



Full wwPDB NMR Structure Validation Report ⓘ

Mar 5, 2026 – 06:42 PM UTC

PDB ID : 1HN6 / pdb_00001hn6
Title : SOLUTION STRUCTURE OF PLASMODIUM FALCIPARUM APICAL
MEMBRANE ANTIGEN 1 (RESIDUES 436-545)
Authors : Nair, M.
Deposited on : 2000-12-07

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

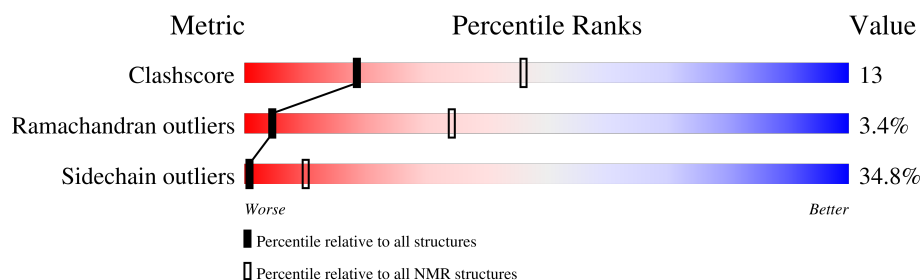
1 Overall quality at a glance

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	110	

2 Ensemble composition and analysis

This entry contains 20 models. Model 18 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *closest to the average*.

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:441-A:450, A:481-A:509 (39)	0.95	18
2	A:513-A:525 (13)	2.69	9
3	A:526-A:534 (9)	1.54	10

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 3 clusters. No single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 1772 atoms, of which 871 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called APICAL MEMBRANE ANTIGEN 1.

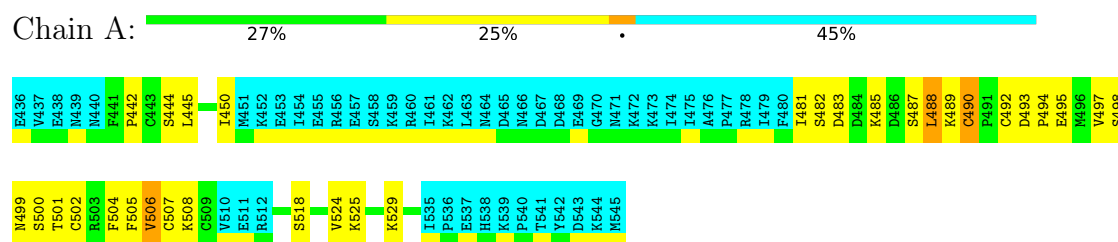
Mol	Chain	Residues	Atoms						Trace
1	A	110	Total	C	H	N	O	S	0
			1772	556	871	151	185	9	

