



Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 04:15 PM BST

PDB ID : 1PQS
Title : Solution structure of the C-terminal OPCA domain of yCdc24p
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Deposited on : 2003-06-19

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
<http://wwpdb.org/validation/2016/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:

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20027457
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

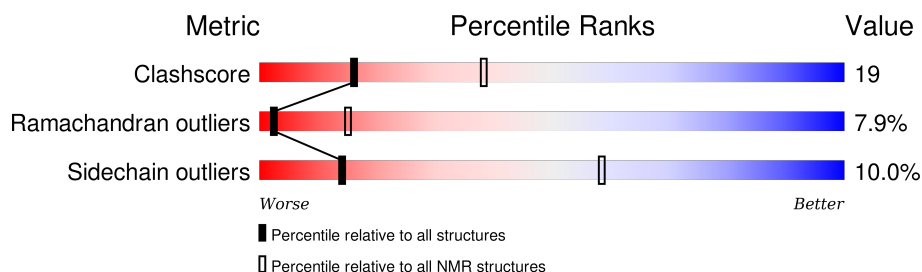
1 Overall quality at a glance

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	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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	77	<div> <div style="width: 47%; background-color: green;"></div> <div style="width: 38%; background-color: yellow;"></div> <div style="width: 13%; background-color: cyan;"></div> <div style="width: 5%; background-color: orange;"></div> <div style="width: 1%; background-color: red;"></div> <div style="width: 1%; background-color: grey;"></div> </div> <div> <div style="width: 47%; text-align: center;">47%</div> <div style="width: 38%; text-align: center;">38%</div> <div style="width: 13%; text-align: center;">• 13%</div> </div>

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:779-A:802, A:812-A:854 (67)	0.39	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 3 clusters. No single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 1247 atoms, of which 615 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Cell division control protein 24.

Mol	Chain	Residues	Atoms						Trace
1	A	77	Total	C	H	N	O	S	0
			1247	402	615	101	127	2	

4 Residue-property plots [i](#)

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA 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: Cell division control protein 24

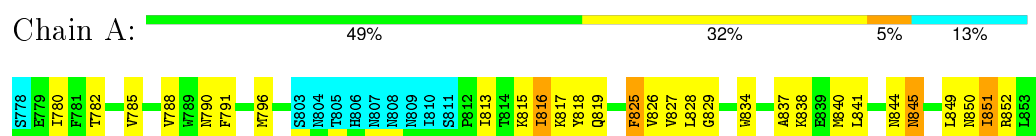


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

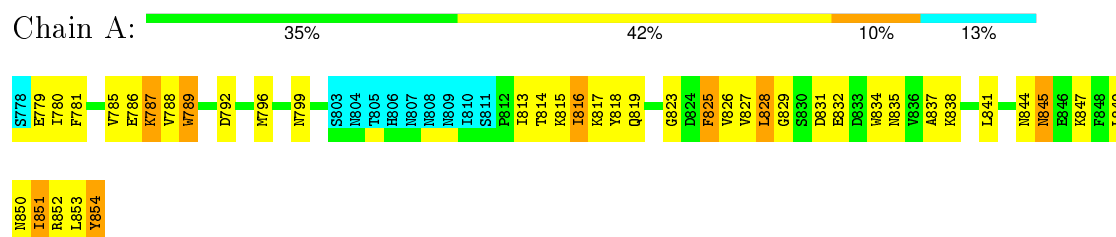
4.2.1 Score per residue for model 1 (medoid)

