



Full wwPDB NMR Structure Validation Report ⓘ

Mar 8, 2026 – 11:46 AM UTC

PDB ID : 1OPI / pdb_00001opi
Title : SOLUTION STRUCTURE OF THE THIRD RNA RECOGNITION MOTIF (RRM) OF U2AF65 IN COMPLEX WITH AN N-TERMINAL SF1 PEPTIDE
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Deposited on : 2003-03-05

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

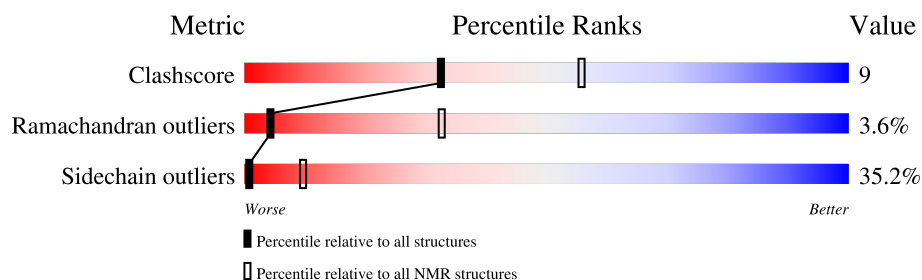
1 Overall quality at a glance

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	104	54% 39% 7%
2	B	13	8% 8% 85%

2 Ensemble composition and analysis

This entry contains 10 models. Model 3 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:374-A:424, A:428-A:473, B:22-B:23 (99)	0.65	3

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. No single-model clusters were found.

Cluster number	Models
1	2, 3, 5, 7, 8, 9, 10
2	1, 4, 6

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1889 atoms, of which 933 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called SPLICING FACTOR U2AF 65 KDA SUBUNIT.

Mol	Chain	Residues	Atoms						Trace
1	A	104	Total	C	H	N	O	S	0
			1647	529	810	137	163	8	

- Molecule 2 is a protein called SPLICING FACTOR SF1.

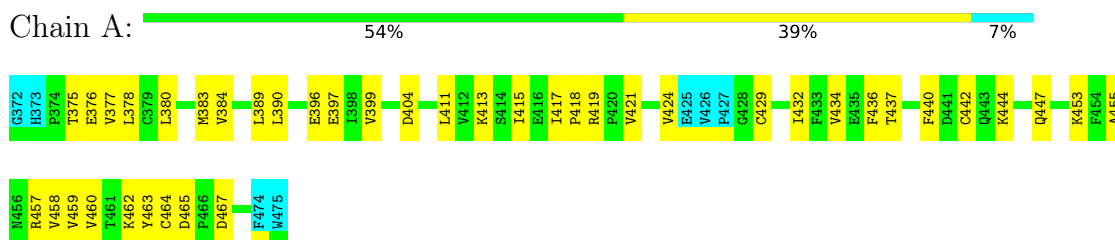
Mol	Chain	Residues	Atoms					Trace
2	B	13	Total	C	H	N	O	0
			242	71	123	28	20	

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: SPLICING FACTOR U2AF 65 KDA SUBUNIT



- Molecule 2: SPLICING FACTOR SF1

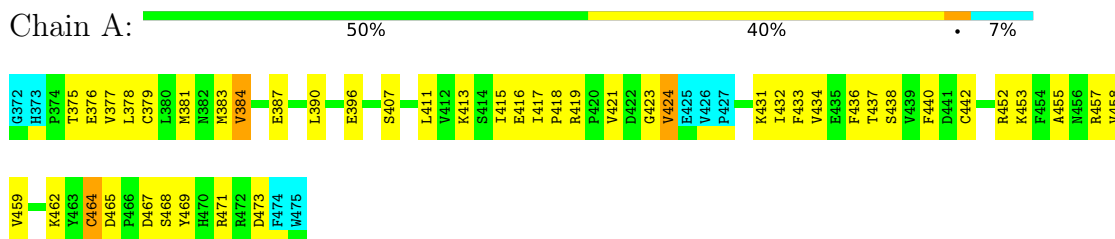


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: SPLICING FACTOR U2AF 65 KDA SUBUNIT