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: APICAL MEMBRANE ANTIGEN 1

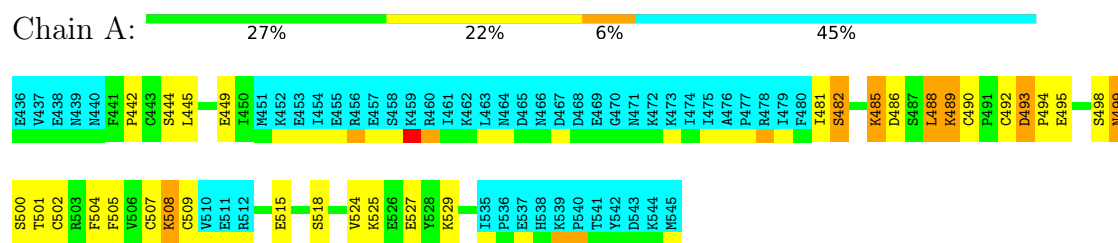


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: APICAL MEMBRANE ANTIGEN 1



4.2.2 Score per residue for model 2

• Molecule 1: APICAL MEMBRANE ANTIGEN 1

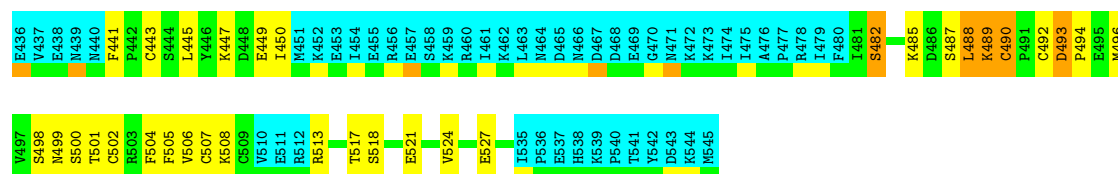




4.2.3 Score per residue for model 3

- Molecule 1: APICAL MEMBRANE ANTIGEN 1

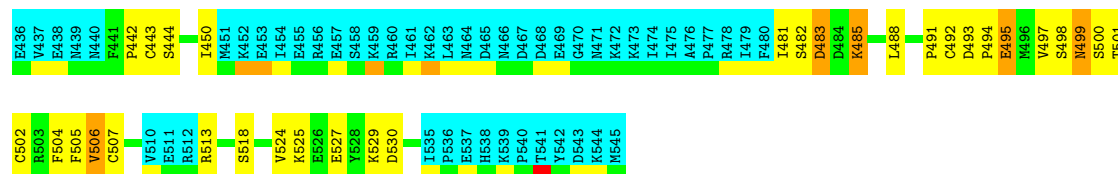
Chain A: 26% 25% 5% 45%



4.2.4 Score per residue for model 4

- Molecule 1: APICAL MEMBRANE ANTIGEN 1

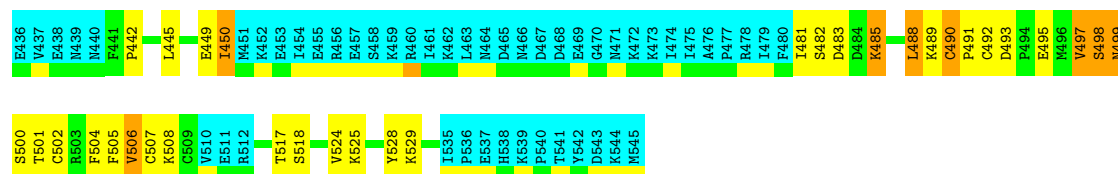
Chain A: 27% 24% 5% 45%



4.2.5 Score per residue for model 5

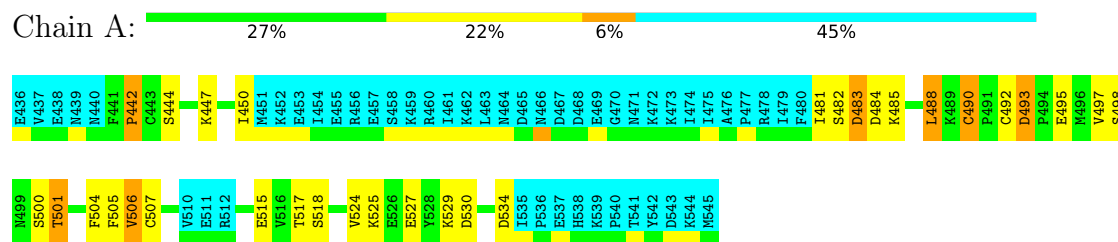