- Molecule 1: Cell division control protein 24



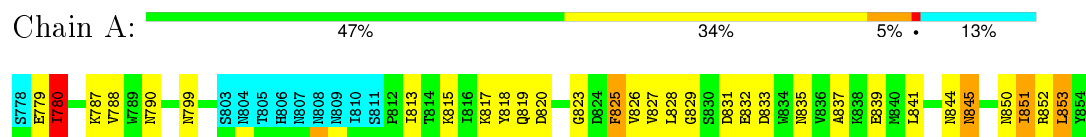
4.2.2 Score per residue for model 2

- Molecule 1: Cell division control protein 24



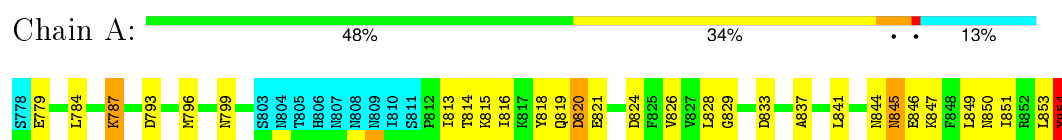
4.2.3 Score per residue for model 3

- Molecule 1: Cell division control protein 24



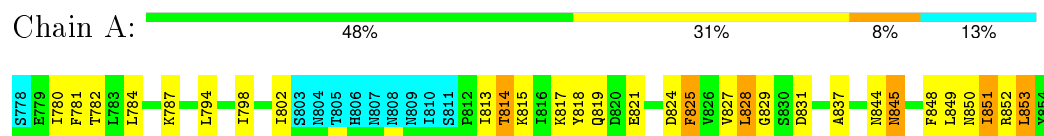
4.2.4 Score per residue for model 4

- Molecule 1: Cell division control protein 24



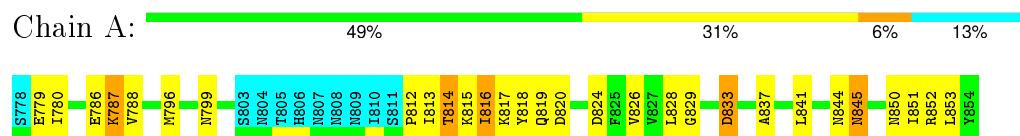
4.2.5 Score per residue for model 5

- Molecule 1: Cell division control protein 24



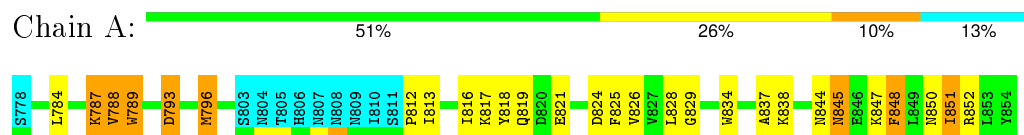
4.2.6 Score per residue for model 6

- Molecule 1: Cell division control protein 24



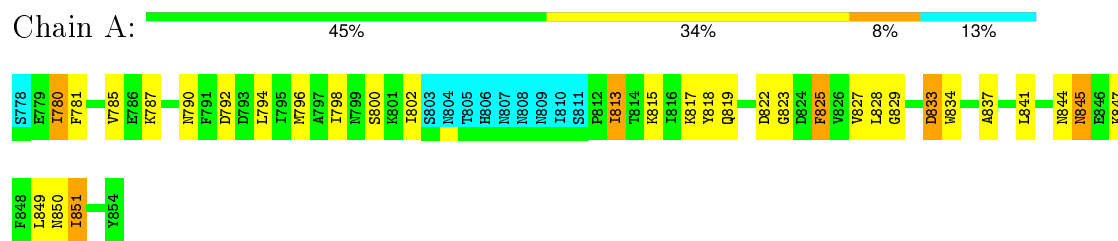
4.2.7 Score per residue for model 7

- Molecule 1: Cell division control protein 24



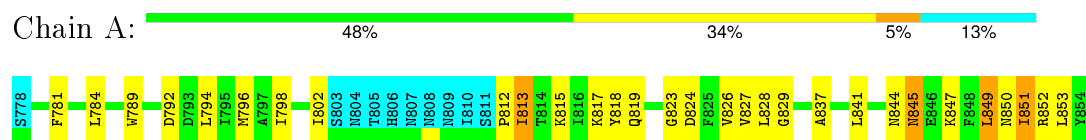
4.2.8 Score per residue for model 8

- Molecule 1: Cell division control protein 24



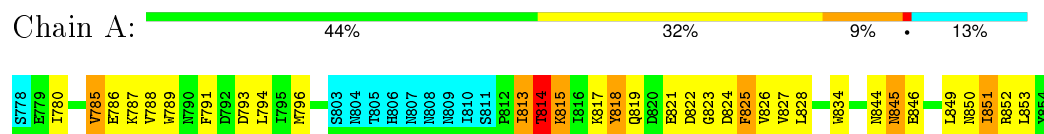
4.2.9 Score per residue for model 9

- Molecule 1: Cell division control protein 24



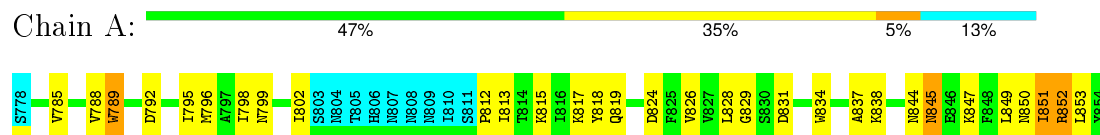
4.2.10 Score per residue for model 10

- Molecule 1: Cell division control protein 24



4.2.11 Score per residue for model 11

- Molecule 1: Cell division control protein 24



4.2.12 Score per residue for model 12

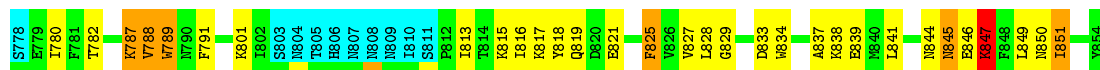
- Molecule 1: Cell division control protein 24





