18 Score per residue for model 18

- Molecule 1: Regulator of G-protein signaling 18



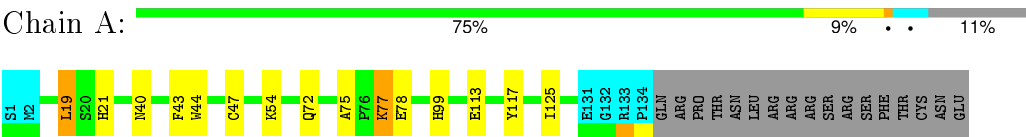
4.2.19 Score per residue for model 19

- Molecule 1: Regulator of G-protein signaling 18



4.2.20 Score per residue for model 20

- Molecule 1: Regulator of G-protein signaling 18



5 Refinement protocol and experimental data overview

The models were refined using the following method: *SIMULATED ANNEALING, MOLECULAR DYNAMICS*.

Of the 200 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
CNS	refinement	1.1
XWINNMR 2.6 AND	structure solution	3.1
CCPNMR ANALYSIS 1.0.9-10	structure solution	1.0.9-10
CYANA	structure solution	2.0
X-PLOR NIH	structure solution	2.14

No chemical shift data was provided. 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](#)

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	1059	1034	1030	11±4
All	All	21180	20680	20600	213

