



Full wwPDB NMR Structure Validation Report ⓘ

Mar 5, 2026 – 11:46 AM UTC

PDB ID : 1NGR / pdb_00001ngr
Title : DEATH DOMAIN OF P75 LOW AFFINITY NEUROTROPHIN RECEPTOR, RESIDUES 334-418, NMR, 20 STRUCTURES
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Deposited on : 1997-01-28

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We welcome your comments at validation@mail.wwpdb.org

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<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
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

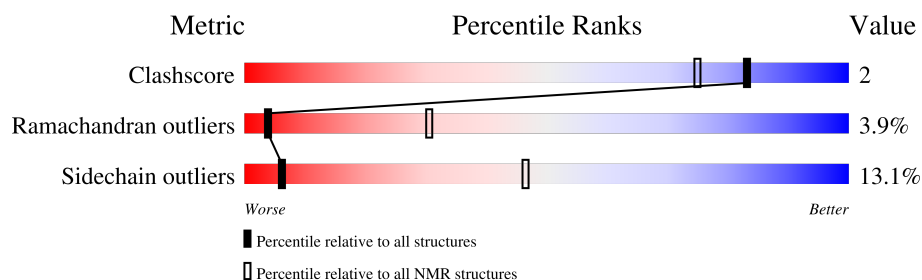
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment 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	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	85	69% 21% 9%

2 Ensemble composition and analysis

This entry contains 20 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:336-A:340, A:344-A:415 (77)	0.63	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 5 clusters. No single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 1314 atoms, of which 651 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called P75 LOW AFFINITY NEUROTROPHIN RECEPTOR.

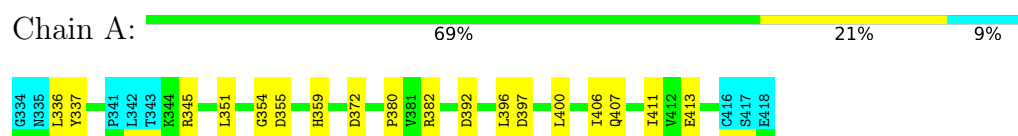
Mol	Chain	Residues	Atoms							Trace
1	A	85	Total	C	H	N	O	S		0
			1314	413	651	118	130	2		

4 Residue-property plots

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: P75 LOW AFFINITY NEUROTROPHIN RECEPTOR

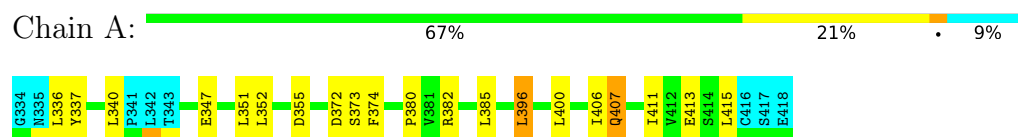


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

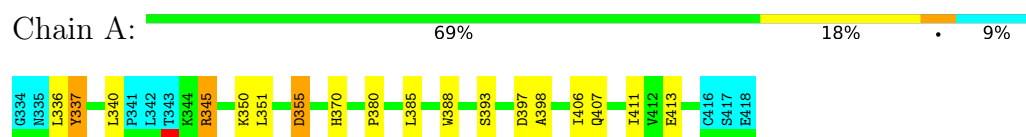
4.2.1 Score per residue for model 1 (medoid)

