



Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 03:56 PM BST

PDB ID : 1MM5
Title : Solution NMR structure of the outer membrane enzyme PagP in OG micelles
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Deposited on : 2002-09-03

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

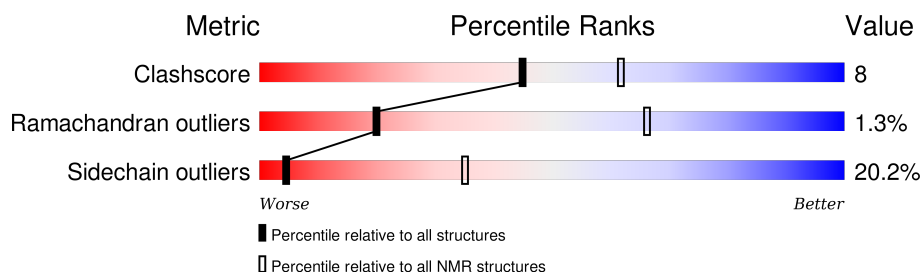
1 Overall quality at a glance

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	170	<div> <div>61%</div> <div>14%</div> <div>26%</div> </div>

2 Ensemble composition and analysis

This entry contains 20 models. Model 15 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:5-A:19 (15)	0.28	5
2	A:22-A:33, A:53-A:114, A:121-A:145, A:152-A:163 (111)	0.75	15

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 and 2 single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2768 atoms, of which 1330 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called CrcA protein.

Mol	Chain	Residues	Atoms						Trace
1	A	170	Total	C	H	N	O	S	0
			2768	937	1330	247	249	5	

There are 9 discrepancies between the modelled and reference sequences:

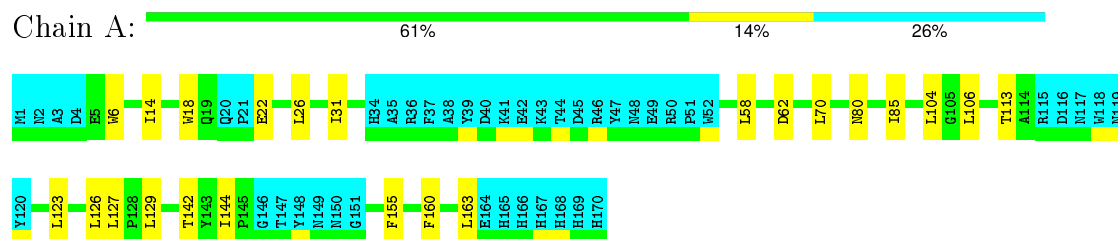
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	EXPRESSION TAG	UNP P37001
A	163	LEU	-	EXPRESSION TAG	UNP P37001
A	164	GLU	-	EXPRESSION TAG	UNP P37001
A	165	HIS	-	EXPRESSION TAG	UNP P37001
A	166	HIS	-	EXPRESSION TAG	UNP P37001
A	167	HIS	-	EXPRESSION TAG	UNP P37001
A	168	HIS	-	EXPRESSION TAG	UNP P37001
A	169	HIS	-	EXPRESSION TAG	UNP P37001
A	170	HIS	-	EXPRESSION TAG	UNP P37001