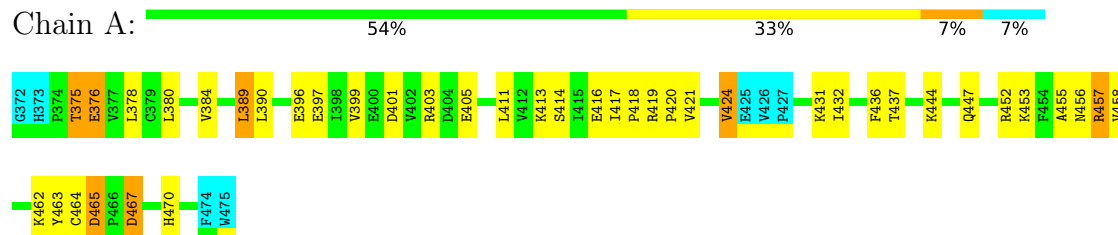


- Molecule 2: SPLICING FACTOR SF1



4.2.2 Score per residue for model 2

- Molecule 1: SPLICING FACTOR U2AF 65 KDA SUBUNIT

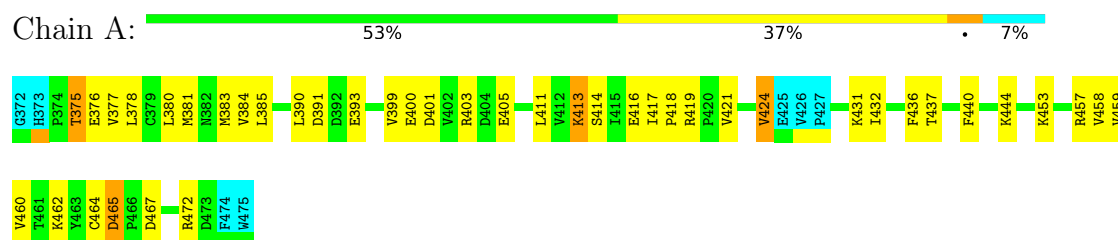


- Molecule 2: SPLICING FACTOR SF1



4.2.3 Score per residue for model 3 (medoid)

- Molecule 1: SPLICING FACTOR U2AF 65 KDA SUBUNIT



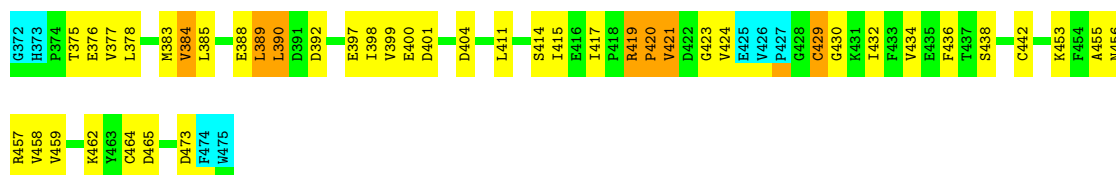
- Molecule 2: SPLICING FACTOR SF1



4.2.4 Score per residue for model 4

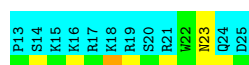
- Molecule 1: SPLICING FACTOR U2AF 65 KDA SUBUNIT





- Molecule 2: SPLICING FACTOR SF1

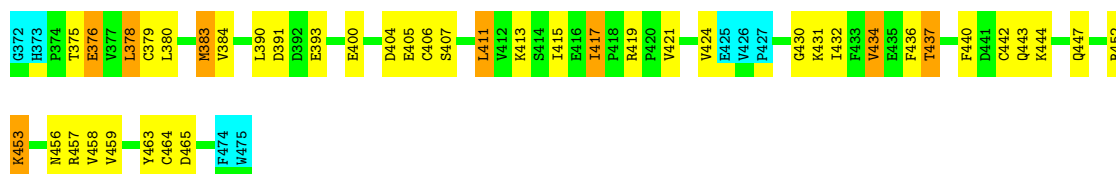
Chain B: 8% 8% 85%



4.2.5 Score per residue for model 5

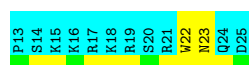
- Molecule 1: SPLICING FACTOR U2AF 65 KDA SUBUNIT

Chain A: 53% 33% 8% 7%



- Molecule 2: SPLICING FACTOR SF1

Chain B: 15% 85%



4.2.6 Score per residue for model 6

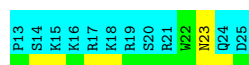
- Molecule 1: SPLICING FACTOR U2AF 65 KDA SUBUNIT