- Molecule 1: P75 LOW AFFINITY NEUROTROPHIN RECEPTOR



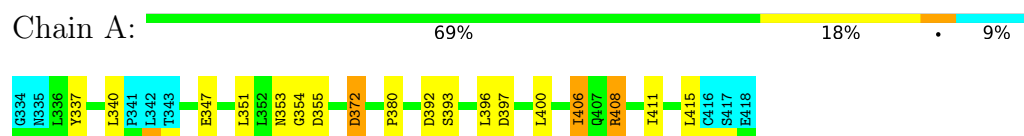
4.2.2 Score per residue for model 2

- Molecule 1: P75 LOW AFFINITY NEUROTROPHIN RECEPTOR



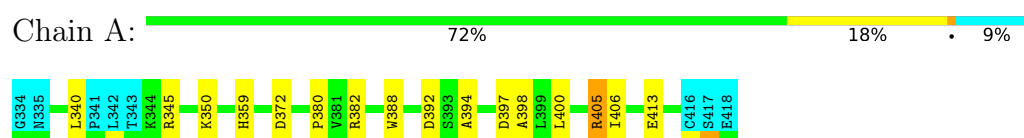
4.2.3 Score per residue for model 3

- Molecule 1: P75 LOW AFFINITY NEUROTROPHIN RECEPTOR



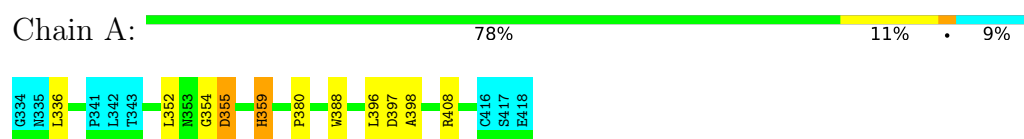
4.2.4 Score per residue for model 4

- Molecule 1: P75 LOW AFFINITY NEUROTROPHIN RECEPTOR



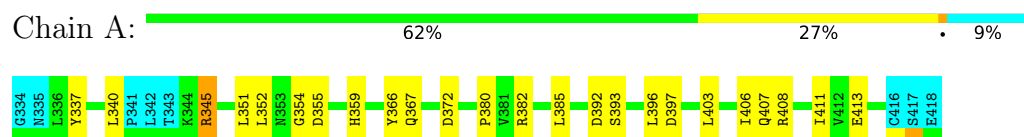
4.2.5 Score per residue for model 5

- Molecule 1: P75 LOW AFFINITY NEUROTROPHIN RECEPTOR



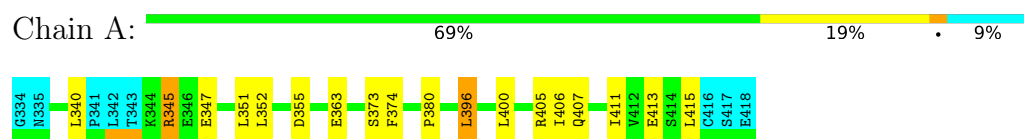
4.2.6 Score per residue for model 6

- Molecule 1: P75 LOW AFFINITY NEUROTROPHIN RECEPTOR



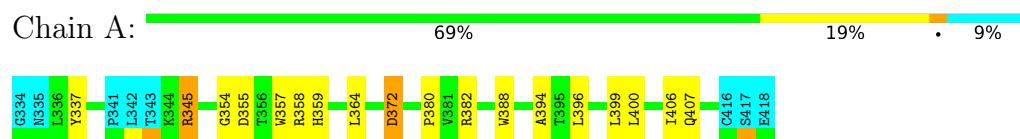
4.2.7 Score per residue for model 7

- Molecule 1: P75 LOW AFFINITY NEUROTROPHIN RECEPTOR



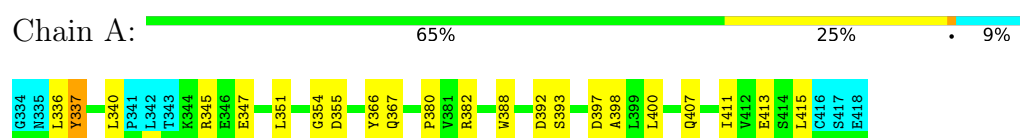
4.2.8 Score per residue for model 8

- Molecule 1: P75 LOW AFFINITY NEUROTROPHIN RECEPTOR



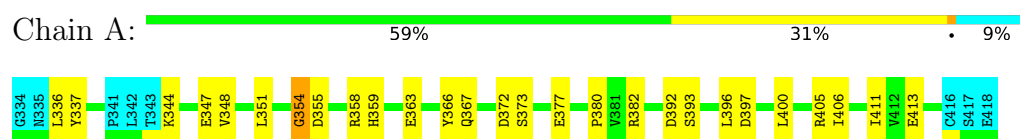
4.2.9 Score per residue for model 9

- Molecule 1: P75 LOW AFFINITY NEUROTROPHIN RECEPTOR



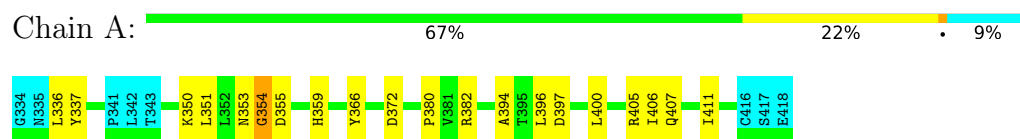
4.2.10 Score per residue for model 10

- Molecule 1: P75 LOW AFFINITY NEUROTROPHIN RECEPTOR



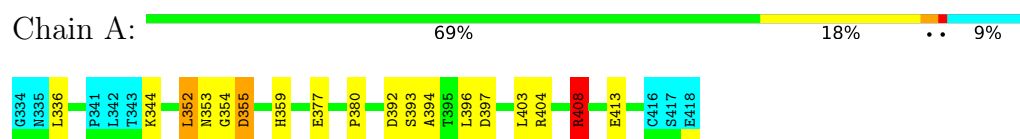
4.2.11 Score per residue for model 11

- Molecule 1: P75 LOW AFFINITY NEUROTROPHIN RECEPTOR



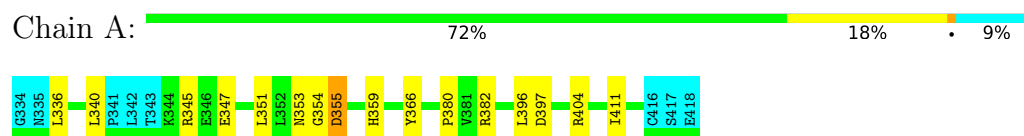
4.2.12 Score per residue for model 12

- Molecule 1: P75 LOW AFFINITY NEUROTROPHIN RECEPTOR