- Molecule 1: APICAL MEMBRANE ANTIGEN 1

Chain A: 26% 22% 7% 45%



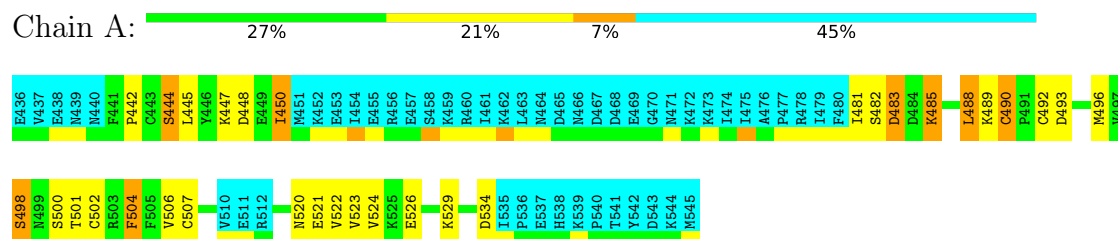
4.2.6 Score per residue for model 6

- Molecule 1: APICAL MEMBRANE ANTIGEN 1



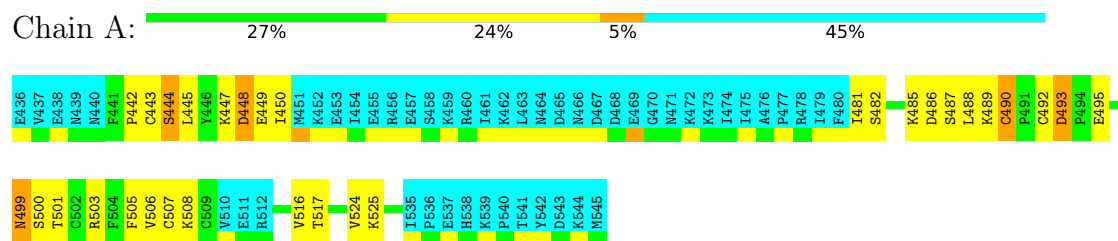
4.2.7 Score per residue for model 7

- Molecule 1: APICAL MEMBRANE ANTIGEN 1



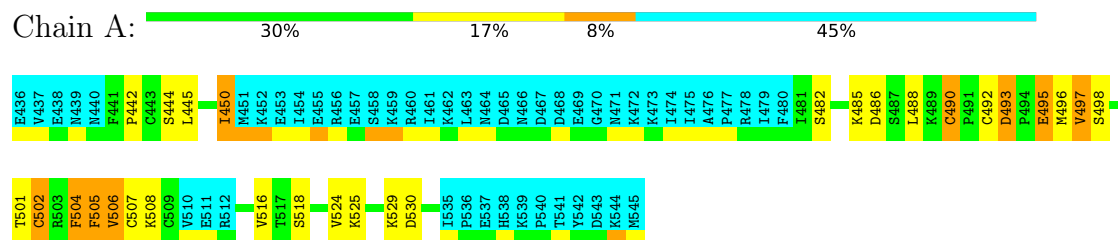
4.2.8 Score per residue for model 8

- Molecule 1: APICAL MEMBRANE ANTIGEN 1



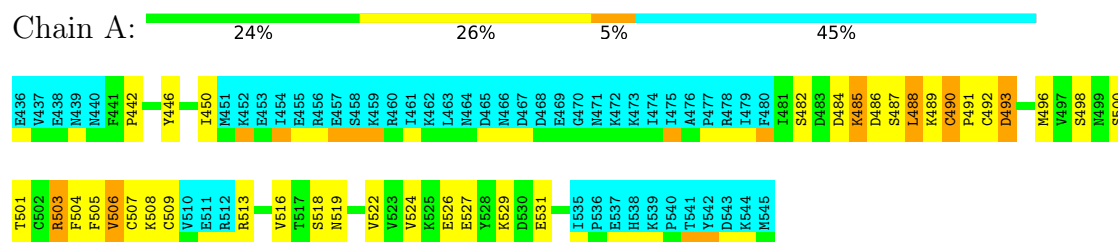
4.2.9 Score per residue for model 9

- Molecule 1: APICAL MEMBRANE ANTIGEN 1



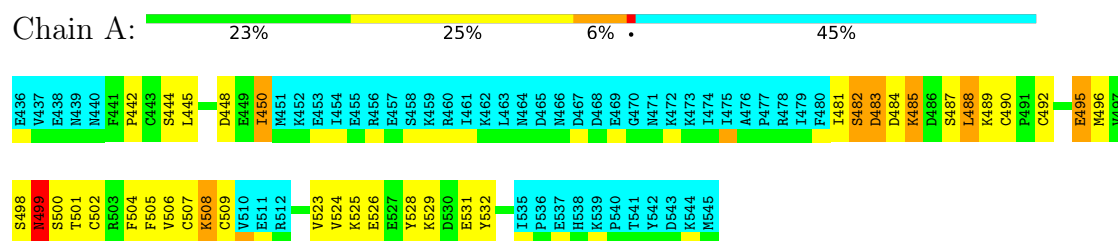
4.2.10 Score per residue for model 10

• Molecule 1: APICAL MEMBRANE ANTIGEN 1