Chain A: 50% 37% 7% 7%



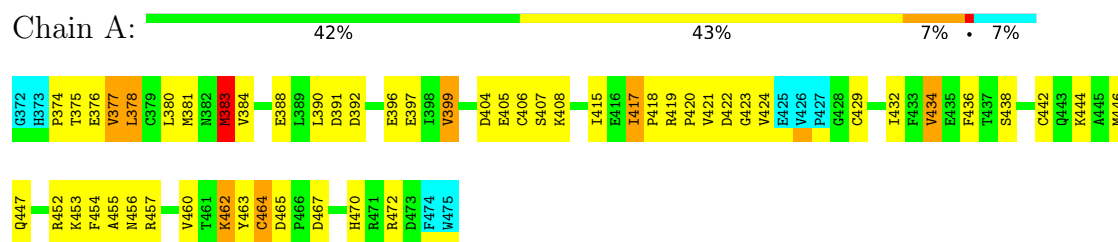
- Molecule 2: SPLICING FACTOR SF1

Chain B: 8% 8% 85%



4.2.7 Score per residue for model 7

- Molecule 1: SPLICING FACTOR U2AF 65 KDA SUBUNIT

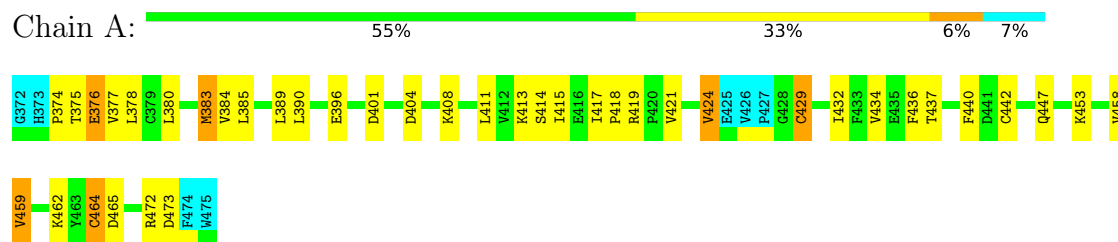


- Molecule 2: SPLICING FACTOR SF1



4.2.8 Score per residue for model 8

- Molecule 1: SPLICING FACTOR U2AF 65 KDA SUBUNIT

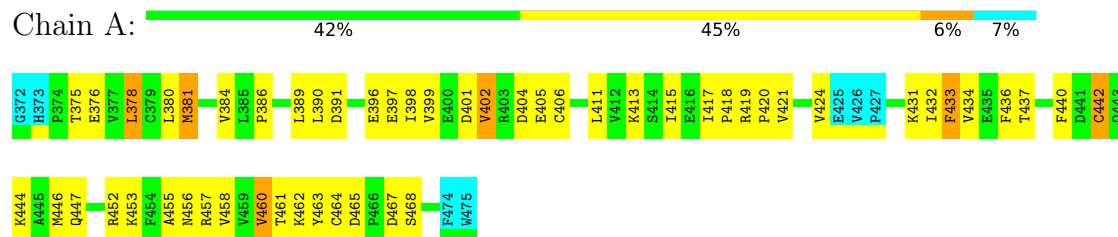


- Molecule 2: SPLICING FACTOR SF1



4.2.9 Score per residue for model 9

- Molecule 1: SPLICING FACTOR U2AF 65 KDA SUBUNIT



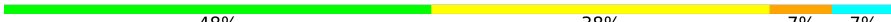
- Molecule 2: SPLICING FACTOR SF1

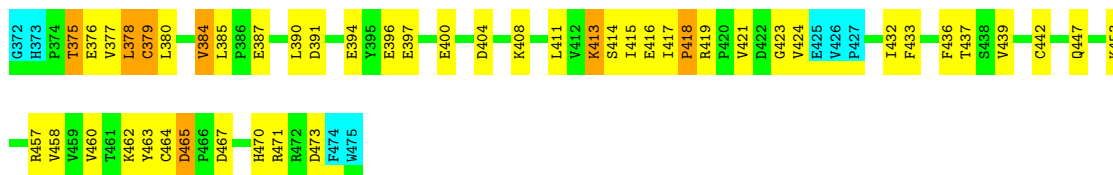
Chain B:  15% 85%



4.2.10 Score per residue for model 10

- Molecule 1: SPLICING FACTOR U2AF 65 KDA SUBUNIT

Chain A:  48% 38% 7% 7%



- Molecule 2: SPLICING FACTOR SF1

Chain B:  8% 8% 85%



5 Refinement protocol and experimental data overview

The models were refined using the following method: *RESTRAINED MOLECULAR DYNAMICS USING CNS AND ARIA FOR AMBIGUOUS DISTANCE RESTRAINTS*.

Of the 100 calculated structures, 10 were deposited, based on the following criterion: *STRUCTURES WITH THE LEAST RESTRAINT VIOLATIONS, 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
ARIA	refinement	1.2

No chemical shift data was provided.