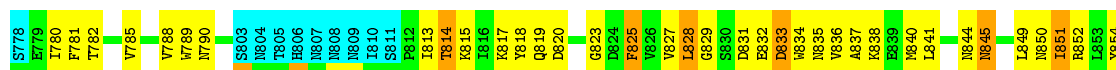
4.2.13 Score per residue for model 13

- Molecule 1: Cell division control protein 24



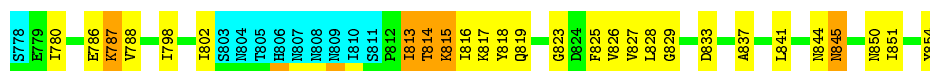
4.2.14 Score per residue for model 14

- Molecule 1: Cell division control protein 24



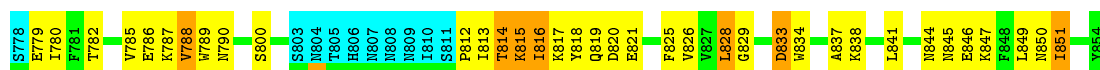
4.2.15 Score per residue for model 15

- Molecule 1: Cell division control protein 24



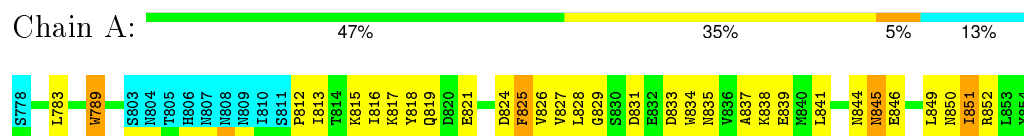
4.2.16 Score per residue for model 16

- Molecule 1: Cell division control protein 24



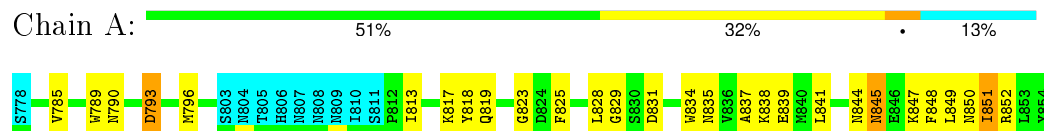
4.2.17 Score per residue for model 17

- Molecule 1: Cell division control protein 24



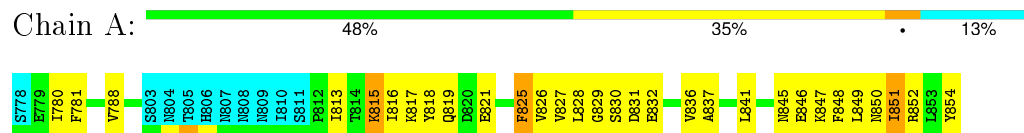
4.2.18 Score per residue for model 18

- Molecule 1: Cell division control protein 24



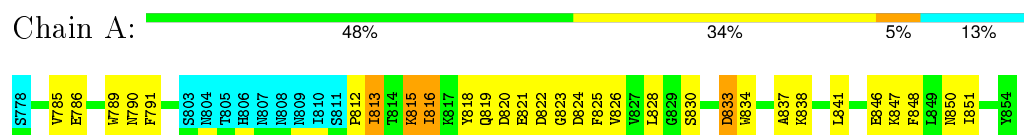
4.2.19 Score per residue for model 19

- Molecule 1: Cell division control protein 24



4.2.20 Score per residue for model 20

- Molecule 1: Cell division control protein 24



5 Refinement protocol and experimental data overview ⓘ

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

Of the 200 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
ARIA/CNS	structure solution	1.2
ARIA/CNS	refinement	1.2

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.

6 Model quality

6.1 Standard geometry

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	0.43±0.07	0±1/567 (0.0±0.1%)	0.49±0.03	0±0/764 (0.0±0.0%)
All	All	0.44	4/11340 (0.0%)	0.49	0/15280 (0.0%)

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	0.0±0.0	0.1±0.4
All	All	0	2

All unique bond 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(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	854	TYR	CE2-CZ	-7.15	1.29	1.38	4	1
1	A	854	TYR	CE1-CZ	6.73	1.47	1.38	4	1
1	A	848	PHE	CE2-CZ	5.83	1.48	1.37	7	2

There are no bond-angle outliers.

There are no chirality outliers.

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	818	TYR	Sidechain	1
1	A	825	PHE	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	557	548	548	21±4
All	All	11140	10960	10960	414