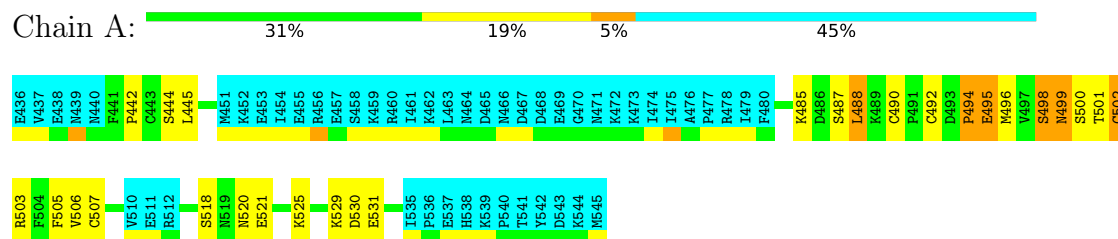
4.2.11 Score per residue for model 11

• Molecule 1: APICAL MEMBRANE ANTIGEN 1



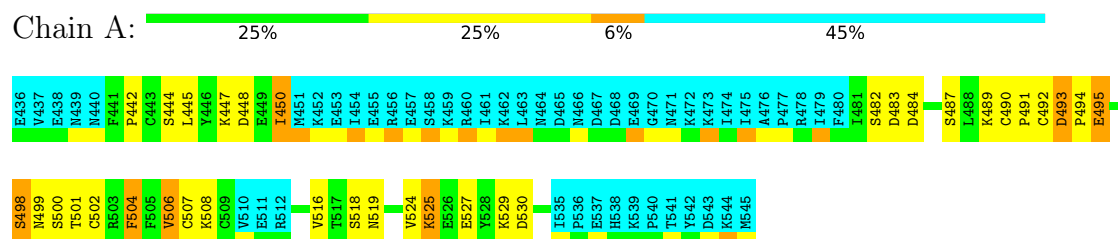
4.2.12 Score per residue for model 12

• Molecule 1: APICAL MEMBRANE ANTIGEN 1



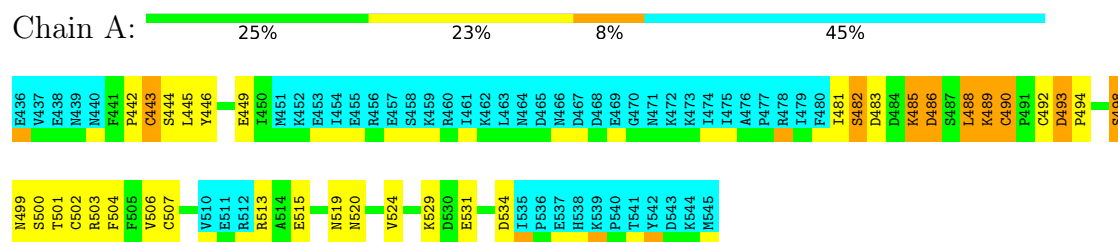
4.2.13 Score per residue for model 13

• Molecule 1: APICAL MEMBRANE ANTIGEN 1



4.2.14 Score per residue for model 14

- Molecule 1: APICAL MEMBRANE ANTIGEN 1



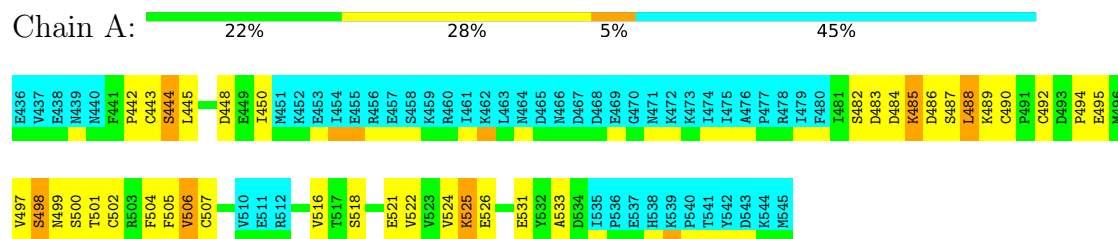
4.2.15 Score per residue for model 15

- Molecule 1: APICAL MEMBRANE ANTIGEN 1



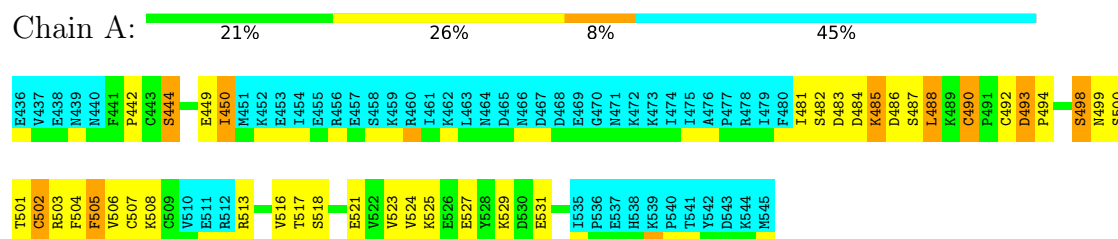
4.2.16 Score per residue for model 16

- Molecule 1: APICAL MEMBRANE ANTIGEN 1