6 Model quality

6.1 Standard geometry

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

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	774	758	757	13±3
2	B	22	16	16	0±0
All	All	7960	7740	7730	134

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 9.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:417:ILE:HG23	1:A:432:ILE:HG21	1.01	1.31	9	7
1:A:417:ILE:HG23	1:A:432:ILE:CG2	0.69	2.17	3	7
1:A:421:VAL:O	1:A:424:VAL:HG23	0.65	1.92	6	6
1:A:418:PRO:HD2	1:A:432:ILE:HG22	0.65	1.68	8	6
1:A:399:VAL:HG22	1:A:417:ILE:HD12	0.64	1.70	6	5
1:A:417:ILE:HG12	1:A:432:ILE:HG23	0.62	1.71	6	2
1:A:413:LYS:HG3	1:A:437:THR:HG22	0.59	1.74	10	6
1:A:399:VAL:HB	1:A:417:ILE:HD11	0.58	1.75	7	1
1:A:415:ILE:HG23	1:A:434:VAL:HG12	0.57	1.75	5	6
1:A:378:LEU:HD12	1:A:442:CYS:SG	0.56	2.40	5	4
1:A:455:ALA:HB3	1:A:457:ARG:NH1	0.55	2.17	2	1
1:A:377:VAL:HG22	1:A:464:CYS:O	0.54	2.01	4	4
1:A:384:VAL:HG21	1:A:432:ILE:HG23	0.54	1.78	4	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:375:THR:O	1:A:439:VAL:HG12	0.54	2.04	10	1
1:A:389:LEU:HD12	1:A:429:CYS:SG	0.53	2.44	8	2
1:A:402:VAL:HG12	1:A:415:ILE:HD12	0.52	1.82	9	1
1:A:375:THR:C	1:A:439:VAL:HG12	0.52	2.30	10	1
1:A:421:VAL:HB	1:A:424:VAL:HB	0.52	1.81	4	6
1:A:417:ILE:HG23	1:A:432:ILE:HG23	0.51	1.83	7	1
1:A:417:ILE:HG22	1:A:418:PRO:HD2	0.50	1.83	7	1
1:A:384:VAL:HG12	1:A:398:ILE:HD13	0.50	1.82	4	1
1:A:386:PRO:O	1:A:390:LEU:HD13	0.50	2.05	9	1
1:A:383:MET:HG3	1:A:459:VAL:HG13	0.49	1.84	6	1
1:A:375:THR:OG1	1:A:376:GLU:N	0.49	2.44	10	1
1:A:383:MET:HB3	1:A:459:VAL:HG13	0.48	1.84	3	2
1:A:375:THR:OG1	1:A:465:ASP:HA	0.47	2.10	10	4
1:A:415:ILE:HD13	1:A:434:VAL:HG22	0.46	1.87	9	1
1:A:384:VAL:HG11	1:A:432:ILE:HD13	0.46	1.88	8	2
1:A:390:LEU:HD11	1:A:420:PRO:HB2	0.46	1.88	9	1
1:A:417:ILE:HG12	1:A:432:ILE:HB	0.46	1.88	1	2
1:A:405:GLU:HG3	2:B:22:TRP:HE1	0.45	1.72	2	1
1:A:417:ILE:CD1	1:A:432:ILE:HD12	0.45	2.41	1	5
1:A:390:LEU:HD21	1:A:423:GLY:N	0.45	2.26	4	2
1:A:415:ILE:HG22	1:A:417:ILE:HG13	0.45	1.89	10	2
1:A:384:VAL:CG1	1:A:432:ILE:HD11	0.45	2.40	6	1
1:A:383:MET:HB2	1:A:454:PHE:HB2	0.45	1.89	7	1
1:A:379:CYS:HA	1:A:433:PHE:HB3	0.44	1.88	10	2
1:A:433:PHE:CD1	1:A:433:PHE:N	0.44	2.85	9	1
1:A:421:VAL:H	1:A:424:VAL:HB	0.44	1.71	8	4
1:A:417:ILE:HG12	1:A:432:ILE:HD12	0.44	1.90	3	4
1:A:415:ILE:CD1	1:A:434:VAL:HG22	0.43	2.44	9	1
1:A:421:VAL:C	1:A:423:GLY:N	0.43	2.74	6	4
1:A:415:ILE:HG23	1:A:433:PHE:O	0.43	2.13	10	1
1:A:419:ARG:O	1:A:420:PRO:C	0.43	2.62	4	1
1:A:381:MET:HE2	1:A:462:LYS:HG2	0.43	1.90	7	1
1:A:383:MET:HB3	1:A:459:VAL:HG12	0.43	1.91	5	1
1:A:389:LEU:HD23	1:A:389:LEU:N	0.42	2.27	4	2
1:A:411:LEU:HB3	1:A:437:THR:HG21	0.42	1.91	5	1
1:A:417:ILE:HG23	1:A:432:ILE:HG12	0.42	1.91	6	1
1:A:378:LEU:HD11	1:A:446:MET:HB3	0.42	1.91	7	1
1:A:375:THR:HG21	1:A:464:CYS:C	0.42	2.39	10	1
1:A:384:VAL:HG23	1:A:430:GLY:O	0.42	2.14	4	1
1:A:398:ILE:O	1:A:402:VAL:HB	0.42	2.15	9	1
1:A:377:VAL:HG23	1:A:464:CYS:HB3	0.42	1.92	6	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:384:VAL:CG1	1:A:389:LEU:HD21	0.42	2.45	6	1
1:A:469:TYR:CD1	1:A:469:TYR:C	0.41	2.98	1	1
1:A:421:VAL:N	1:A:424:VAL:HB	0.41	2.31	1	1
1:A:452:ARG:O	1:A:453:LYS:C	0.41	2.63	5	1
1:A:380:LEU:HD23	1:A:461:THR:HG22	0.41	1.93	9	1
1:A:381:MET:HB2	1:A:460:VAL:HG13	0.40	1.93	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	97/104 (93%)	83±3 (86±4%)	11±2 (11±3%)	3±1 (3±1%)	5	35
2	B	2/13 (15%)	0±0 (25±25%)	1±1 (55±42%)	0±0 (20±24%)	0	2
All	All	990/1170 (85%)	835 (84%)	119 (12%)	36 (4%)	4	32

