



Full wwPDB NMR Structure Validation Report ⓘ

Mar 6, 2022 – 05:13 PM EST

PDB ID : 2KSR
Title : NMR structures of TM domain of the n-Acetylcholine receptor b2 subunit
Authors : Bondarenko, V.; Tillman, T.; Xu, Y.; Tang, P.
Deposited on : 2010-01-12

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:

MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : 2.27
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.27

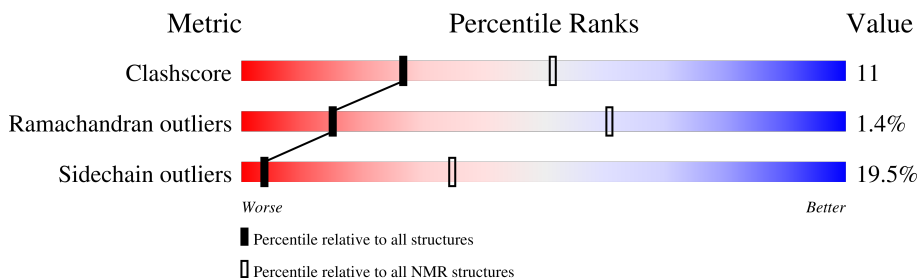
1 Overall quality at a glance

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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	164	 43% 27% • 14% 15%

2 Ensemble composition and analysis i

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:28-A:117, A:130-A:156 (117)	0.79	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 2 clusters and 2 single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2277 atoms, of which 1176 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Neuronal acetylcholine receptor subunit beta-2.

Mol	Chain	Residues	Atoms					Trace	
			Total	C	H	N	O		S
1	A	140	2277	742	1176	171	178	10	0

There are 30 discrepancies between the modelled and reference sequences:

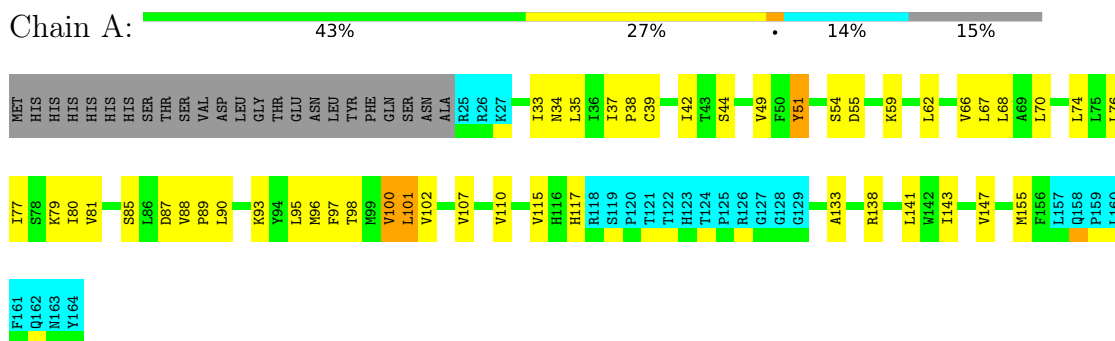
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP P17787
A	2	HIS	-	expression tag	UNP P17787
A	3	HIS	-	expression tag	UNP P17787
A	4	HIS	-	expression tag	UNP P17787
A	5	HIS	-	expression tag	UNP P17787
A	6	HIS	-	expression tag	UNP P17787
A	7	HIS	-	expression tag	UNP P17787
A	8	SER	-	expression tag	UNP P17787
A	9	THR	-	expression tag	UNP P17787
A	10	SER	-	expression tag	UNP P17787
A	11	VAL	-	expression tag	UNP P17787
A	12	ASP	-	expression tag	UNP P17787
A	13	LEU	-	expression tag	UNP P17787
A	14	GLY	-	expression tag	UNP P17787
A	15	THR	-	expression tag	UNP P17787
A	16	GLU	-	expression tag	UNP P17787
A	17	ASN	-	expression tag	UNP P17787
A	18	LEU	-	expression tag	UNP P17787
A	19	TYR	-	expression tag	UNP P17787
A	20	PHE	-	expression tag	UNP P17787
A	21	GLN	-	expression tag	UNP P17787
A	22	SER	-	expression tag	UNP P17787
A	23	ASN	-	expression tag	UNP P17787
A	24	ALA	-	expression tag	UNP P17787
A	125	PRO	-	linker	UNP P17787
A	126	ARG	-	linker	UNP P17787
A	127	GLY	-	linker	UNP P17787
A	128	GLY	-	linker	UNP P17787
A	129	GLY	-	linker	UNP P17787
A	130	GLY	-	linker	UNP P17787