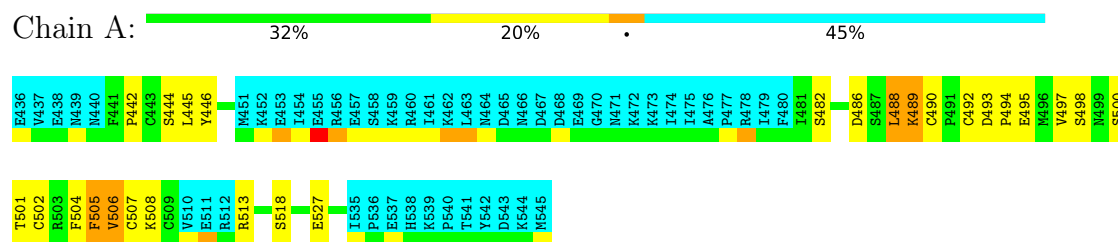
4.2.17 Score per residue for model 17

- Molecule 1: APICAL MEMBRANE ANTIGEN 1



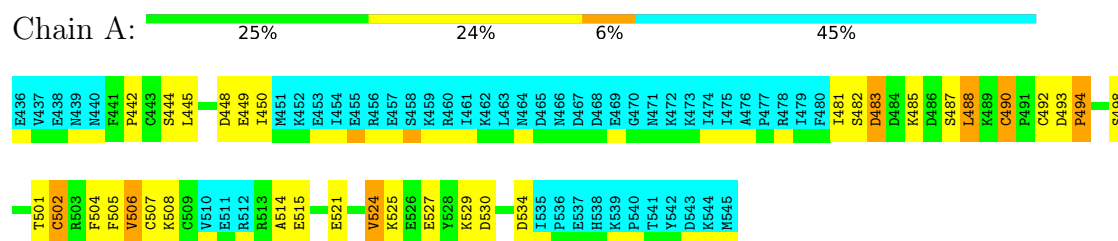
4.2.18 Score per residue for model 18 (medoid)

• Molecule 1: APICAL MEMBRANE ANTIGEN 1



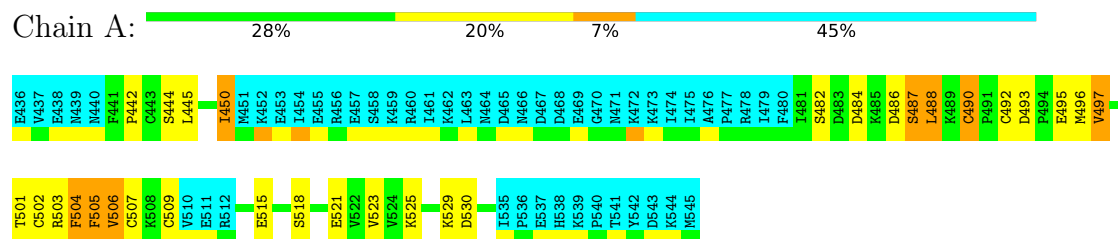
4.2.19 Score per residue for model 19

• Molecule 1: APICAL MEMBRANE ANTIGEN 1



4.2.20 Score per residue for model 20

• Molecule 1: APICAL MEMBRANE ANTIGEN 1



5 Refinement protocol and experimental data overview

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

Of the 256 calculated structures, 20 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
DYANA	structure solution	1.5
CNS	refinement	1.0