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:47:CYS:SG	1:A:101:PHE:HB2	0.71	2.25	17	5
1:A:9:VAL:HG12	1:A:130:MET:SD	0.68	2.28	4	2
1:A:44:TRP:HA	1:A:47:CYS:SG	0.66	2.31	2	3
1:A:8:ALA:HB3	1:A:130:MET:SD	0.65	2.31	9	1
1:A:122:LYS:HE2	1:A:122:LYS:HA	0.61	1.70	18	2
1:A:99:HIS:HB3	1:A:102:ASP:HB2	0.60	1.72	18	2
1:A:49:ASP:HA	1:A:52:LYS:HE3	0.59	1.73	5	3
1:A:113:GLU:O	1:A:117:TYR:HB3	0.59	1.97	2	18
1:A:49:ASP:HA	1:A:52:LYS:HE2	0.58	1.74	11	1
1:A:122:LYS:HE3	1:A:122:LYS:HA	0.58	1.76	17	1
1:A:106:SER:O	1:A:110:GLN:HG3	0.57	1.98	13	4
1:A:77:LYS:HA	1:A:77:LYS:HE2	0.57	1.76	10	2
1:A:48:GLU:O	1:A:51:LYS:HG2	0.56	2.00	13	4
1:A:122:LYS:HA	1:A:122:LYS:HE2	0.55	1.76	7	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:17:LYS:HB2	1:A:17:LYS:NZ	0.55	2.16	11	2
1:A:6:GLU:O	1:A:9:VAL:HG22	0.54	2.03	7	9
1:A:48:GLU:HA	1:A:51:LYS:HG2	0.53	1.79	6	1
1:A:122:LYS:HA	1:A:122:LYS:HE3	0.53	1.78	10	2
1:A:99:HIS:O	1:A:101:PHE:N	0.53	2.41	16	2
1:A:26:GLU:O	1:A:30:ARG:HG2	0.53	2.04	18	3
1:A:40:ASN:O	1:A:43:PHE:HB3	0.53	2.04	16	10
1:A:29:THR:O	1:A:33:LYS:HG3	0.52	2.04	19	7
1:A:38:GLU:O	1:A:41:ILE:HG22	0.52	2.03	18	1
1:A:6:GLU:O	1:A:10:LYS:HG2	0.52	2.05	12	6
1:A:22:ARG:HB3	1:A:22:ARG:NH1	0.52	2.19	3	1
1:A:72:GLN:HG3	1:A:74:ASP:H	0.52	1.64	7	1
1:A:51:LYS:HB2	1:A:51:LYS:NZ	0.52	2.19	3	2
1:A:48:GLU:O	1:A:52:LYS:HG3	0.51	2.04	15	2
1:A:109:TYR:HA	1:A:112:MET:SD	0.51	2.46	9	1
1:A:10:LYS:O	1:A:13:GLU:HG2	0.50	2.06	3	3
1:A:26:GLU:O	1:A:29:THR:HG22	0.50	2.07	13	2
1:A:31:PHE:O	1:A:34:THR:HG22	0.49	2.07	18	13
1:A:44:TRP:HB2	1:A:105:GLN:HG3	0.49	1.82	8	2
1:A:45:ILE:O	1:A:48:GLU:HG3	0.49	2.06	14	1
1:A:61:LEU:HD12	1:A:62:LYS:N	0.48	2.23	7	4
1:A:10:LYS:O	1:A:17:LYS:HD2	0.48	2.08	18	3
1:A:49:ASP:O	1:A:52:LYS:HG2	0.47	2.09	3	1
1:A:44:TRP:CA	1:A:47:CYS:SG	0.47	3.02	2	1
1:A:110:GLN:NE2	1:A:111:LEU:HD12	0.47	2.25	10	1
1:A:58:GLN:OE1	1:A:61:LEU:HD11	0.47	2.09	9	1
1:A:47:CYS:O	1:A:50:PHE:HB3	0.47	2.10	18	1
1:A:115:ASP:O	1:A:119:ARG:HG3	0.47	2.09	19	1
1:A:51:LYS:HE3	1:A:99:HIS:CE1	0.47	2.45	18	1
1:A:103:ALA:O	1:A:107:ARG:HG2	0.47	2.10	10	2
1:A:113:GLU:HA	1:A:117:TYR:HB3	0.46	1.85	17	1
1:A:22:ARG:HH11	1:A:26:GLU:HB2	0.46	1.70	11	1
1:A:52:LYS:N	1:A:52:LYS:HE2	0.46	2.25	18	1
1:A:115:ASP:O	1:A:119:ARG:HD3	0.46	2.11	13	1
1:A:86:LYS:O	1:A:90:THR:HG23	0.46	2.11	11	5
1:A:58:GLN:O	1:A:62:LYS:HB2	0.46	2.10	11	1
1:A:72:GLN:NE2	1:A:74:ASP:HB3	0.46	2.26	2	1
1:A:77:LYS:HE3	1:A:77:LYS:HA	0.45	1.87	16	1
1:A:107:ARG:O	1:A:111:LEU:HG	0.45	2.11	7	3
1:A:81:LEU:O	1:A:86:LYS:NZ	0.45	2.49	13	1
1:A:22:ARG:NH1	1:A:26:GLU:HB2	0.45	2.27	11	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:26:GLU:O	1:A:30:ARG:HG3	0.45	2.10	17	2
1:A:40:ASN:ND2	1:A:112:MET:HB3	0.45	2.27	10	1
1:A:17:LYS:HA	1:A:20:SER:OG	0.45	2.11	17	1
1:A:125:ILE:O	1:A:129:LEU:HG	0.44	2.11	12	2
1:A:47:CYS:SG	1:A:105:GLN:OE1	0.44	2.74	18	1
1:A:49:ASP:HA	1:A:52:LYS:CD	0.44	2.43	15	1
1:A:102:ASP:HA	1:A:105:GLN:NE2	0.44	2.28	13	1
1:A:108:VAL:O	1:A:112:MET:SD	0.44	2.75	19	2
1:A:27:ALA:O	1:A:30:ARG:HB2	0.44	2.13	5	1
1:A:85:THR:OG1	1:A:107:ARG:HG3	0.43	2.13	9	1
1:A:110:GLN:O	1:A:114:GLN:HG2	0.43	2.13	5	1
1:A:14:SER:O	1:A:17:LYS:HG2	0.43	2.14	2	1
1:A:108:VAL:O	1:A:112:MET:HG3	0.43	2.14	15	1
1:A:33:LYS:HG2	1:A:38:GLU:HB3	0.43	1.91	10	1
1:A:77:LYS:O	1:A:77:LYS:HD3	0.43	2.13	11	1
1:A:39:GLU:O	1:A:43:PHE:HB2	0.43	2.14	16	1
1:A:107:ARG:O	1:A:110:GLN:HG2	0.43	2.12	7	1
1:A:35:GLU:O	1:A:37:SER:N	0.43	2.51	16	1
1:A:42:GLU:HA	1:A:45:ILE:HG22	0.42	1.91	15	1
1:A:67:TYR:HA	1:A:71:ILE:HB	0.42	1.90	3	3
1:A:55:GLY:O	1:A:59:ILE:HG12	0.42	2.14	11	3
1:A:29:THR:OG1	1:A:33:LYS:HE2	0.42	2.13	5	1
1:A:40:ASN:OD1	1:A:41:ILE:N	0.42	2.52	10	2
1:A:107:ARG:O	1:A:110:GLN:HG3	0.42	2.14	10	1
1:A:3:VAL:HG11	1:A:129:LEU:HD13	0.42	1.92	13	1
1:A:95:GLN:N	1:A:96:PRO:HD3	0.42	2.29	10	1
1:A:42:GLU:HA	1:A:45:ILE:HB	0.42	1.91	16	1
1:A:44:TRP:O	1:A:48:GLU:HG2	0.42	2.15	18	2
1:A:126:TYR:O	1:A:130:MET:HG2	0.41	2.15	4	1
1:A:33:LYS:HD2	1:A:38:GLU:HB3	0.41	1.91	3	1
1:A:57:GLN:OE1	1:A:57:GLN:N	0.41	2.53	5	1
1:A:62:LYS:HA	1:A:62:LYS:HE2	0.41	1.91	12	1
1:A:29:THR:OG1	1:A:33:LYS:NZ	0.41	2.54	17	1
1:A:19:LEU:HD23	1:A:44:TRP:CZ2	0.41	2.50	20	1
1:A:102:ASP:O	1:A:105:GLN:HB3	0.41	2.16	12	2
1:A:51:LYS:HE3	1:A:99:HIS:ND1	0.41	2.31	18	1
1:A:7:GLU:O	1:A:10:LYS:HB2	0.41	2.16	6	1
1:A:48:GLU:O	1:A:51:LYS:HG3	0.41	2.15	19	1
1:A:6:GLU:O	1:A:10:LYS:HD3	0.41	2.16	3	1
1:A:54:LYS:HB2	1:A:54:LYS:NZ	0.41	2.31	10	1
1:A:26:GLU:HA	1:A:29:THR:HG22	0.41	1.93	18	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:77:LYS:HD2	1:A:78:GLU:O	0.40	2.17	15	1
1:A:125:ILE:N	1:A:125:ILE:HD12	0.40	2.30	7	1
1:A:48:GLU:HA	1:A:51:LYS:HB3	0.40	1.92	17	1
1:A:15:PHE:CZ	1:A:112:MET:SD	0.40	3.14	4	1
1:A:75:ALA:HB1	1:A:76:PRO:HD2	0.40	1.93	15	1
1:A:71:ILE:O	1:A:86:LYS:NZ	0.40	2.50	14	1
1:A:3:VAL:HG21	1:A:11:TRP:CZ2	0.40	2.52	6	1
1:A:72:GLN:HB2	1:A:75:ALA:HB2	0.40	1.93	20	1
1:A:81:LEU:HD23	1:A:86:LYS:HB3	0.40	1.94	18	1