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: Neuronal acetylcholine receptor subunit beta-2

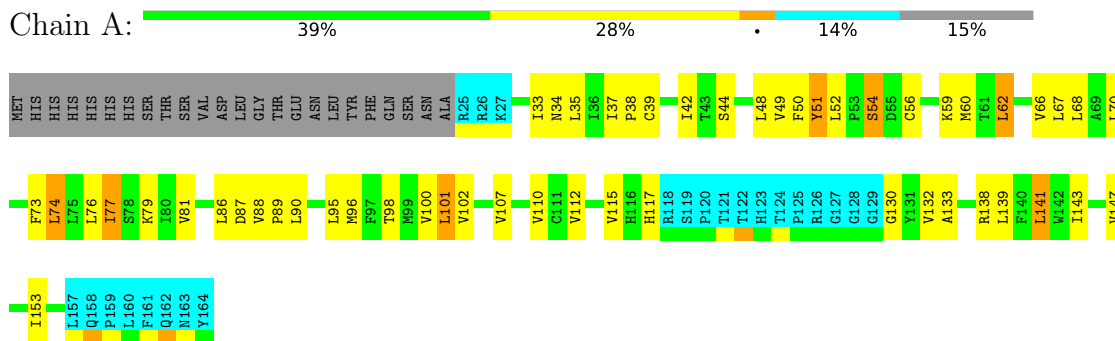


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Neuronal acetylcholine receptor subunit beta-2

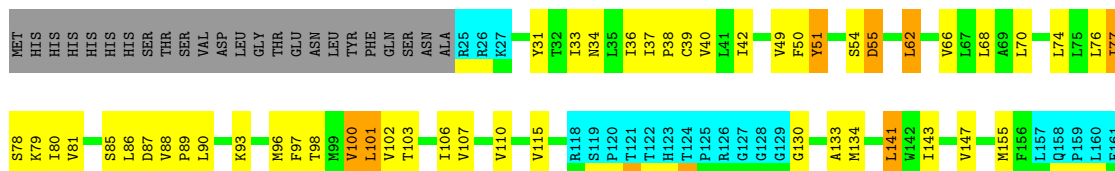




4.2.9 Score per residue for model 9

- Molecule 1: Neuronal acetylcholine receptor subunit beta-2

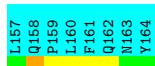
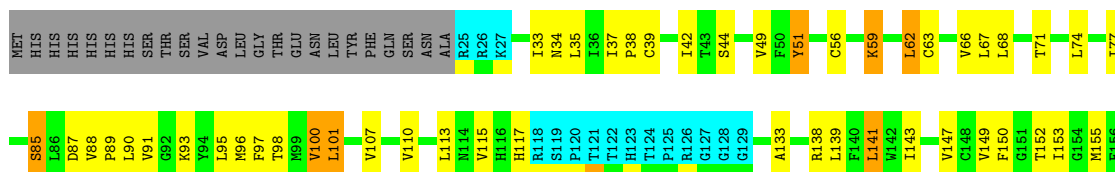
Chain A: 41% 26% 14% 15%