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 19.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:819:GLN:HB3	1:A:850:ASN:HB2	0.98	1.35	17	20
1:A:817:LYS:HB2	1:A:852:ARG:HB3	0.90	1.44	14	4
1:A:841:LEU:HG	1:A:847:LYS:HA	0.86	1.44	9	1
1:A:788:VAL:HG23	1:A:838:LYS:HD2	0.85	1.46	16	1
1:A:817:LYS:HB3	1:A:852:ARG:HB3	0.82	1.50	6	7
1:A:783:LEU:HD11	1:A:789:TRP:HZ3	0.81	1.35	17	1
1:A:841:LEU:HA	1:A:846:GLU:HG2	0.79	1.52	4	1
1:A:819:GLN:HB2	1:A:825:PHE:CD1	0.78	2.13	5	4
1:A:817:LYS:HG2	1:A:827:VAL:HG22	0.78	1.53	14	2
1:A:819:GLN:HB2	1:A:825:PHE:HD1	0.76	1.40	5	1
1:A:821:GLU:HG2	1:A:846:GLU:HG2	0.75	1.56	20	2
1:A:819:GLN:HE21	1:A:822:ASP:HA	0.73	1.43	10	2
1:A:817:LYS:HG3	1:A:827:VAL:HB	0.72	1.61	1	4
1:A:848:PHE:HE2	1:A:850:ASN:HD21	0.71	1.27	18	1
1:A:785:VAL:HG23	1:A:789:TRP:CE3	0.71	2.20	12	1
1:A:819:GLN:HG2	1:A:850:ASN:HD22	0.71	1.46	1	5
1:A:817:LYS:HG2	1:A:827:VAL:HB	0.69	1.62	2	4
1:A:788:VAL:HG22	1:A:838:LYS:HD2	0.69	1.64	7	1
1:A:813:ILE:HG22	1:A:815:LYS:HE2	0.69	1.63	20	1
1:A:783:LEU:HD11	1:A:789:TRP:CZ3	0.68	2.23	17	1
1:A:817:LYS:HE3	1:A:825:PHE:HB3	0.68	1.64	10	1
1:A:821:GLU:HB3	1:A:846:GLU:HB3	0.67	1.67	16	1
1:A:780:ILE:HD11	1:A:850:ASN:HB3	0.66	1.67	15	9
1:A:787:LYS:HD3	1:A:787:LYS:H	0.66	1.51	6	4
1:A:818:TYR:CD2	1:A:828:LEU:HD23	0.66	2.26	10	11
1:A:817:LYS:HG3	1:A:827:VAL:HG22	0.65	1.69	9	3
1:A:819:GLN:NE2	1:A:822:ASP:HA	0.65	2.07	20	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:787:LYS:HD2	1:A:788:VAL:H	0.64	1.52	13	1
1:A:813:ILE:HG23	1:A:815:LYS:HG2	0.64	1.70	9	1
1:A:821:GLU:HB2	1:A:848:PHE:HB3	0.63	1.71	19	3
1:A:812:PRO:HB2	1:A:816:ILE:HG23	0.63	1.71	20	1
1:A:815:LYS:HA	1:A:815:LYS:HE2	0.63	1.69	12	5
1:A:844:ASN:O	1:A:845:ASN:HB3	0.63	1.93	11	17
1:A:813:ILE:HG22	1:A:814:THR:HG22	0.62	1.69	6	4
1:A:785:VAL:HG13	1:A:789:TRP:CE3	0.61	2.31	16	4
1:A:784:LEU:HD23	1:A:847:LYS:HE3	0.61	1.72	9	1
1:A:818:TYR:CZ	1:A:837:ALA:HB2	0.60	2.32	16	15
1:A:819:GLN:HG3	1:A:825:PHE:CE1	0.60	2.32	12	2
1:A:818:TYR:CE2	1:A:826:VAL:HB	0.60	2.32	9	11