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	487	452	452	12±2
All	All	9740	9040	9040	245

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 13.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:497:VAL:HG22	1:A:506:VAL:HG22	1.09	1.21	20	3
1:A:482:SER:HB3	1:A:504:PHE:HA	0.90	1.43	18	2
1:A:442:PRO:HB2	1:A:445:LEU:HB2	0.86	1.48	8	11
1:A:488:LEU:HB3	1:A:506:VAL:HA	0.77	1.57	19	6
1:A:494:PRO:HA	1:A:505:PHE:HB2	0.76	1.56	19	1
1:A:497:VAL:HG23	1:A:506:VAL:HG21	0.76	1.57	4	5
1:A:495:GLU:O	1:A:505:PHE:HA	0.75	1.81	16	11
1:A:492:CYS:SG	1:A:494:PRO:HG3	0.74	2.23	12	1
1:A:450:ILE:HG12	1:A:485:LYS:HB3	0.73	1.59	3	1
1:A:482:SER:HB3	1:A:504:PHE:HB3	0.71	1.61	17	3
1:A:445:LEU:HB3	1:A:450:ILE:HD13	0.68	1.66	8	1
1:A:485:LYS:HE3	1:A:488:LEU:HD21	0.67	1.66	4	1
1:A:442:PRO:HB3	1:A:445:LEU:HD12	0.67	1.66	11	4
1:A:490:CYS:O	1:A:507:CYS:HB2	0.66	1.90	8	13