All 13 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	376	GLU	9
1	A	455	ALA	5
2	B	22	TRP	4
1	A	383	MET	3
1	A	467	ASP	3
1	A	452	ARG	2
1	A	421	VAL	2
1	A	456	ASN	2
1	A	374	PRO	2
1	A	420	PRO	1
1	A	430	GLY	1
1	A	458	VAL	1
1	A	418	PRO	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	89/95 (94%)	58±3 (65±3%)	31±3 (35±3%)	1 9
2	B	2/13 (15%)	1±0 (70±24%)	1±0 (30±24%)	1 17
All	All	910/1080 (84%)	590 (65%)	320 (35%)	1 10

All 70 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	375	THR	10
1	A	378	LEU	10
1	A	419	ARG	10
1	A	436	PHE	10
1	A	453	LYS	10
1	A	465	ASP	10
1	A	390	LEU	9
1	A	411	LEU	9
1	A	457	ARG	9
1	A	384	VAL	8
1	A	458	VAL	8
1	A	462	LYS	8
1	A	464	CYS	7
1	A	380	LEU	7
1	A	404	ASP	7
1	A	396	GLU	6
1	A	440	PHE	6
2	B	23	ASN	6
1	A	397	GLU	6
1	A	444	LYS	6
1	A	447	GLN	6
1	A	463	TYR	6
1	A	416	GLU	5
1	A	431	LYS	5
1	A	467	ASP	5
1	A	473	ASP	5
1	A	401	ASP	5
1	A	414	SER	5

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Mol	Chain	Res	Type	Models (Total)
1	A	391	ASP	5
1	A	400	GLU	5
1	A	460	VAL	5
1	A	424	VAL	4
1	A	438	SER	4
1	A	442	CYS	4
1	A	376	GLU	4
1	A	385	LEU	4
1	A	405	GLU	4
1	A	472	ARG	4
1	A	429	CYS	4
1	A	381	MET	3
1	A	407	SER	3
1	A	459	VAL	3
1	A	471	ARG	3
1	A	389	LEU	3
1	A	456	ASN	3
1	A	470	HIS	3
1	A	377	VAL	3
1	A	413	LYS	3
1	A	383	MET	3
1	A	392	ASP	3
1	A	406	CYS	3
1	A	434	VAL	3
1	A	408	LYS	3
1	A	387	GLU	2
1	A	468	SER	2
1	A	403	ARG	2
1	A	452	ARG	2
1	A	393	GLU	2
1	A	388	GLU	2
1	A	379	CYS	2
1	A	417	ILE	2
1	A	394	GLU	2
1	A	422	ASP	2
1	A	437	THR	1
1	A	443	GLN	1
1	A	409	TYR	1
1	A	399	VAL	1
1	A	402	VAL	1
1	A	433	PHE	1
1	A	446	MET	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

No chemical shift data were provided