4.2.10 Score per residue for model 10

- Molecule 1: Neuronal acetylcholine receptor subunit beta-2

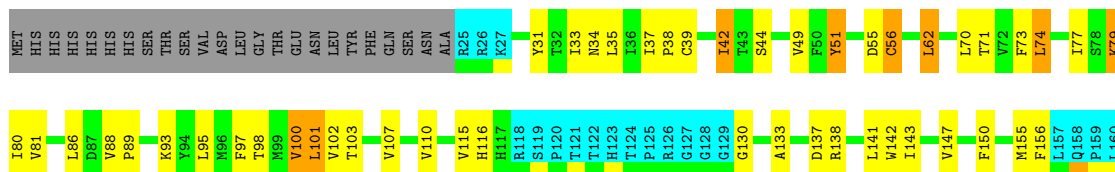
Chain A: 41% 26% 14% 15%

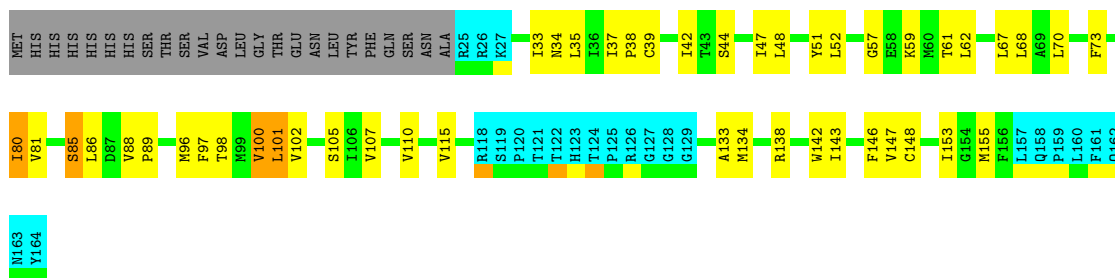


4.2.11 Score per residue for model 11

- Molecule 1: Neuronal acetylcholine receptor subunit beta-2

Chain A: 42% 24% 5% 14% 15%

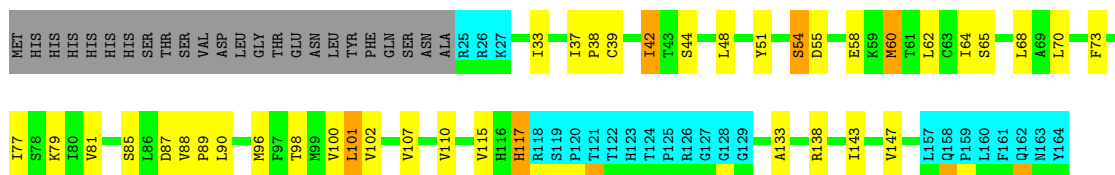




4.2.16 Score per residue for model 16

- Molecule 1: Neuronal acetylcholine receptor subunit beta-2

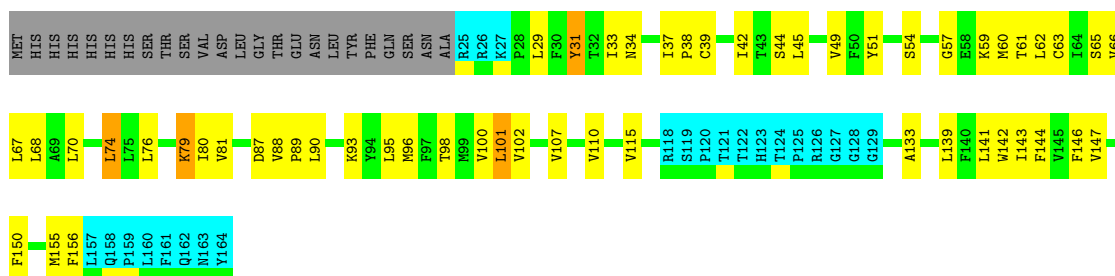
Chain A: 48% 21% 14% 15%



4.2.17 Score per residue for model 17

- Molecule 1: Neuronal acetylcholine receptor subunit beta-2

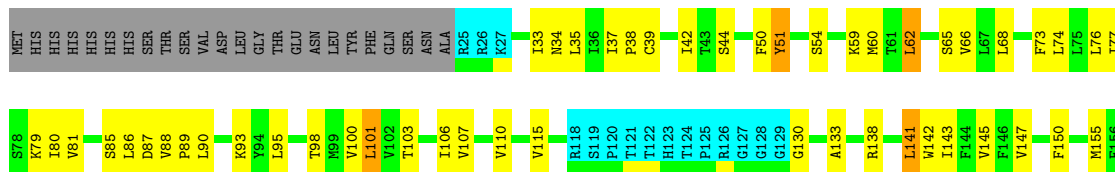
Chain A: 38% 30% 14% 15%



4.2.18 Score per residue for model 18

- Molecule 1: Neuronal acetylcholine receptor subunit beta-2

Chain A: 41% 28% 14% 15%



L157
Q158
P159
L160
F161
Q162
M163
Y164

4.2.19 Score per residue for model 19

- Molecule 1: Neuronal acetylcholine receptor subunit beta-2

Chain A: 42% 26% 14% 15%

MET
HIS
HIS
HIS
HIS
HIS
HIS
HIS
HIS
SER
THR
THR
SER
SER
VAL
VAL
ASP
ASP
LEU
LEU
GLY
THR
GLU
GLU
ASN
ASN
LEU
LEU
TYR
PHE
GLN
SER
SER
ASN
ASN
ALA
R25
R26
R27
I33
N34
L35
L36
I37
P38
C39
V40
L41
I42