1:A:816:ILE:HD13	1:A:816:ILE:H	0.60	1.57	1	3
1:A:828:LEU:HB2	1:A:833:ASP:HB2	0.59	1.73	13	2
1:A:794:LEU:O	1:A:798:ILE:HG12	0.58	1.98	8	3
1:A:818:TYR:HA	1:A:850:ASN:O	0.58	1.97	5	15
1:A:817:LYS:HE3	1:A:854:TYR:HE2	0.58	1.58	2	1
1:A:837:ALA:O	1:A:841:LEU:HG	0.58	1.98	17	14
1:A:817:LYS:HE2	1:A:825:PHE:HB3	0.58	1.76	18	2
1:A:786:GLU:HA	1:A:847:LYS:HD2	0.58	1.74	16	1
1:A:815:LYS:HE3	1:A:815:LYS:HA	0.58	1.74	16	2
1:A:815:LYS:O	1:A:816:ILE:HG12	0.56	1.99	6	2
1:A:798:ILE:O	1:A:802:ILE:HG12	0.56	2.01	5	2
1:A:817:LYS:O	1:A:851:ILE:HA	0.56	2.01	3	15
1:A:785:VAL:HG21	1:A:841:LEU:HD13	0.56	1.76	14	1
1:A:825:PHE:CZ	1:A:852:ARG:HB2	0.55	2.36	5	2
1:A:815:LYS:HB3	1:A:854:TYR:CZ	0.55	2.36	14	1
1:A:814:THR:HG23	1:A:815:LYS:HG2	0.55	1.78	6	1
1:A:786:GLU:O	1:A:787:LYS:HG2	0.55	2.01	10	1
1:A:782:THR:HG22	1:A:850:ASN:OD1	0.55	2.02	5	5
1:A:817:LYS:HG3	1:A:854:TYR:CE1	0.55	2.37	15	1
1:A:818:TYR:CD1	1:A:828:LEU:HD23	0.53	2.38	1	2
1:A:787:LYS:O	1:A:788:VAL:HG12	0.53	2.04	7	2
1:A:815:LYS:HE3	1:A:815:LYS:C	0.53	2.24	19	1
1:A:841:LEU:HG	1:A:847:LYS:CA	0.53	2.23	9	1
1:A:787:LYS:HD2	1:A:789:TRP:CD1	0.53	2.38	7	1
1:A:785:VAL:HA	1:A:789:TRP:CH2	0.53	2.38	16	2
1:A:812:PRO:O	1:A:813:ILE:HG22	0.53	2.04	9	1
1:A:844:ASN:HB3	1:A:846:GLU:HG3	0.53	1.79	16	1
1:A:834:TRP:O	1:A:838:LYS:HG3	0.53	2.04	2	10
1:A:793:ASP:O	1:A:796:MET:HG2	0.53	2.04	4	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:815:LYS:HE2	1:A:815:LYS:HA	0.52	1.79	2	1
1:A:853:LEU:N	1:A:853:LEU:HD13	0.52	2.20	5	2
1:A:828:LEU:CB	1:A:833:ASP:HB2	0.52	2.34	14	3
1:A:819:GLN:O	1:A:849:LEU:HD12	0.52	2.05	18	12
1:A:798:ILE:HG23	1:A:802:ILE:HD12	0.52	1.81	9	1
1:A:819:GLN:HA	1:A:824:ASP:O	0.52	2.04	12	9
1:A:802:ILE:HD13	1:A:853:LEU:HD21	0.51	1.80	9	1
1:A:784:LEU:HD21	1:A:847:LYS:HD2	0.51	1.82	7	1
1:A:818:TYR:CD2	1:A:849:LEU:HD11	0.51	2.41	13	1
1:A:785:VAL:HG11	1:A:834:TRP:HH2	0.51	1.64	1	5
1:A:813:ILE:HG23	1:A:815:LYS:CG	0.51	2.36	9	1
1:A:818:TYR:HD2	1:A:828:LEU:HD12	0.51	1.66	14	4