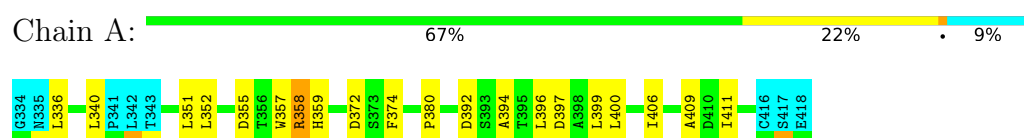
4.2.13 Score per residue for model 13

- Molecule 1: P75 LOW AFFINITY NEUROTROPHIN RECEPTOR



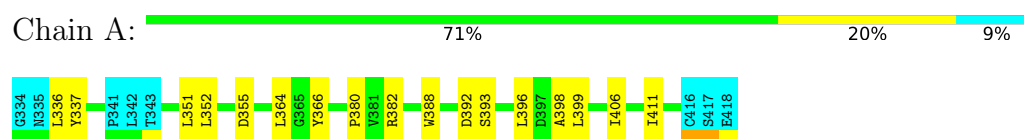
4.2.14 Score per residue for model 14

- Molecule 1: P75 LOW AFFINITY NEUROTROPHIN RECEPTOR



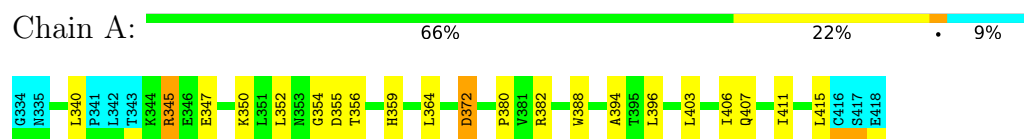
4.2.15 Score per residue for model 15

- Molecule 1: P75 LOW AFFINITY NEUROTROPHIN RECEPTOR



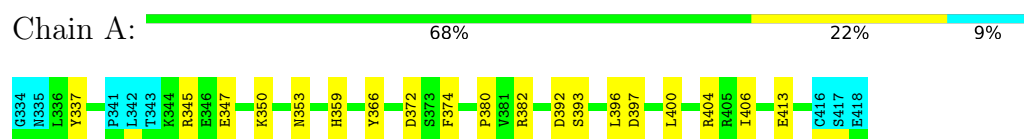
4.2.16 Score per residue for model 16

- Molecule 1: P75 LOW AFFINITY NEUROTROPHIN RECEPTOR



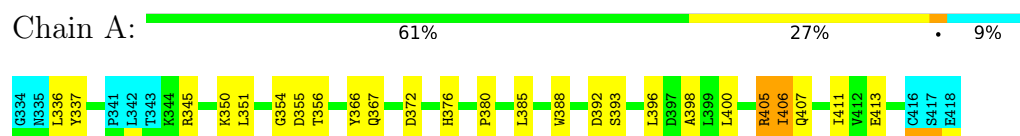
4.2.17 Score per residue for model 17

- Molecule 1: P75 LOW AFFINITY NEUROTROPHIN RECEPTOR



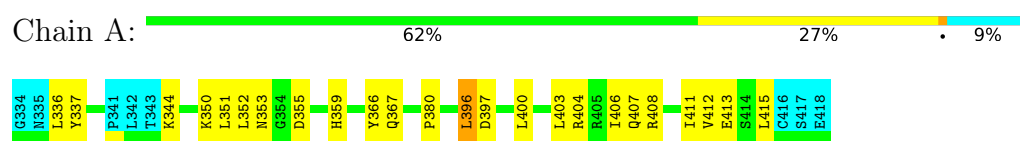
4.2.18 Score per residue for model 18

- Molecule 1: P75 LOW AFFINITY NEUROTROPHIN RECEPTOR



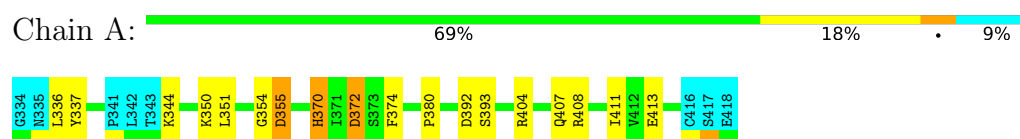
4.2.19 Score per residue for model 19

- Molecule 1: P75 LOW AFFINITY NEUROTROPHIN RECEPTOR



4.2.20 Score per residue for model 20

- Molecule 1: P75 LOW AFFINITY NEUROTROPHIN RECEPTOR



5 Refinement protocol and experimental data overview

The models were refined using the following method: *VARIABLE TARGET FUNCTION (DIANA) APPROACH*.

Of the 50 calculated structures, 20 were deposited, based on the following criterion: *LOWEST TARGET FUNCTION AFTER DIANA*.

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

Software name	Classification	Version
OPAL	refinement	
EASY	structure solution	
HABAS	structure solution	
DIANA	structure solution	
OPAL	structure solution	