V49
F50
Y51
S54
D55
K59
M60
L67
L68
A69
L70
L76
L77
S78
K79
I80
V81

S85
L86
D87
V88
P89
L90
K93
M96
F97
T98
M99
V100
L101
V102
S105
L113
M114
V115
H116
H117
R118
S119
P120
T121
T122
H123
T124
P125
R126
G127
G128
G129
V132
A133
R138
L139
F140
L141
W142
T143
F144
V145
F146
V147
C148
M155
F156
L157
Q158
P159
L160
F161

Q162
M163
Y164

4.2.20 Score per residue for model 20

- Molecule 1: Neuronal acetylcholine receptor subunit beta-2

Chain A: 42% 26% 14% 15%

MET
HIS
HIS
HIS
HIS
HIS
HIS
HIS
SER
THR
THR
SER
SER
VAL
VAL
ASP
ASP
LEU
LEU
GLY
THR
GLU
GLU
ASN
ASN
LEU
LEU
TYR
PHE
GLN
SER
SER
ASN
ASN
ALA
R25
R26
R27
I33
I37
P38
C39
V40
L41
I42
V49
F50
Y51
S54
E58
K59
M60
T61
L62
S65
V66
L68
T71
L74
L75
L76

K79
I80
V81
S85
L86
D87
V88
P89
L90
K93
M94
L95
M96
F97
T98
M99
V100
L101
V107
T108
S109
V110
V115
H116
H117
R118
S119
P120
T121
T122
H123
T124
P125
R126
G127
G128
G129
G130
A133
D137
R138
L141
W142
T143
F146
V147
F150
M155
F156
L157

Q158
P159
L160
F161
Q162
M163
Y164

5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing, torsion angle dynamics*.

Of the 100 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
CYANA	structure solution	2.1
CYANA	refinement	2.1

No chemical shift data was provided.