1:A:815:LYS:HB3	1:A:854:TYR:OH	0.50	2.05	15	1
1:A:846:GLU:HG3	1:A:847:LYS:H	0.50	1.66	13	1
1:A:817:LYS:HG2	1:A:827:VAL:CB	0.50	2.35	8	3
1:A:788:VAL:HG13	1:A:838:LYS:HD2	0.50	1.84	11	1
1:A:832:GLU:HA	1:A:835:ASN:HD22	0.50	1.67	3	2
1:A:818:TYR:HD2	1:A:849:LEU:HD11	0.50	1.67	13	1
1:A:785:VAL:HG12	1:A:789:TRP:CE3	0.50	2.42	14	1
1:A:816:ILE:HD11	1:A:828:LEU:HD11	0.50	1.82	4	3
1:A:798:ILE:O	1:A:802:ILE:HG13	0.49	2.07	11	2
1:A:819:GLN:O	1:A:849:LEU:HA	0.49	2.07	5	2
1:A:835:ASN:O	1:A:839:GLU:HG2	0.49	2.08	17	2
1:A:792:ASP:O	1:A:796:MET:HG3	0.48	2.08	9	3
1:A:837:ALA:HA	1:A:840:MET:HE2	0.48	1.84	1	2
1:A:825:PHE:CE1	1:A:852:ARG:HB2	0.48	2.42	17	4
1:A:781:PHE:HD2	1:A:851:ILE:HG13	0.48	1.68	9	4
1:A:841:LEU:HB3	1:A:847:LYS:HA	0.48	1.86	20	2
1:A:812:PRO:HB2	1:A:816:ILE:HG22	0.47	1.86	16	1
1:A:779:GLU:HG2	1:A:853:LEU:HB2	0.47	1.84	2	2
1:A:825:PHE:CE2	1:A:852:ARG:HB2	0.47	2.44	5	3
1:A:818:TYR:CZ	1:A:826:VAL:HB	0.47	2.45	6	5
1:A:834:TRP:NE1	1:A:838:LYS:HD3	0.46	2.26	11	6
1:A:781:PHE:O	1:A:850:ASN:HA	0.46	2.10	12	3
1:A:812:PRO:HB2	1:A:816:ILE:CG2	0.46	2.41	7	1
1:A:789:TRP:CD1	1:A:793:ASP:HB3	0.46	2.46	7	1
1:A:820:ASP:OD2	1:A:824:ASP:HB3	0.46	2.10	6	2
1:A:816:ILE:O	1:A:827:VAL:HG23	0.46	2.11	19	1
1:A:785:VAL:O	1:A:847:LYS:HE3	0.46	2.10	11	1
1:A:813:ILE:HG12	1:A:853:LEU:HD12	0.46	1.86	6	1
1:A:819:GLN:OE1	1:A:825:PHE:CE1	0.45	2.69	20	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:854:TYR:CD1	1:A:854:TYR:N	0.45	2.85	4	2
1:A:817:LYS:HE2	1:A:825:PHE:HD2	0.45	1.72	8	1
1:A:786:GLU:CA	1:A:847:LYS:HD2	0.45	2.40	16	1
1:A:779:GLU:HB2	1:A:853:LEU:HB2	0.45	1.88	6	1
1:A:813:ILE:O	1:A:814:THR:HG23	0.45	2.11	10	1
1:A:848:PHE:CE2	1:A:850:ASN:ND2	0.44	2.79	18	1
1:A:817:LYS:HE3	1:A:854:TYR:CE2	0.44	2.43	2	1
1:A:788:VAL:CG1	1:A:838:LYS:HD2	0.44	2.42	2	1
1:A:796:MET:HA	1:A:796:MET:CE	0.44	2.42	18	1
1:A:817:LYS:HD3	1:A:852:ARG:HD3	0.44	1.88	17	1
1:A:795:ILE:HG23	1:A:812:PRO:HD3	0.44	1.89	11	1
1:A:789:TRP:HB3	1:A:793:ASP:HB2	0.44	1.90	18	1
1:A:788:VAL:O	1:A:789:TRP:HB2	0.44	2.13	13	1