4 Residue-property plots

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: CrcA protein

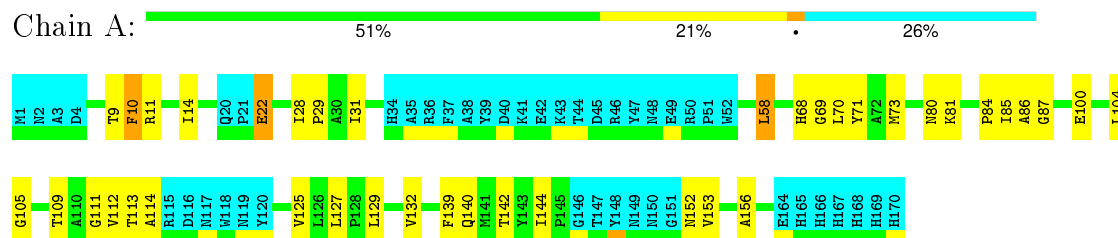


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: CrcA protein



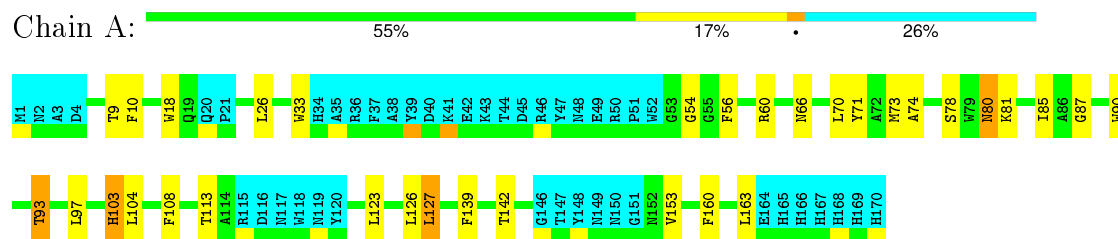
4.2.2 Score per residue for model 2

- Molecule 1: CrcA protein



4.2.6 Score per residue for model 6

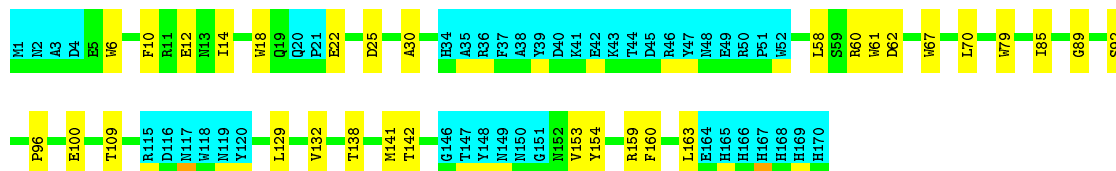
- Molecule 1: CrcA protein





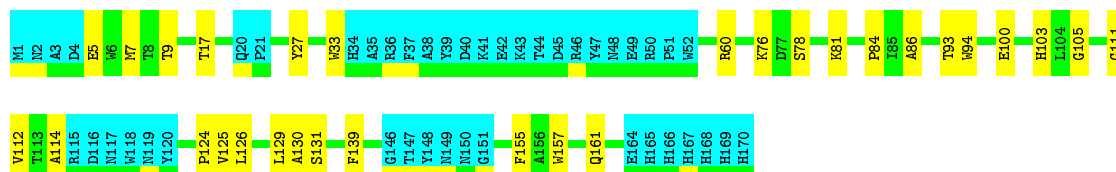
4.2.10 Score per residue for model 10

- Molecule 1: CrcA protein



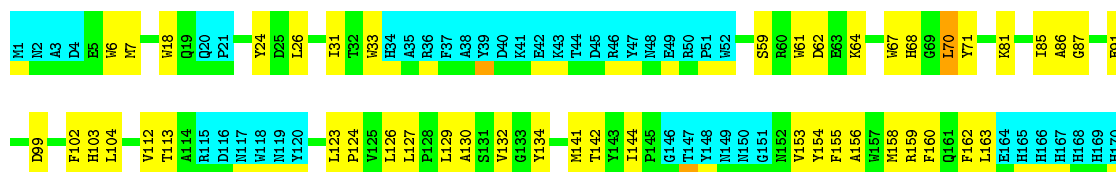
4.2.11 Score per residue for model 11

- Molecule 1: CrcA protein



4.2.12 Score per residue for model 12

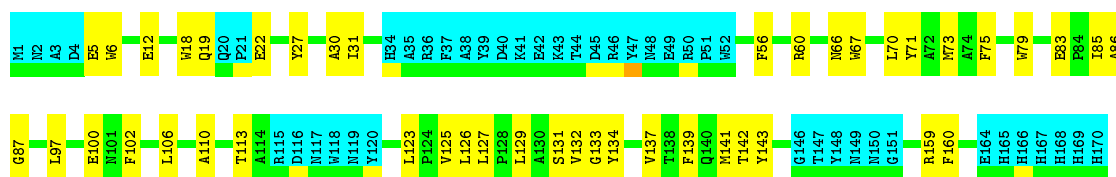
- Molecule 1: CrcA protein



4.2.13 Score per residue for model 13

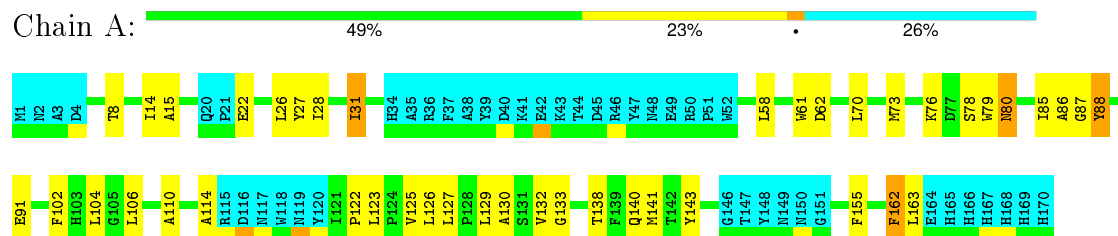
- Molecule 1: CrcA protein





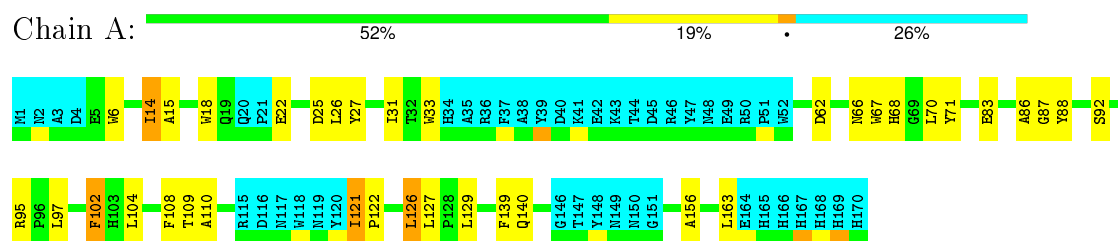
4.2.14 Score per residue for model 14

- Molecule 1: CrcA protein



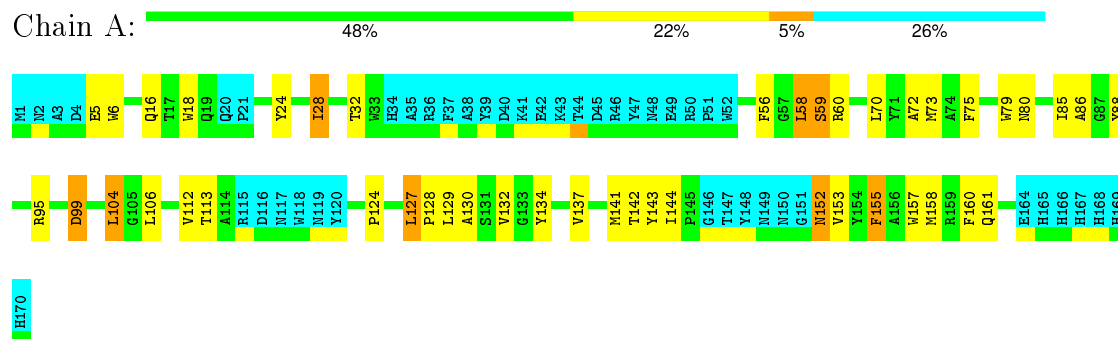
4.2.15 Score per residue for model 15 (medoid)