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	913	986	986	21±3
All	All	18260	19720	19720	419

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 11.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:LEU:HD11	1:A:102:VAL:HG11	0.81	1.50	15	1
1:A:49:VAL:HG11	1:A:62:LEU:HD13	0.80	1.52	1	1
1:A:74:LEU:HD11	1:A:95:LEU:HD13	0.73	1.61	11	4
1:A:70:LEU:HD22	1:A:102:VAL:HG11	0.66	1.66	14	10
1:A:149:VAL:HG12	1:A:153:ILE:HD11	0.66	1.66	14	1
1:A:79:LYS:O	1:A:81:VAL:HG23	0.64	1.93	9	17
1:A:143:ILE:O	1:A:147:VAL:HG23	0.64	1.93	6	19
1:A:115:VAL:HG11	1:A:133:ALA:HB2	0.64	1.70	20	20
1:A:62:LEU:O	1:A:66:VAL:HG23	0.63	1.94	9	9
1:A:70:LEU:CD1	1:A:102:VAL:HG11	0.63	2.23	15	3
1:A:51:TYR:CZ	1:A:141:LEU:HD13	0.63	2.29	11	5
1:A:74:LEU:HD23	1:A:95:LEU:HD13	0.63	1.69	20	1
1:A:57:GLY:O	1:A:61:THR:HG23	0.62	1.95	15	3
1:A:103:THR:O	1:A:107:VAL:HG23	0.61	1.95	6	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:49:VAL:HG13	1:A:62:LEU:HD22	0.61	1.73	20	1
1:A:49:VAL:HG22	1:A:59:LYS:HD3	0.60	1.71	19	1
1:A:70:LEU:HD13	1:A:102:VAL:HG11	0.60	1.71	16	5
1:A:98:THR:HA	1:A:101:LEU:HD23	0.59	1.75	1	20
1:A:49:VAL:CG1	1:A:62:LEU:HD22	0.58	2.28	20	2
1:A:149:VAL:HG12	1:A:153:ILE:CD1	0.58	2.28	14	1
1:A:49:VAL:HG23	1:A:54:SER:CB	0.58	2.29	12	2
1:A:112:VAL:HG13	1:A:130:GLY:O	0.58	1.97	1	1
1:A:49:VAL:HG21	1:A:59:LYS:HA	0.57	1.77	6	3
1:A:31:TYR:CE1	1:A:80:ILE:HG22	0.56	2.36	8	2
1:A:39:CYS:O	1:A:42:ILE:HG22	0.54	2.03	11	20
1:A:35:LEU:HG	1:A:77:ILE:HD12	0.54	1.78	12	4
1:A:58:GLU:O	1:A:62:LEU:HD12	0.54	2.02	12	1
1:A:51:TYR:CZ	1:A:141:LEU:HD23	0.54	2.37	18	1
1:A:51:TYR:CE2	1:A:141:LEU:HD22	0.54	2.38	11	6
1:A:67:LEU:HD22	1:A:70:LEU:HD12	0.53	1.80	6	1
1:A:141:LEU:O	1:A:145:VAL:HG23	0.53	2.04	7	6
1:A:51:TYR:CD2	1:A:141:LEU:HD22	0.53	2.39	9	2
1:A:115:VAL:CG1	1:A:133:ALA:HB2	0.52	2.35	1	20
1:A:51:TYR:CE1	1:A:141:LEU:HD13	0.52	2.40	6	2
1:A:132:VAL:O	1:A:135:VAL:HG22	0.52	2.05	7	1
1:A:74:LEU:HD11	1:A:95:LEU:CD1	0.52	2.35	10	3
1:A:74:LEU:HD21	1:A:95:LEU:CD1	0.51	2.35	10	1
1:A:49:VAL:HG23	1:A:59:LYS:HD3	0.51	1.83	17	1
1:A:74:LEU:CD2	1:A:95:LEU:HD13	0.50	2.36	20	1
1:A:77:ILE:O	1:A:80:ILE:HG23	0.50	2.06	9	4
1:A:74:LEU:HG	1:A:95:LEU:HD13	0.50	1.83	6	1
1:A:103:THR:HA	1:A:106:ILE:HD12	0.50	1.84	9	4
1:A:37:ILE:N	1:A:38:PRO:HD2	0.49	2.23	4	20
1:A:73:PHE:O	1:A:77:ILE:HG22	0.49	2.07	16	6
1:A:60:MET:O	1:A:64:ILE:HG23	0.49	2.07	16	1
1:A:74:LEU:CG	1:A:95:LEU:HD13	0.49	2.37	6	1
1:A:59:LYS:HE2	1:A:113:LEU:HD21	0.49	1.85	19	1
1:A:71:THR:O	1:A:75:LEU:HD13	0.49	2.08	20	1
1:A:49:VAL:HG12	1:A:62:LEU:HD22	0.48	1.85	12	1
1:A:84:THR:HG23	1:A:86:LEU:H	0.48	1.67	14	1
1:A:35:LEU:CB	1:A:77:ILE:HD12	0.48	2.38	1	1
1:A:88:VAL:N	1:A:89:PRO:HD2	0.48	2.24	15	20
1:A:49:VAL:HG21	1:A:62:LEU:HD13	0.48	1.85	14	1
1:A:70:LEU:CD2	1:A:102:VAL:HG11	0.48	2.38	11	3
1:A:107:VAL:O	1:A:110:VAL:HG12	0.48	2.09	7	19