No chemical shift data was provided.

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	0.72±0.01	0±0/619 (0.0± 0.0%)	1.56±0.04	5±3/842 (0.6± 0.3%)
All	All	0.72	0/12380 (0.0%)	1.56	100/16840 (0.6%)

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	0.1±0.2	1.9±1.0
All	All	1	39

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	413	GLU	CB-CA-C	9.19	127.62	110.63	2	6
1	A	359	HIS	CA-CB-CG	8.00	121.80	113.80	5	6
1	A	345	ARG	CD-NE-CZ	7.60	135.04	124.40	2	1
1	A	359	HIS	CB-CG-CD2	-7.36	121.64	131.20	5	12
1	A	406	ILE	CA-CB-CG1	6.49	121.43	110.40	18	2
1	A	374	PHE	CA-CB-CG	6.16	119.96	113.80	1	5
1	A	392	ASP	CA-C-N	6.07	133.13	121.54	18	9
1	A	392	ASP	C-N-CA	6.07	133.13	121.54	18	9
1	A	355	ASP	CA-CB-CG	-6.04	106.56	112.60	13	5
1	A	345	ARG	CA-CB-CG	5.78	125.65	114.10	8	1
1	A	354	GLY	CA-C-N	5.67	132.36	121.54	12	10
1	A	354	GLY	C-N-CA	5.67	132.36	121.54	12	10
1	A	352	LEU	CA-C-N	5.66	129.75	121.31	12	4
1	A	352	LEU	C-N-CA	5.66	129.75	121.31	12	4
1	A	372	ASP	CA-CB-CG	-5.57	107.03	112.60	16	4

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	359	HIS	CA-C-N	5.29	127.37	120.28	6	1
1	A	359	HIS	C-N-CA	5.29	127.37	120.28	6	1
1	A	404	ARG	CA-C-N	5.28	127.67	120.54	20	2
1	A	404	ARG	C-N-CA	5.28	127.67	120.54	20	2
1	A	408	ARG	CB-CG-CD	5.20	123.26	111.30	12	1
1	A	409	ALA	CA-C-N	5.19	127.55	120.54	14	1
1	A	409	ALA	C-N-CA	5.19	127.55	120.54	14	1
1	A	359	HIS	CB-CG-ND1	5.12	130.39	122.70	5	1
1	A	413	GLU	N-CA-C	5.12	117.59	111.71	10	1
1	A	370	HIS	CB-CG-CD2	-5.10	124.57	131.20	20	1

All unique chiral outliers are listed below.