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	128/151 (85%)	118±3 (92±2%)	9±3 (7±2%)	1±1 (1±1%)	26	73
All	All	2560/3020 (85%)	2355 (92%)	181 (7%)	24 (1%)	26	73

All 11 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	78	GLU	11
1	A	75	ALA	3
1	A	100	SER	2
1	A	54	LYS	1
1	A	130	MET	1
1	A	80	ASN	1
1	A	36	PHE	1
1	A	98	LEU	1
1	A	77	LYS	1
1	A	67	TYR	1
1	A	74	ASP	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	117/139 (84%)	111±2 (95±2%)	6±2 (5±2%)	37 80
All	All	2340/2780 (84%)	2229 (95%)	111 (5%)	37 80

All 32 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	54	LYS	18
1	A	21	HIS	9
1	A	77	LYS	6
1	A	112	MET	6
1	A	110	GLN	6
1	A	42	GLU	5
1	A	22	ARG	5
1	A	51	LYS	5
1	A	99	HIS	5
1	A	38	GLU	4
1	A	39	GLU	4
1	A	122	LYS	4
1	A	125	ILE	4
1	A	105	GLN	3
1	A	30	ARG	3
1	A	78	GLU	3
1	A	17	LYS	2
1	A	6	GLU	2
1	A	34	THR	2
1	A	72	GLN	2
1	A	130	MET	2
1	A	49	ASP	1
1	A	57	GLN	1
1	A	95	GLN	1
1	A	86	LYS	1
1	A	91	ASN	1
1	A	19	LEU	1
1	A	80	ASN	1
1	A	13	GLU	1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	107	ARG	1
1	A	48	GLU	1
1	A	74	ASP	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

No chemical shift data were provided