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:150:PHE:O	1:A:153:ILE:HG22	0.48	2.08	10	1
1:A:38:PRO:HA	1:A:41:LEU:HD23	0.47	1.86	20	1
1:A:48:LEU:O	1:A:52:LEU:HD22	0.47	2.10	2	3
1:A:74:LEU:CD1	1:A:95:LEU:HD13	0.47	2.37	1	3
1:A:51:TYR:CE2	1:A:141:LEU:HD23	0.47	2.44	18	1
1:A:48:LEU:O	1:A:52:LEU:HD13	0.46	2.10	4	3
1:A:49:VAL:HG23	1:A:55:ASP:CB	0.46	2.40	9	1
1:A:74:LEU:HD11	1:A:95:LEU:HD11	0.46	1.88	7	4
1:A:59:LYS:CE	1:A:113:LEU:HD21	0.46	2.41	19	1
1:A:113:LEU:HD22	1:A:117:HIS:O	0.46	2.11	10	1
1:A:149:VAL:O	1:A:152:THR:HG22	0.46	2.11	10	1
1:A:35:LEU:HD13	1:A:76:LEU:HD22	0.45	1.88	3	1
1:A:81:VAL:HG22	1:A:81:VAL:O	0.45	2.11	18	2
1:A:35:LEU:CD1	1:A:76:LEU:HD22	0.45	2.42	3	2
1:A:70:LEU:HD13	1:A:102:VAL:HG21	0.45	1.89	4	2
1:A:42:ILE:CD1	1:A:66:VAL:HG23	0.45	2.42	20	1
1:A:35:LEU:HD12	1:A:77:ILE:HD12	0.45	1.89	5	1
1:A:70:LEU:HD13	1:A:102:VAL:CG1	0.45	2.42	16	1
1:A:101:LEU:C	1:A:101:LEU:HD12	0.44	2.33	16	2
1:A:101:LEU:HD12	1:A:101:LEU:C	0.44	2.33	7	17
1:A:87:ASP:O	1:A:91:VAL:HG23	0.44	2.12	10	2
1:A:58:GLU:O	1:A:62:LEU:HD23	0.44	2.11	13	1
1:A:74:LEU:HD11	1:A:95:LEU:CD2	0.44	2.43	10	1
1:A:48:LEU:O	1:A:52:LEU:HD23	0.44	2.13	15	1
1:A:87:ASP:HA	1:A:90:LEU:HD23	0.44	1.90	1	14
1:A:63:CYS:O	1:A:66:VAL:HG12	0.43	2.13	5	2
1:A:131:TYR:CZ	1:A:132:VAL:HG13	0.43	2.48	6	1
1:A:51:TYR:CE2	1:A:141:LEU:HD13	0.43	2.49	14	2
1:A:49:VAL:HG23	1:A:55:ASP:HB2	0.43	1.88	9	1
1:A:68:LEU:C	1:A:68:LEU:HD13	0.43	2.34	20	16
1:A:36:ILE:O	1:A:40:VAL:HG12	0.43	2.12	19	2
1:A:74:LEU:HD21	1:A:95:LEU:HD13	0.42	1.91	10	1
1:A:80:ILE:O	1:A:81:VAL:C	0.42	2.57	15	2
1:A:115:VAL:HG21	1:A:132:VAL:CG2	0.42	2.44	1	1
1:A:68:LEU:HD13	1:A:68:LEU:C	0.41	2.35	16	2
1:A:97:PHE:O	1:A:100:VAL:HG22	0.41	2.16	5	13
1:A:88:VAL:CB	1:A:89:PRO:CD	0.41	2.99	6	10
1:A:35:LEU:CD1	1:A:77:ILE:HD12	0.41	2.46	19	1
1:A:89:PRO:HG2	1:A:90:LEU:HD22	0.41	1.92	10	2
1:A:51:TYR:CG	1:A:141:LEU:HD22	0.41	2.50	12	1
1:A:35:LEU:HD21	1:A:80:ILE:HG21	0.41	1.93	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:35:LEU:HD12	1:A:73:PHE:CE2	0.40	2.50	15	1
1:A:88:VAL:HG12	1:A:89:PRO:N	0.40	2.31	10	1
1:A:49:VAL:HG11	1:A:62:LEU:HG	0.40	1.92	11	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	117/164 (71%)	108±2 (92±2%)	8±2 (7±2%)	2±1 (1±1%)	15	61
All	All	2340/3280 (71%)	2152 (92%)	155 (7%)	33 (1%)	15	61