1:A:816:ILE:CD1	1:A:816:ILE:H	0.44	2.24	20	1
1:A:828:LEU:HB3	1:A:833:ASP:HB2	0.43	1.89	20	2
1:A:821:GLU:HB3	1:A:846:GLU:HG3	0.43	1.90	17	1
1:A:817:LYS:HE3	1:A:825:PHE:CD2	0.43	2.48	13	1
1:A:787:LYS:HE2	1:A:789:TRP:CD1	0.43	2.48	10	1
1:A:792:ASP:O	1:A:796:MET:HG2	0.43	2.13	11	1
1:A:779:GLU:O	1:A:780:ILE:HB	0.43	2.14	3	1
1:A:821:GLU:OE1	1:A:821:GLU:HA	0.43	2.14	5	1
1:A:815:LYS:HG2	1:A:815:LYS:O	0.43	2.14	20	1
1:A:852:ARG:NE	1:A:854:TYR:HB3	0.43	2.29	19	1
1:A:813:ILE:O	1:A:814:THR:HB	0.43	2.14	15	1
1:A:821:GLU:HG2	1:A:846:GLU:CG	0.43	2.44	13	1
1:A:813:ILE:O	1:A:813:ILE:HG22	0.42	2.14	8	1
1:A:819:GLN:O	1:A:849:LEU:HD23	0.42	2.14	9	1
1:A:793:ASP:O	1:A:796:MET:HG3	0.42	2.14	7	1
1:A:791:PHE:HB2	1:A:834:TRP:CD1	0.42	2.49	1	1
1:A:832:GLU:CD	1:A:832:GLU:H	0.42	2.18	2	1
1:A:817:LYS:HE3	1:A:827:VAL:HB	0.42	1.91	5	1
1:A:814:THR:O	1:A:815:LYS:HE2	0.42	2.15	4	1
1:A:817:LYS:HG3	1:A:827:VAL:CG2	0.42	2.44	10	1
1:A:779:GLU:H	1:A:779:GLU:CD	0.42	2.17	16	1
1:A:799:ASN:HD21	1:A:812:PRO:HD3	0.41	1.74	6	1
1:A:817:LYS:HE2	1:A:827:VAL:HG22	0.41	1.92	9	1
1:A:785:VAL:HA	1:A:789:TRP:CZ3	0.41	2.50	16	2
1:A:815:LYS:CA	1:A:815:LYS:HE2	0.41	2.44	12	1
1:A:832:GLU:O	1:A:836:VAL:HG23	0.41	2.15	19	1
1:A:833:ASP:O	1:A:836:VAL:HG22	0.41	2.16	14	1
1:A:853:LEU:N	1:A:853:LEU:HD22	0.41	2.30	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:834:TRP:NE1	1:A:838:LYS:HD2	0.41	2.30	12	1
1:A:835:ASN:HA	1:A:838:LYS:HE2	0.41	1.92	2	1
1:A:828:LEU:HD22	1:A:834:TRP:HB2	0.41	1.93	18	1
1:A:844:ASN:O	1:A:845:ASN:CB	0.40	2.68	6	1
1:A:821:GLU:HA	1:A:821:GLU:OE1	0.40	2.16	10	1
1:A:791:PHE:CE1	1:A:828:LEU:HD13	0.40	2.51	20	1
1:A:784:LEU:HD12	1:A:848:PHE:HA	0.40	1.92	5	1
1:A:833:ASP:N	1:A:833:ASP:OD1	0.40	2.54	16	1
1:A:781:PHE:CD2	1:A:851:ILE:HG13	0.40	2.51	14	1
1:A:821:GLU:HB2	1:A:846:GLU:HG2	0.40	1.94	10	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	66/77 (86%)	52±2 (79±2%)	9±2 (13±3%)	5±2 (8±2%)	2	15
All	All	1320/1540 (86%)	1045 (79%)	171 (13%)	104 (8%)	2	15