- Molecule 1: CrcA protein



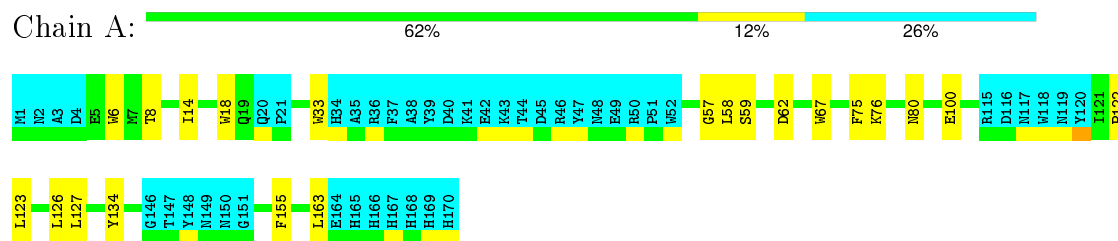
4.2.16 Score per residue for model 16

- Molecule 1: CrcA protein



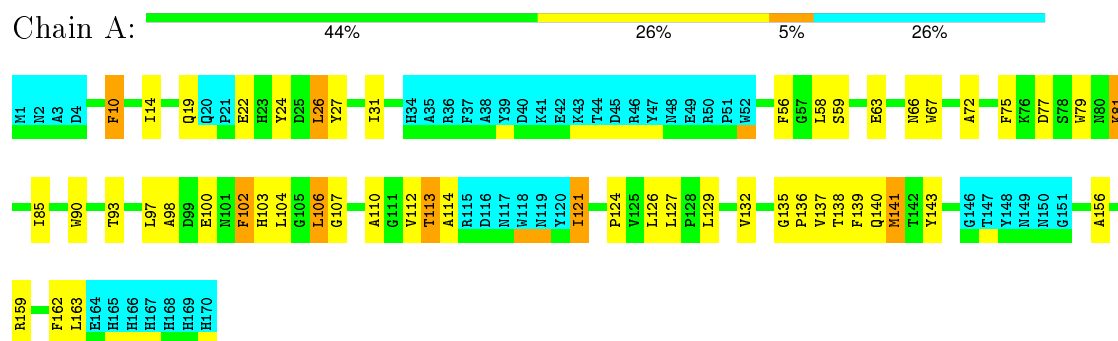
4.2.17 Score per residue for model 17

- Molecule 1: CrcA protein



4.2.18 Score per residue for model 18

- Molecule 1: CrcA protein



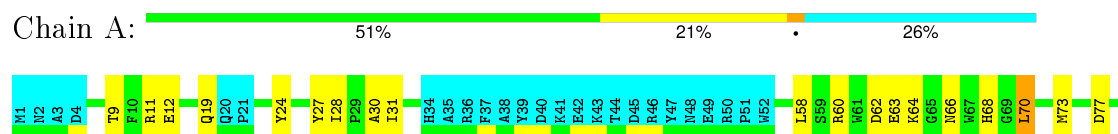
4.2.19 Score per residue for model 19

- Molecule 1: CrcA protein



4.2.20 Score per residue for model 20

- Molecule 1: CrcA protein



E83	F84	I85	A86	G87	Y88	E100	M101	F102	H103	L104	G105	L106	R115	D116	N117	M118	M119	Y120	I121	P122	L123	P124	V125	L126	L127	P128	L129	T138	I144	P145	G146	T147	Y148	M149	M150	G151	M158	R159	F160	Q161	F162	L163	E164	H165	H166	H167	H168	H169	H170
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5 Refinement protocol and experimental data overview

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

Of the 250 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
CNS	structure solution	1.0
CNS	refinement	1.0

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 ⓘ

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	1043	986	972	16±7
All	All	20860	19720	19440	329