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:497:VAL:CG2	1:A:506:VAL:HG22	0.66	2.09	5	1
1:A:485:LYS:HE2	1:A:488:LEU:HD11	0.65	1.68	7	1
1:A:482:SER:HB3	1:A:505:PHE:H	0.65	1.50	1	2
1:A:485:LYS:HA	1:A:488:LEU:HD21	0.64	1.68	8	4
1:A:450:ILE:HD11	1:A:485:LYS:HD2	0.64	1.68	6	2
1:A:494:PRO:HA	1:A:505:PHE:HB3	0.64	1.70	3	1
1:A:493:ASP:HB2	1:A:509:CYS:HB3	0.62	1.71	1	3
1:A:492:CYS:O	1:A:507:CYS:HA	0.62	1.94	5	10
1:A:494:PRO:HG2	1:A:507:CYS:HA	0.61	1.73	12	1
1:A:482:SER:HB3	1:A:504:PHE:HB2	0.61	1.72	4	2
1:A:488:LEU:H	1:A:488:LEU:HD23	0.61	1.55	4	3
1:A:442:PRO:HG2	1:A:446:TYR:HB2	0.60	1.73	2	2
1:A:442:PRO:HA	1:A:483:ASP:OD1	0.59	1.97	7	4
1:A:498:SER:HA	1:A:502:CYS:O	0.59	1.97	3	12
1:A:482:SER:HB2	1:A:505:PHE:HB2	0.58	1.75	8	1
1:A:495:GLU:HB3	1:A:506:VAL:HB	0.58	1.76	9	7
1:A:444:SER:HA	1:A:447:LYS:HB3	0.58	1.73	8	1
1:A:488:LEU:HD12	1:A:490:CYS:O	0.58	1.98	8	1
1:A:492:CYS:SG	1:A:507:CYS:SG	0.56	3.03	14	19
1:A:488:LEU:HD22	1:A:506:VAL:HG13	0.56	1.77	5	1
1:A:496:MET:SD	1:A:498:SER:HB2	0.56	2.41	9	1
1:A:499:ASN:HD21	1:A:502:CYS:HB2	0.56	1.59	11	2
1:A:485:LYS:HE2	1:A:491:PRO:HB3	0.56	1.77	2	1
1:A:492:CYS:SG	1:A:493:ASP:N	0.55	2.79	8	3
1:A:495:GLU:HG2	1:A:508:LYS:HD3	0.55	1.77	15	3
1:A:496:MET:HA	1:A:504:PHE:O	0.54	2.02	11	2
1:A:488:LEU:HD13	1:A:506:VAL:HA	0.54	1.78	4	2
1:A:484:ASP:O	1:A:488:LEU:HD21	0.54	2.01	17	3
1:A:485:LYS:NZ	1:A:491:PRO:HA	0.53	2.18	4	2
1:A:494:PRO:HA	1:A:505:PHE:HD1	0.53	1.64	17	1
1:A:486:ASP:O	1:A:489:LYS:HG2	0.52	2.02	14	3
1:A:488:LEU:CD1	1:A:506:VAL:HA	0.52	2.35	4	1
1:A:503:ARG:HD2	1:A:505:PHE:HE1	0.52	1.64	10	1
1:A:442:PRO:HB3	1:A:445:LEU:HB2	0.52	1.79	5	2
1:A:496:MET:HG3	1:A:503:ARG:HG3	0.52	1.82	15	2
1:A:495:GLU:HB3	1:A:506:VAL:CB	0.52	2.34	5	3
1:A:496:MET:SD	1:A:503:ARG:HG3	0.52	2.44	10	1
1:A:506:VAL:HG12	1:A:507:CYS:H	0.52	1.65	13	1
1:A:442:PRO:O	1:A:446:TYR:HB2	0.51	2.06	10	2
1:A:483:ASP:HB2	1:A:502:CYS:HB3	0.51	1.81	16	1
1:A:484:ASP:OD1	1:A:487:SER:HB2	0.50	2.07	20	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:483:ASP:N	1:A:504:PHE:HB3	0.50	2.22	14	3
1:A:444:SER:HB2	1:A:484:ASP:HA	0.49	1.84	16	3
1:A:494:PRO:HA	1:A:505:PHE:CD1	0.49	2.42	17	1
1:A:502:CYS:HB2	1:A:504:PHE:CE1	0.49	2.43	1	1
1:A:488:LEU:O	1:A:489:LYS:HG2	0.48	2.08	3	1
1:A:442:PRO:CB	1:A:445:LEU:HB2	0.48	2.37	9	4
1:A:482:SER:HB3	1:A:504:PHE:CB	0.48	2.39	4	2
1:A:524:VAL:HG11	1:A:527:GLU:HB2	0.48	1.85	19	2
1:A:488:LEU:HD22	1:A:504:PHE:CE1	0.48	2.43	4	1
1:A:483:ASP:CG	1:A:502:CYS:HB3	0.47	2.34	19	1
1:A:488:LEU:HD22	1:A:505:PHE:O	0.47	2.09	10	3
1:A:444:SER:HB2	1:A:483:ASP:O	0.47	2.10	7	1
1:A:443:CYS:SG	1:A:483:ASP:HB3	0.47	2.49	14	1
1:A:524:VAL:HB	1:A:527:GLU:HB2	0.47	1.87	6	1
1:A:485:LYS:HG3	1:A:488:LEU:HD11	0.46	1.86	16	1
1:A:499:ASN:HD21	1:A:504:PHE:HE2	0.46	1.52	2	2
1:A:531:GLU:HG3	1:A:532:TYR:H	0.46	1.71	11	1
1:A:495:GLU:CB	1:A:508:LYS:HB2	0.45	2.41	13	1
1:A:483:ASP:HB3	1:A:504:PHE:HB3	0.45	1.89	13	1
1:A:450:ILE:HD11	1:A:485:LYS:HE3	0.45	1.88	17	1
1:A:488:LEU:HB3	1:A:506:VAL:HG13	0.45	1.88	7	1
1:A:485:LYS:HA	1:A:485:LYS:HE3	0.44	1.89	5	1
1:A:482:SER:HB3	1:A:504:PHE:CA	0.44	2.31	18	1
1:A:497:VAL:HB	1:A:504:PHE:CD2	0.43	2.48	9	1
1:A:494:PRO:HG2	1:A:506:VAL:O	0.43	2.13	12	1
1:A:495:GLU:HB3	1:A:508:LYS:HB2	0.43	1.88	13	1
1:A:497:VAL:HG23	1:A:504:PHE:O	0.43	2.13	9	2
1:A:483:ASP:H	1:A:504:PHE:HB3	0.43	1.74	14	1
1:A:484:ASP:CG	1:A:487:SER:HB2	0.43	2.39	20	2
1:A:443:CYS:O	1:A:447:LYS:HB2	0.43	2.13	15	1
1:A:490:CYS:SG	1:A:492:CYS:HB3	0.43	2.54	19	1
1:A:504:PHE:CE1	1:A:506:VAL:HG22	0.43	2.49	16	2
1:A:485:LYS:HE3	1:A:488:LEU:HD11	0.42	1.90	1	2
1:A:442:PRO:HA	1:A:483:ASP:CB	0.42	2.44	4	1
1:A:483:ASP:HB3	1:A:504:PHE:HD2	0.42	1.74	13	1
1:A:484:ASP:HB3	1:A:504:PHE:CD1	0.42	2.50	10	1
1:A:442:PRO:HA	1:A:483:ASP:CG	0.42	2.39	17	1
1:A:450:ILE:HD11	1:A:485:LYS:HB3	0.41	1.91	19	1
1:A:504:PHE:CE2	1:A:506:VAL:HG22	0.41	2.50	7	1
1:A:445:LEU:HD23	1:A:482:SER:O	0.41	2.16	3	1
1:A:493:ASP:HA	1:A:494:PRO:HD3	0.41	1.78	1	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:494:PRO:HG2	1:A:507:CYS:CA	0.41	2.44	12	1
1:A:525:LYS:HB3	1:A:525:LYS:HE3	0.41	1.55	2	1
1:A:484:ASP:H	1:A:504:PHE:CB	0.41	2.29	13	1
1:A:504:PHE:HD1	1:A:506:VAL:CG2	0.40	2.30	13	1
1:A:450:ILE:HD11	1:A:485:LYS:CB	0.40	2.46	19	1
1:A:488:LEU:C	1:A:490:CYS:H	0.40	2.24	20	1
1:A:497:VAL:HB	1:A:504:PHE:HB2	0.40	1.92	6	1
1:A:495:GLU:HB3	1:A:506:VAL:CG2	0.40	2.45	9	1
1:A:482:SER:HB3	1:A:505:PHE:N	0.40	2.30	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	61/110 (55%)	47±3 (77±5%)	12±3 (20±5%)	2±1 (3±2%)	4	34
All	All	1220/2200 (55%)	936 (77%)	242 (20%)	42 (3%)	4	34

