



wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 1P9D / pdb_00001p9d
Title : High-resolution structure of the complex of HHR23A ubiquitin-like domain and the C-terminal ubiquitin-interacting motif of proteasome subunit S5a
Authors : Mueller, T.D.; Feigon, J.
Deposited on : 2003-05-10

This is a wwPDB NMR Structure Validation Summary 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

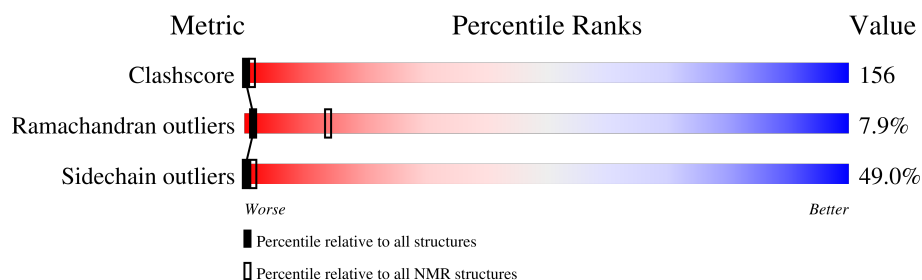
1 Overall quality at a glance

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	S	45	
2	U	78	

2 Ensemble composition and analysis

This entry contains 10 models. Model 8 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	S:284-S:295, U:2-U:76 (87)	0.48	8

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	1, 3, 4, 5, 6, 8, 9, 10
2	2, 7

3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 1764 atoms, of which 895 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called 26S proteasome non-ATPase regulatory subunit 4.

Mol	Chain	Residues	Atoms						Trace
1	S	32	Total	C	H	N	O	S	0
			468	150	226	38	51	3	

- Molecule 2 is a protein called UV excision repair protein RAD23 homolog A.

Mol	Chain	Residues	Atoms						Trace
2	U	78	Total	C	H	N	O	S	0
			1296	402	669	105	117	3	

I61	R62	D63	Y64	R65	I66	D67	E68	K69	N70	F71	V72	V73	V74	M75	V76	T77	K78
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5 Refinement protocol and experimental data overview ⓘ

The models were refined using the following method: *simulated annealing*.

Of the 30 calculated structures, 10 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
X-PLOR	structure solution	3.1
X-PLOR	refinement	3.1

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	S	96	92	92	42±5
2	U	602	638	638	205±14
All	All	6980	7300	7300	2234

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 156.

5 of 760 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:U:7:LEU:HD12	2:U:72:VAL:HG12	1.05	1.05	6	4
2:U:48:LEU:HD23	2:U:72:VAL:HG11	1.02	1.29	6	3
2:U:19:MET:HE1	2:U:61:ILE:HG21	0.99	1.32	1	2
2:U:25:VAL:HG13	2:U:59:VAL:O	0.99	1.58	7	10
2:U:5:ILE:HD13	2:U:7:LEU:HD11	0.97	1.32	6	3

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	S	12/45 (27%)	11±1 (92±6%)	1±1 (8±6%)	0±0 (0±0%)	100	100
2	U	75/78 (96%)	57±2 (76±2%)	11±2 (15±2%)	7±2 (9±2%)	1	11
All	All	870/1230 (71%)	681 (78%)	120 (14%)	69 (8%)	1	14

5 of 14 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
2	U	25	VAL	10
2	U	43	VAL	10
2	U	23	GLU	8
2	U	10	LEU	7
2	U	12	GLN	7

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	S	10/36 (28%)	6±1 (57±11%)	4±1 (43±11%)	0	3
2	U	67/70 (96%)	34±1 (50±2%)	33±1 (50±2%)	0	1
All	All	770/1060 (73%)	393 (51%)	377 (49%)	0	1

5 of 61 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	S	291	MET	10
1	S	293	MET	10
2	U	5	ILE	10
2	U	7	LEU	10
2	U	24	THR	10

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