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 8.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:109:THR:HG23	1:A:129:LEU:HD21	0.91	1.42	9	2
1:A:70:LEU:HD21	1:A:86:ALA:HB1	0.88	1.45	13	3
1:A:144:ILE:HD13	1:A:153:VAL:HG23	0.86	1.46	8	2
1:A:70:LEU:HD21	1:A:86:ALA:CB	0.78	2.08	13	2
1:A:93:THR:HG22	1:A:103:HIS:CE1	0.78	2.13	6	1
1:A:110:ALA:HB2	1:A:126:LEU:HD22	0.78	1.54	15	1
1:A:129:LEU:HD12	1:A:142:THR:HG23	0.77	1.55	8	1
1:A:89:GLY:CA	1:A:109:THR:HG22	0.76	2.10	19	1
1:A:70:LEU:HD22	1:A:88:TYR:CE1	0.76	2.16	20	1
1:A:86:ALA:HB3	1:A:112:VAL:CG2	0.76	2.11	11	2
1:A:110:ALA:HB2	1:A:126:LEU:CD2	0.72	2.14	15	2
1:A:70:LEU:HD23	1:A:71:TYR:N	0.71	2.01	13	4
1:A:111:GLY:O	1:A:125:VAL:HG22	0.70	1.86	11	2
1:A:70:LEU:HD12	1:A:87:GLY:O	0.70	1.86	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:LEU:HD13	1:A:88:TYR:OH	0.69	1.88	20	1
1:A:104:LEU:HD23	1:A:132:VAL:HG12	0.68	1.65	14	1
1:A:126:LEU:O	1:A:127:LEU:HD12	0.68	1.88	19	1
1:A:70:LEU:HD22	1:A:86:ALA:HB1	0.68	1.66	12	1
1:A:6:TRP:O	1:A:9:THR:HG22	0.67	1.90	2	1
1:A:84:PRO:HG2	1:A:114:ALA:HB3	0.67	1.66	1	4
1:A:56:PHE:O	1:A:72:ALA:HB3	0.67	1.89	3	6
1:A:73:MET:HB3	1:A:85:ILE:HD13	0.66	1.66	2	1
1:A:110:ALA:HB2	1:A:126:LEU:HD12	0.66	1.68	14	2
1:A:110:ALA:HB2	1:A:126:LEU:CD1	0.66	2.21	14	1
1:A:5:GLU:O	1:A:9:THR:HG23	0.65	1.90	11	1
1:A:27:TYR:O	1:A:28:ILE:HD13	0.64	1.92	20	2
1:A:129:LEU:HD22	1:A:140:GLN:HG2	0.64	1.70	18	1
1:A:85:ILE:HG12	1:A:113:THR:HG23	0.64	1.69	6	2
1:A:83:GLU:OE2	1:A:113:THR:HG21	0.64	1.93	4	1
1:A:128:PRO:O	1:A:142:THR:HG23	0.63	1.92	7	1
1:A:109:THR:HG21	1:A:129:LEU:HD21	0.63	1.70	15	1
1:A:70:LEU:HD21	1:A:88:TYR:CZ	0.62	2.30	2	1
1:A:70:LEU:HD13	1:A:87:GLY:O	0.61	1.93	1	1
1:A:70:LEU:HD12	1:A:88:TYR:CZ	0.61	2.30	19	2
1:A:31:ILE:O	1:A:156:ALA:HB3	0.61	1.93	12	2
1:A:110:ALA:HB2	1:A:126:LEU:HG	0.61	1.70	8	1
1:A:112:VAL:HG12	1:A:124:PRO:HA	0.61	1.71	16	3
1:A:89:GLY:HA3	1:A:109:THR:HG22	0.60	1.70	19	1
1:A:132:VAL:HG22	1:A:141:MET:CE	0.60	2.27	12	1
1:A:132:VAL:HG22	1:A:141:MET:HE3	0.59	1.74	12	1
1:A:89:GLY:HA2	1:A:109:THR:HG22	0.59	1.72	19	2
1:A:57:GLY:C	1:A:58:LEU:HD22	0.59	2.17	17	1
1:A:14:ILE:HG22	1:A:18:TRP:CD1	0.59	2.33	7	2
1:A:109:THR:CG2	1:A:129:LEU:HD21	0.58	2.27	15	2
1:A:70:LEU:HD12	1:A:87:GLY:C	0.58	2.19	14	1
1:A:144:ILE:HG23	1:A:144:ILE:O	0.58	1.99	5	2
1:A:129:LEU:HD11	1:A:140:GLN:OE1	0.58	1.98	19	1
1:A:70:LEU:HD12	1:A:88:TYR:CE2	0.58	2.33	15	1
1:A:106:LEU:HD23	1:A:130:ALA:HB2	0.58	1.73	16	2
1:A:129:LEU:HD12	1:A:142:THR:CG2	0.58	2.28	8	1
1:A:121:ILE:O	1:A:121:ILE:HG23	0.58	1.99	18	1
1:A:28:ILE:N	1:A:28:ILE:HD13	0.58	2.14	3	2
1:A:129:LEU:HD23	1:A:141:MET:O	0.58	1.99	18	1
1:A:32:THR:HG21	1:A:155:PHE:CE2	0.57	2.33	2	2
1:A:129:LEU:HD12	1:A:142:THR:OG1	0.57	1.99	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:LEU:HD13	1:A:88:TYR:CZ	0.57	2.34	20	1
1:A:73:MET:HB3	1:A:85:ILE:HD12	0.57	1.75	16	1
1:A:30:ALA:HB2	1:A:158:MET:HG3	0.57	1.77	20	2
1:A:57:GLY:C	1:A:58:LEU:HD12	0.57	2.20	5	1
1:A:144:ILE:O	1:A:144:ILE:HG23	0.57	2.00	20	2
1:A:85:ILE:HD12	1:A:113:THR:HG22	0.57	1.76	13	1
1:A:144:ILE:HD12	1:A:144:ILE:N	0.57	2.15	16	1
1:A:31:ILE:N	1:A:31:ILE:HD13	0.57	2.14	14	1
1:A:137:VAL:HG13	1:A:137:VAL:O	0.56	2.00	18	2
1:A:26:LEU:HD11	1:A:56:PHE:CZ	0.56	2.36	6	1
1:A:129:LEU:HB3	1:A:142:THR:HG23	0.56	1.77	13	1
1:A:127:LEU:HD12	1:A:142:THR:OG1	0.56	2.00	6	1
1:A:70:LEU:CD2	1:A:86:ALA:HB1	0.56	2.27	13	2
1:A:121:ILE:HD12	1:A:122:PRO:O	0.56	2.01	19	1
1:A:85:ILE:O	1:A:85:ILE:HD12	0.56	2.00	20	1
1:A:106:LEU:HD13	1:A:107:GLY:N	0.55	2.17	18	2
1:A:144:ILE:HD12	1:A:153:VAL:O	0.55	2.01	7	1
1:A:30:ALA:HB1	1:A:31:ILE:HD12	0.55	1.78	9	1
1:A:109:THR:OG1	1:A:129:LEU:HD21	0.55	2.01	2	2
1:A:32:THR:HG22	1:A:155:PHE:CD1	0.55	2.37	3	1
1:A:84:PRO:C	1:A:85:ILE:HD12	0.55	2.22	2	1
1:A:86:ALA:O	1:A:112:VAL:HG22	0.55	2.01	16	1
1:A:58:LEU:HD23	1:A:59:SER:O	0.55	2.02	2	2
1:A:70:LEU:HD23	1:A:87:GLY:N	0.55	2.16	12	1
1:A:127:LEU:HD23	1:A:143:TYR:O	0.55	2.01	19	1
1:A:85:ILE:CG2	1:A:113:THR:HG22	0.55	2.31	12	1
1:A:126:LEU:C	1:A:127:LEU:HD12	0.54	2.22	2	1
1:A:31:ILE:HG13	1:A:156:ALA:HB3	0.54	1.79	1	2
1:A:85:ILE:HG23	1:A:112:VAL:O	0.54	2.03	16	2
1:A:104:LEU:HA	1:A:132:VAL:HG12	0.53	1.80	8	1
1:A:70:LEU:HD11	1:A:88:TYR:CE2	0.53	2.38	16	1
1:A:129:LEU:HD23	1:A:130:ALA:N	0.53	2.18	11	4