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	499	ASN	9
1	A	493	ASP	8
1	A	494	PRO	8
1	A	513	ARG	4
1	A	448	ASP	3
1	A	508	LYS	2
1	A	525	LYS	2
1	A	442	PRO	1
1	A	501	THR	1
1	A	519	ASN	1
1	A	521	GLU	1
1	A	533	ALA	1
1	A	514	ALA	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	59/106 (56%)	38±3 (65±6%)	21±3 (35±6%)	1	10
All	All	1180/2120 (56%)	769 (65%)	411 (35%)	1	10

All 49 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	501	THR	20
1	A	490	CYS	18
1	A	488	LEU	17
1	A	500	SER	17
1	A	444	SER	15
1	A	524	VAL	15
1	A	525	LYS	15
1	A	529	LYS	15
1	A	506	VAL	15
1	A	518	SER	14
1	A	498	SER	13
1	A	482	SER	12
1	A	489	LYS	12
1	A	487	SER	12
1	A	493	ASP	12
1	A	481	ILE	11
1	A	485	LYS	11
1	A	508	LYS	11
1	A	450	ILE	10
1	A	449	GLU	8
1	A	499	ASN	8
1	A	516	VAL	8
1	A	530	ASP	8
1	A	483	ASP	7
1	A	502	CYS	7
1	A	486	ASP	7
1	A	515	GLU	6
1	A	527	GLU	6
1	A	443	CYS	6

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Mol	Chain	Res	Type	Models (Total)
1	A	531	GLU	6
1	A	521	GLU	6
1	A	517	THR	5
1	A	495	GLU	5
1	A	504	PHE	5
1	A	503	ARG	5
1	A	447	LYS	4
1	A	534	ASP	4
1	A	448	ASP	4
1	A	523	VAL	4
1	A	526	GLU	4
1	A	505	PHE	4
1	A	497	VAL	3
1	A	520	ASN	3
1	A	522	VAL	3
1	A	441	PHE	2
1	A	513	ARG	2
1	A	528	TYR	2
1	A	496	MET	2
1	A	519	ASN	2

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.6 Ligand geometry ⓘ

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