All 16 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	829	GLY	18
1	A	813	ILE	16
1	A	845	ASN	12
1	A	788	VAL	10
1	A	823	GLY	10
1	A	789	TRP	8
1	A	831	ASP	6
1	A	814	THR	6
1	A	847	LYS	4
1	A	786	GLU	3
1	A	780	ILE	3
1	A	816	ILE	3

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Mol	Chain	Res	Type	Models (Total)
1	A	791	PHE	2
1	A	785	VAL	1
1	A	821	GLU	1
1	A	830	SER	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	62/72 (86%)	56±2 (90±3%)	6±2 (10±3%)	14	58
All	All	1240/1440 (86%)	1116 (90%)	124 (10%)	14	58

All 30 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	851	ILE	19
1	A	815	LYS	11
1	A	787	LYS	11
1	A	825	PHE	10
1	A	833	ASP	9
1	A	790	ASN	7
1	A	845	ASN	7
1	A	820	ASP	5
1	A	796	MET	4
1	A	828	LEU	4
1	A	780	ILE	4
1	A	847	LYS	3
1	A	793	ASP	3
1	A	826	VAL	3
1	A	816	ILE	3
1	A	830	SER	2
1	A	839	GLU	2
1	A	831	ASP	2
1	A	853	LEU	2
1	A	854	TYR	2
1	A	814	THR	2

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Mol	Chain	Res	Type	Models (Total)
1	A	846	GLU	1
1	A	799	ASN	1
1	A	788	VAL	1
1	A	852	ARG	1
1	A	784	LEU	1
1	A	794	LEU	1
1	A	849	LEU	1
1	A	786	GLU	1
1	A	812	PRO	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 carbohydrates 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