1:A:122:PRO:O	1:A:123:LEU:HD22	0.53	2.04	17	1
1:A:27:TYR:C	1:A:28:ILE:HD12	0.52	2.24	8	1
1:A:105:GLY:C	1:A:106:LEU:HD12	0.52	2.24	20	1
1:A:70:LEU:HD11	1:A:86:ALA:HB1	0.52	1.80	19	2
1:A:98:ALA:HB3	1:A:102:PHE:CB	0.52	2.35	18	1
1:A:71:TYR:CE2	1:A:109:THR:HG21	0.52	2.39	7	2
1:A:26:LEU:HB3	1:A:28:ILE:HD11	0.52	1.81	8	1
1:A:109:THR:HG21	1:A:129:LEU:HD12	0.52	1.80	3	1
1:A:28:ILE:N	1:A:28:ILE:HD12	0.52	2.19	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:28:ILE:HD13	1:A:28:ILE:H	0.52	1.64	3	1
1:A:71:TYR:HE2	1:A:109:THR:HG21	0.51	1.65	7	1
1:A:10:PHE:CD2	1:A:14:ILE:HD11	0.51	2.40	1	1
1:A:70:LEU:HD22	1:A:88:TYR:CZ	0.51	2.39	20	1
1:A:163:LEU:O	1:A:163:LEU:HD12	0.51	2.04	5	2
1:A:129:LEU:HD21	1:A:140:GLN:CG	0.51	2.36	14	1
1:A:125:VAL:HG12	1:A:127:LEU:CD2	0.51	2.36	20	2
1:A:127:LEU:O	1:A:129:LEU:HD23	0.51	2.06	9	2
1:A:106:LEU:CD2	1:A:130:ALA:HB2	0.51	2.35	2	1
1:A:105:GLY:O	1:A:130:ALA:HB1	0.51	2.06	11	1
1:A:127:LEU:HD12	1:A:142:THR:HG23	0.50	1.83	16	1
1:A:58:LEU:HD22	1:A:58:LEU:N	0.50	2.21	17	1
1:A:127:LEU:HD21	1:A:144:ILE:HD12	0.50	1.82	19	1
1:A:121:ILE:HD13	1:A:121:ILE:C	0.50	2.27	15	1
1:A:144:ILE:HD12	1:A:153:VAL:HG13	0.50	1.83	12	1
1:A:54:GLY:O	1:A:74:ALA:HB3	0.49	2.07	6	1
1:A:129:LEU:HD13	1:A:140:GLN:NE2	0.49	2.22	5	1
1:A:110:ALA:HB2	1:A:126:LEU:HD23	0.49	1.83	13	1
1:A:160:PHE:CD1	1:A:162:PHE:CE2	0.49	3.00	7	1
1:A:11:ARG:HA	1:A:14:ILE:HD12	0.49	1.84	2	1
1:A:26:LEU:HD11	1:A:162:PHE:HB2	0.49	1.83	14	1
1:A:122:PRO:C	1:A:123:LEU:HD22	0.49	2.28	17	1
1:A:26:LEU:HD11	1:A:56:PHE:CE2	0.49	2.43	2	2
1:A:105:GLY:O	1:A:106:LEU:HD12	0.49	2.08	20	1
1:A:129:LEU:HD23	1:A:142:THR:OG1	0.48	2.07	1	1
1:A:130:ALA:HB3	1:A:141:MET:HB2	0.48	1.85	19	1
1:A:5:GLU:O	1:A:9:THR:HG22	0.48	2.08	4	1
1:A:113:THR:HG23	1:A:123:LEU:HD12	0.48	1.85	5	1
1:A:125:VAL:O	1:A:127:LEU:HD23	0.48	2.07	20	1
1:A:31:ILE:HD13	1:A:31:ILE:H	0.48	1.66	14	1
1:A:26:LEU:HD12	1:A:26:LEU:N	0.48	2.24	14	1
1:A:123:LEU:HD12	1:A:123:LEU:O	0.48	2.08	8	1
1:A:31:ILE:HB	1:A:156:ALA:HB3	0.48	1.85	18	2
1:A:104:LEU:HD23	1:A:105:GLY:N	0.48	2.23	1	1
1:A:10:PHE:O	1:A:14:ILE:HG22	0.48	2.09	19	3
1:A:69:GLY:O	1:A:70:LEU:HD22	0.48	2.09	1	1
1:A:134:TYR:O	1:A:137:VAL:HG12	0.47	2.09	9	1
1:A:70:LEU:HD21	1:A:88:TYR:CE2	0.47	2.43	2	1
1:A:22:GLU:HG3	1:A:58:LEU:HD22	0.47	1.85	18	1
1:A:139:PHE:CE1	1:A:156:ALA:HB1	0.47	2.43	18	1
1:A:13:ASN:O	1:A:17:THR:HG23	0.47	2.10	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:73:MET:O	1:A:85:ILE:HG22	0.47	2.09	14	1
1:A:30:ALA:CB	1:A:31:ILE:HD12	0.47	2.39	9	1
1:A:134:TYR:CZ	1:A:137:VAL:HG13	0.47	2.44	13	1
1:A:121:ILE:HG23	1:A:121:ILE:O	0.47	2.09	20	2
1:A:125:VAL:HG13	1:A:125:VAL:O	0.47	2.08	14	1
1:A:110:ALA:HB1	1:A:126:LEU:CD2	0.47	2.40	18	1
1:A:26:LEU:HD23	1:A:27:TYR:H	0.47	1.69	18	1
1:A:132:VAL:HG13	1:A:132:VAL:O	0.47	2.09	10	1
1:A:61:TRP:CD1	1:A:67:TRP:CE2	0.47	3.03	12	1
1:A:113:THR:CG2	1:A:123:LEU:HD12	0.47	2.40	5	1
1:A:114:ALA:HB2	1:A:122:PRO:CA	0.47	2.40	14	1
1:A:104:LEU:HG	1:A:132:VAL:HG12	0.46	1.86	2	1
1:A:112:VAL:HG12	1:A:124:PRO:CA	0.46	2.39	16	3
1:A:125:VAL:HG12	1:A:127:LEU:HD13	0.46	1.85	19	1
1:A:125:VAL:HG22	1:A:127:LEU:CD1	0.46	2.41	2	1
1:A:125:VAL:HG12	1:A:127:LEU:HD22	0.46	1.87	8	1
1:A:123:LEU:HD23	1:A:123:LEU:O	0.46	2.10	20	1
1:A:129:LEU:C	1:A:129:LEU:HD12	0.46	2.31	15	1
1:A:110:ALA:CB	1:A:126:LEU:HD23	0.46	2.40	2	1
1:A:127:LEU:CD2	1:A:144:ILE:HG23	0.46	2.41	3	1
1:A:104:LEU:CD2	1:A:132:VAL:HG23	0.46	2.41	18	1
1:A:163:LEU:N	1:A:163:LEU:HD12	0.46	2.26	7	1
1:A:132:VAL:O	1:A:132:VAL:HG13	0.46	2.11	1	1
1:A:112:VAL:O	1:A:112:VAL:HG23	0.45	2.12	1	1
1:A:126:LEU:HD13	1:A:127:LEU:N	0.45	2.26	15	1
1:A:129:LEU:CD1	1:A:142:THR:HG23	0.45	2.36	8	1
1:A:125:VAL:HG23	1:A:125:VAL:O	0.45	2.12	13	2
1:A:70:LEU:CD2	1:A:88:TYR:CZ	0.45	2.99	2	1
1:A:26:LEU:CD1	1:A:56:PHE:CE2	0.45	3.00	2	2
1:A:129:LEU:HD21	1:A:140:GLN:HG3	0.45	1.88	14	1
1:A:134:TYR:CE2	1:A:137:VAL:CG1	0.45	3.00	13	1
1:A:127:LEU:HD13	1:A:128:PRO:HD2	0.45	1.88	16	1
1:A:127:LEU:HD11	1:A:144:ILE:HG22	0.45	1.87	1	1
1:A:113:THR:HG23	1:A:123:LEU:HB2	0.45	1.88	7	1
1:A:85:ILE:HG23	1:A:112:VAL:C	0.45	2.33	19	1
1:A:82:TRP:N	1:A:82:TRP:CE3	0.45	2.85	2	1
1:A:106:LEU:HD23	1:A:107:GLY:N	0.45	2.27	9	1
1:A:108:PHE:CD1	1:A:108:PHE:N	0.45	2.85	2	1
1:A:134:TYR:CZ	1:A:137:VAL:CG1	0.45	3.00	13	1
1:A:73:MET:HB2	1:A:85:ILE:HD11	0.45	1.88	20	1
1:A:59:SER:CB	1:A:67:TRP:CH2	0.45	3.00	18	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:85:ILE:CD1	1:A:113:THR:HG23	0.45	2.41	1	1
1:A:30:ALA:O	1:A:31:ILE:HG23	0.45	2.11	20	2
1:A:24:TYR:CE1	1:A:58:LEU:CD2	0.44	3.00	3	1
1:A:85:ILE:HG23	1:A:113:THR:HG22	0.44	1.89	12	1
1:A:143:TYR:N	1:A:143:TYR:CD1	0.44	2.85	14	1
1:A:135:GLY:N	1:A:136:PRO:HD2	0.44	2.27	18	1
1:A:104:LEU:HD23	1:A:132:VAL:CG1	0.44	2.41	14	1
1:A:69:GLY:C	1:A:70:LEU:HD22	0.44	2.33	1	1
1:A:105:GLY:O	1:A:106:LEU:HD22	0.44	2.12	19	1
1:A:85:ILE:HG23	1:A:85:ILE:O	0.44	2.13	13	1
1:A:70:LEU:HA	1:A:87:GLY:O	0.44	2.12	20	1
1:A:160:PHE:CD1	1:A:160:PHE:N	0.44	2.85	12	1
1:A:129:LEU:HD22	1:A:140:GLN:CG	0.44	2.42	18	1
1:A:85:ILE:CD1	1:A:113:THR:HG22	0.44	2.43	13	1
1:A:104:LEU:HG	1:A:132:VAL:HG22	0.44	1.90	16	1
1:A:132:VAL:O	1:A:132:VAL:HG23	0.44	2.12	2	1
1:A:14:ILE:HG23	1:A:15:ALA:N	0.43	2.28	15	1
1:A:26:LEU:CB	1:A:160:PHE:CZ	0.43	3.01	12	1
1:A:23:HIS:O	1:A:58:LEU:HD12	0.43	2.13	9	1
1:A:155:PHE:CD2	1:A:157:TRP:CZ2	0.43	3.07	16	1
1:A:70:LEU:HD23	1:A:71:TYR:H	0.43	1.72	7	1
1:A:70:LEU:HD12	1:A:70:LEU:N	0.43	2.29	2	1
1:A:96:PRO:CG	1:A:102:PHE:CE2	0.43	3.01	8	1
1:A:28:ILE:N	1:A:28:ILE:CD1	0.43	2.81	16	2
1:A:71:TYR:CE2	1:A:87:GLY:O	0.43	2.72	15	3
1:A:154:TYR:CD1	1:A:154:TYR:N	0.43	2.87	12	1
1:A:14:ILE:HD12	1:A:15:ALA:N	0.43	2.28	3	2
1:A:153:VAL:HG22	1:A:154:TYR:N	0.43	2.29	10	1
1:A:61:TRP:NE1	1:A:67:TRP:CZ2	0.42	2.87	12	1
1:A:28:ILE:HD12	1:A:29:PRO:O	0.42	2.14	1	1
1:A:132:VAL:HG23	1:A:139:PHE:HB2	0.42	1.90	3	1
1:A:144:ILE:HD12	1:A:153:VAL:CG1	0.42	2.44	12	1
1:A:85:ILE:CG1	1:A:113:THR:HG23	0.42	2.41	6	1
1:A:31:ILE:N	1:A:31:ILE:CD1	0.42	2.82	14	1
1:A:106:LEU:HD13	1:A:107:GLY:H	0.42	1.74	18	1
1:A:134:TYR:CD1	1:A:134:TYR:N	0.42	2.88	13	1
1:A:86:ALA:HB3	1:A:112:VAL:HG21	0.42	1.90	11	1
1:A:126:LEU:N	1:A:126:LEU:HD12	0.42	2.30	2	1
1:A:134:TYR:O	1:A:137:VAL:HG22	0.42	2.14	16	2
1:A:71:TYR:O	1:A:71:TYR:CD1	0.42	2.73	15	2
1:A:58:LEU:N	1:A:58:LEU:HD12	0.42	2.29	1	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:132:VAL:HG12	1:A:133:GLY:N	0.42	2.30	13	1
1:A:98:ALA:HB3	1:A:102:PHE:HB2	0.42	1.92	18	1
1:A:153:VAL:HG12	1:A:154:TYR:N	0.42	2.30	7	1
1:A:32:THR:HG23	1:A:155:PHE:CE1	0.42	2.50	4	1
1:A:103:HIS:C	1:A:104:LEU:HD12	0.42	2.34	5	1
1:A:70:LEU:HD12	1:A:88:TYR:N	0.42	2.29	14	1
1:A:85:ILE:HD12	1:A:113:THR:OG1	0.42	2.15	18	1
1:A:73:MET:CB	1:A:85:ILE:HD12	0.42	2.44	8	1
1:A:27:TYR:CE2	1:A:159:ARG:CD	0.42	3.02	18	1
1:A:85:ILE:HD12	1:A:85:ILE:O	0.41	2.14	10	1
1:A:129:LEU:HD11	1:A:140:GLN:NE2	0.41	2.31	14	1
1:A:106:LEU:HD22	1:A:130:ALA:HB2	0.41	1.92	4	1
1:A:121:ILE:HD13	1:A:122:PRO:N	0.41	2.30	15	1
1:A:123:LEU:HD23	1:A:125:VAL:HG13	0.41	1.92	3	1
1:A:71:TYR:CD2	1:A:71:TYR:O	0.41	2.74	13	1
1:A:86:ALA:HB3	1:A:112:VAL:HG22	0.41	1.87	11	2
1:A:56:PHE:HB2	1:A:72:ALA:HB3	0.41	1.92	2	1
1:A:108:PHE:N	1:A:108:PHE:CD1	0.41	2.88	15	1
1:A:68:HIS:CD2	1:A:90:TRP:NE1	0.41	2.88	3	1
1:A:134:TYR:O	1:A:137:VAL:CG2	0.41	2.68	16	1
1:A:144:ILE:CD1	1:A:153:VAL:HG23	0.41	2.33	8	1
1:A:106:LEU:HD23	1:A:130:ALA:CB	0.41	2.44	16	1
1:A:142:THR:HG23	1:A:155:PHE:HB2	0.41	1.92	12	1
1:A:109:THR:HG23	1:A:129:LEU:HB3	0.41	1.93	10	1
1:A:129:LEU:HD11	1:A:142:THR:HG23	0.41	1.92	16	1
1:A:102:PHE:CD1	1:A:133:GLY:O	0.41	2.74	14	1
1:A:71:TYR:CD2	1:A:87:GLY:O	0.41	2.74	15	1
1:A:61:TRP:NE1	1:A:67:TRP:CE2	0.40	2.89	12	1
1:A:88:TYR:CD1	1:A:110:ALA:O	0.40	2.74	5	1
1:A:73:MET:CG	1:A:85:ILE:CG2	0.40	2.99	14	1
1:A:96:PRO:HG2	1:A:102:PHE:CE2	0.40	2.51	8	1
1:A:138:THR:HG23	1:A:159:ARG:HB2	0.40	1.92	18	1
1:A:71:TYR:CD1	1:A:87:GLY:O	0.40	2.74	13	1
1:A:143:TYR:CG	1:A:143:TYR:O	0.40	2.75	13	1
1:A:70:LEU:CB	1:A:87:GLY:O	0.40	2.70	20	1
1:A:104:LEU:HD21	1:A:132:VAL:HG23	0.40	1.91	18	1
1:A:71:TYR:CD1	1:A:71:TYR:O	0.40	2.74	6	1
1:A:90:TRP:CD1	1:A:90:TRP:O	0.40	2.74	6	1
1:A:88:TYR:O	1:A:90:TRP:CZ3	0.40	2.75	19	1
1:A:75:PHE:CD1	1:A:75:PHE:O	0.40	2.74	19	1
1:A:134:TYR:CD1	1:A:134:TYR:O	0.40	2.75	12	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:27:TYR:CE2	1:A:56:PHE:O	0.40	2.74	2	1
1:A:127:LEU:O	1:A:127:LEU:HD12	0.40	2.16	15	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	126/170 (74%)	114±2 (91±1%)	10±2 (8±1%)	2±1 (1±1%)	20	66
All	All	2520/3400 (74%)	2286 (91%)	200 (8%)	34 (1%)	20	66

All 11 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	80	ASN	8
1	A	96	PRO	7
1	A	22	GLU	7
1	A	152	ASN	3
1	A	99	ASP	2
1	A	100	GLU	2
1	A	77	ASP	1
1	A	79	TRP	1
1	A	81	LYS	1
1	A	30	ALA	1
1	A	102	PHE	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	103/142 (73%)	82±4 (80±4%)	21±4 (20±4%)	4	35
All	All	2060/2840 (73%)	1643 (80%)	417 (20%)	4	35

All 88 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	126	LEU	12
1	A	62	ASP	11
1	A	6	TRP	11
1	A	18	TRP	10
1	A	163	LEU	10
1	A	160	PHE	10
1	A	79	TRP	9
1	A	66	ASN	9
1	A	33	TRP	9
1	A	60	ARG	8
1	A	68	HIS	8
1	A	127	LEU	8
1	A	76	LYS	7
1	A	162	PHE	7
1	A	139	PHE	7
1	A	104	LEU	7
1	A	97	LEU	7
1	A	70	LEU	7
1	A	67	TRP	7
1	A	141	MET	7
1	A	11	ARG	6
1	A	10	PHE	6
1	A	103	HIS	6
1	A	81	LYS	6
1	A	95	ARG	6
1	A	161	GLN	6
1	A	102	PHE	6
1	A	155	PHE	6
1	A	24	TYR	6
1	A	106	LEU	6
1	A	75	PHE	6
1	A	58	LEU	6
1	A	138	THR	5
1	A	100	GLU	5
1	A	99	ASP	5
1	A	26	LEU	5

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Mol	Chain	Res	Type	Models (Total)
1	A	80	ASN	5
1	A	19	GLN	5
1	A	123	LEU	5
1	A	129	LEU	5
1	A	12	GLU	5
1	A	73	MET	5
1	A	83	GLU	5
1	A	59	SER	5
1	A	27	TYR	5
1	A	5	GLU	4
1	A	93	THR	4
1	A	140	GLN	4
1	A	63	GLU	4
1	A	158	MET	4
1	A	9	THR	4
1	A	77	ASP	4
1	A	157	TRP	4
1	A	78	SER	4
1	A	159	ARG	4
1	A	64	LYS	4
1	A	143	TYR	4
1	A	121	ILE	3
1	A	16	GLN	3
1	A	144	ILE	3
1	A	94	TRP	3
1	A	22	GLU	3
1	A	113	THR	3
1	A	23	HIS	3
1	A	92	SER	3
1	A	101	ASN	3
1	A	7	MET	3
1	A	131	SER	2
1	A	91	GLU	2
1	A	108	PHE	2
1	A	17	THR	2
1	A	82	TRP	2
1	A	28	ILE	2
1	A	8	THR	2
1	A	61	TRP	2
1	A	142	THR	2
1	A	25	ASP	2
1	A	14	ILE	1

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Mol	Chain	Res	Type	Models (Total)
1	A	32	THR	1
1	A	154	TYR	1
1	A	152	ASN	1
1	A	88	TYR	1
1	A	71	TYR	1
1	A	31	ILE	1
1	A	134	TYR	1
1	A	56	PHE	1
1	A	90	TRP	1
1	A	13	ASN	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