All 7 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	117	HIS	7
1	A	54	SER	6
1	A	55	ASP	6
1	A	130	GLY	6
1	A	85	SER	4
1	A	56	CYS	2
1	A	116	HIS	2

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	109/151 (72%)	88±3 (81±3%)	21±3 (19±3%)	4	35
All	All	2180/3020 (72%)	1755 (81%)	425 (19%)	4	35

All 55 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	33	ILE	20
1	A	51	TYR	20
1	A	100	VAL	20
1	A	101	LEU	20
1	A	34	ASN	16
1	A	62	LEU	16
1	A	138	ARG	15
1	A	141	LEU	15
1	A	44	SER	14
1	A	96	MET	14
1	A	93	LYS	14
1	A	155	MET	14
1	A	85	SER	13
1	A	54	SER	12
1	A	67	LEU	12
1	A	59	LYS	9
1	A	60	MET	9
1	A	74	LEU	9
1	A	76	LEU	9
1	A	86	LEU	9
1	A	139	LEU	9
1	A	31	TYR	8
1	A	50	PHE	7
1	A	56	CYS	7
1	A	148	CYS	7
1	A	142	TRP	7
1	A	146	PHE	7
1	A	150	PHE	7
1	A	65	SER	7
1	A	55	ASP	6
1	A	117	HIS	6
1	A	42	ILE	6
1	A	77	ILE	5
1	A	134	MET	5
1	A	79	LYS	5
1	A	48	LEU	4
1	A	47	ILE	4
1	A	137	ASP	4
1	A	45	LEU	3
1	A	63	CYS	3
1	A	78	SER	3

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Mol	Chain	Res	Type	Models (Total)
1	A	58	GLU	3
1	A	105	SER	3
1	A	156	PHE	3
1	A	52	LEU	2
1	A	80	ILE	2
1	A	87	ASP	2
1	A	109	SER	2
1	A	71	THR	2
1	A	35	LEU	1
1	A	116	HIS	1
1	A	131	TYR	1
1	A	29	LEU	1
1	A	144	PHE	1
1	A	98	THR	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 monosaccharides 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