Mol	Chain	Res	Type	Atoms	Models (Total)
1	A	413	GLU	CA	1

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	366	TYR	Sidechain	9
1	A	382	ARG	Sidechain	8
1	A	337	TYR	Sidechain	6
1	A	405	ARG	Sidechain	5
1	A	408	ARG	Sidechain	4
1	A	345	ARG	Sidechain	4
1	A	373	SER	Mainchain	2
1	A	404	ARG	Sidechain	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	607	599	599	3±2
All	All	12140	11980	11980	57

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:351:LEU:HB3	1:A:411:ILE:HG23	0.71	1.62	9	14
1:A:364:LEU:HD22	1:A:388:TRP:CZ2	0.52	2.39	15	3
1:A:396:LEU:HD11	1:A:415:LEU:HD22	0.52	1.82	1	3
1:A:337:TYR:OH	1:A:415:LEU:HD21	0.51	2.05	19	4
1:A:351:LEU:CB	1:A:411:ILE:HG23	0.50	2.37	3	1
1:A:364:LEU:HD21	1:A:399:LEU:HA	0.49	1.84	15	1
1:A:352:LEU:HD21	1:A:403:LEU:HD11	0.48	1.84	16	2
1:A:356:THR:HG21	1:A:411:ILE:HD12	0.48	1.85	18	2
1:A:352:LEU:HD23	1:A:411:ILE:HD13	0.46	1.88	16	1
1:A:388:TRP:CH2	1:A:394:ALA:HA	0.46	2.45	16	2
1:A:388:TRP:HH2	1:A:398:ALA:HB3	0.46	1.71	4	6
1:A:337:TYR:CE2	1:A:385:LEU:HD13	0.44	2.47	2	1
1:A:356:THR:HG21	1:A:411:ILE:CD1	0.44	2.42	18	1
1:A:337:TYR:CD1	1:A:385:LEU:HD22	0.43	2.47	1	1
1:A:337:TYR:CE1	1:A:385:LEU:HD22	0.43	2.49	18	2
1:A:400:LEU:HG	1:A:412:VAL:HG13	0.43	1.89	19	1
1:A:337:TYR:OH	1:A:348:VAL:HG21	0.42	2.14	10	1
1:A:344:LYS:O	1:A:348:VAL:HG23	0.42	2.14	10	1
1:A:347:GLU:CD	1:A:350:LYS:HZ1	0.42	2.22	16	1
1:A:337:TYR:CD2	1:A:399:LEU:HD22	0.41	2.50	8	1
1:A:352:LEU:CD2	1:A:403:LEU:HD21	0.41	2.45	12	2
1:A:364:LEU:HD22	1:A:388:TRP:CE2	0.41	2.50	15	1
1:A:352:LEU:HD11	1:A:399:LEU:HD21	0.41	1.90	14	1
1:A:352:LEU:HD23	1:A:411:ILE:CD1	0.41	2.46	16	1
1:A:357:TRP:CG	1:A:358:ARG:N	0.40	2.89	8	2
1:A:352:LEU:CD2	1:A:411:ILE:HG21	0.40	2.46	15	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	77/85 (91%)	62±2 (81±2%)	12±2 (15±2%)	3±1 (4±1%)	4	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1540/1700 (91%)	1247 (81%)	233 (15%)	60 (4%)	4	30

All 8 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	380	PRO	20
1	A	355	ASP	18
1	A	393	SER	10
1	A	394	ALA	4
1	A	354	GLY	4
1	A	392	ASP	2
1	A	407	GLN	1
1	A	377	GLU	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	63/70 (90%)	55±2 (87±4%)	8±2 (13±4%)	6	46
All	All	1260/1400 (90%)	1095 (87%)	165 (13%)	6	46

All 27 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	396	LEU	16
1	A	406	ILE	15
1	A	336	LEU	13
1	A	397	ASP	13
1	A	372	ASP	12
1	A	400	LEU	11
1	A	407	GLN	11
1	A	340	LEU	10
1	A	345	ARG	9
1	A	347	GLU	7
1	A	350	LYS	7

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Mol	Chain	Res	Type	Models (Total)
1	A	413	GLU	6
1	A	353	ASN	6
1	A	367	GLN	5
1	A	408	ARG	4
1	A	382	ARG	3
1	A	370	HIS	2
1	A	405	ARG	2
1	A	363	GLU	2
1	A	358	ARG	2
1	A	404	ARG	2
1	A	344	LYS	2
1	A	359	HIS	1
1	A	373	SER	1
1	A	377	GLU	1
1	A	415	LEU	1
1	A	376	HIS	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

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided