Full wwPDB NMR Structure Validation Report (i)

Feb 26, 2022 – 02:41 PM EST

PDB ID	:	2CR3
Title	:	Solution structure of the first Ig-like domain of human fibroblast growth factor receptor 1
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Deposited on	:	2005-05-20

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 (i) symbol.

The following versions of software and data (see references (i)) were used in the production of this report:

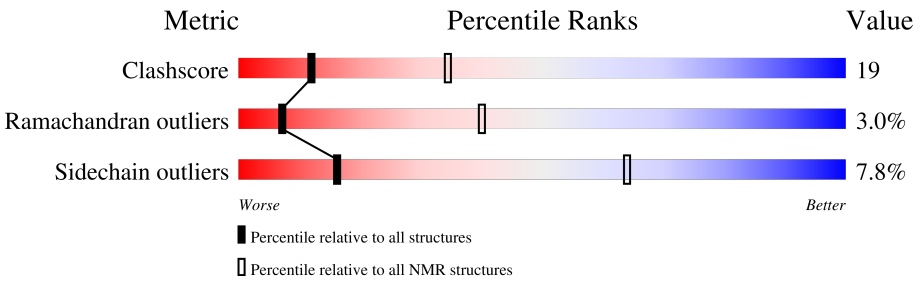
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.27
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.27

1 Overall quality at a glance (i)

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	99	42% 26% • 29%

2 Ensemble composition and analysis (i)

This entry contains 20 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:10-A:26, A:33-A:74, A:80-A:90 (70)	0.07	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 4 clusters and 3 single-model clusters were found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1417 atoms, of which 688 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Basic fibroblast growth factor receptor 1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	99	1417	441	688	127	159	2	0

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	cloning artifact	UNP P11362
A	2	SER	-	cloning artifact	UNP P11362
A	3	SER	-	cloning artifact	UNP P11362
A	4	GLY	-	cloning artifact	UNP P11362
A	5	SER	-	cloning artifact	UNP P11362
A	6	SER	-	cloning artifact	UNP P11362
A	7	GLY	-	cloning artifact	UNP P11362
A	94	SER	-	cloning artifact	UNP P11362
A	95	GLY	-	cloning artifact	UNP P11362
A	96	PRO	-	cloning artifact	UNP P11362
A	97	SER	-	cloning artifact	UNP P11362
A	98	SER	-	cloning artifact	UNP P11362
A	99	GLY	-	cloning artifact	UNP P11362

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: Basic fibroblast growth factor receptor 1

Chain A: 42% 26% • 29%

G1 S2 S3 G4 S5 S6 G7 V8 E9 F13 L14 V15 H16 P17 L20 R24 L27 R28 D29 D30 V31 Q32 W36 L37 R38 V41 Q42 N47 R48 T49 R50 I51 E57 V58 Q59 D60 S61 V62 S66 Y69 A70 C71 S75 P76 S77 G78 S79 T82

Y83 F84 S85 V88 S89 D90 A91 L92 P93 S94 G95 P96 S97 S98 G99

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: Basic fibroblast growth factor receptor 1

Chain A: 39% 28% • 29%

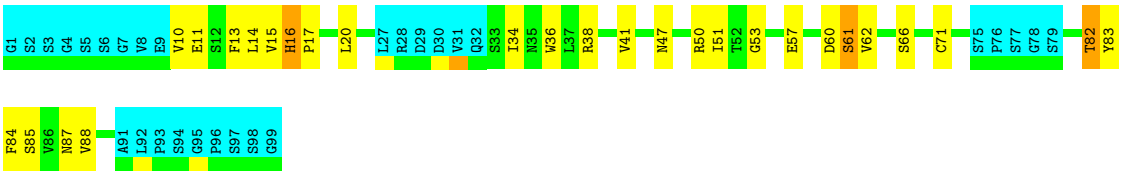
G1 S2 S3 G4 S5 S6 G7 V8 E9 L14 V15 H16 P17 L20 R24 L27 R28 D29 D30 V31 Q32 S33 I34 N35 W36 L37 R38 V41 Q42 E45 T49 R50 I51 T52 G53 E57 V58 Q59 D60 S61 V62 Y69 A70 C71 V72 T73 S74 S75 P76 S77 G78

S79 T82 Y83 F84 S85 V86 N87 V88 S89 D90 A91 L92 P93 S94 G95 P96 S97 S98 G99

4.2.2 Score per residue for model 2

• Molecule 1: Basic fibroblast growth factor receptor 1

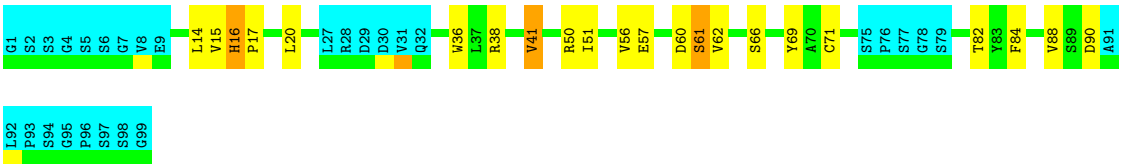
Chain A: 42% 25% • 29%



4.2.3 Score per residue for model 3 (medoid)

- Molecule 1: Basic fibroblast growth factor receptor 1

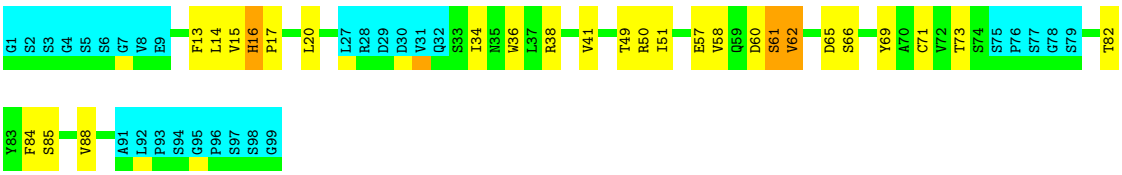
Chain A: 48% 19% • 29%



4.2.4 Score per residue for model 4

- Molecule 1: Basic fibroblast growth factor receptor 1

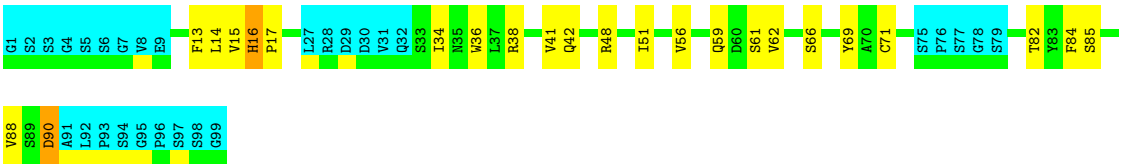
Chain A: 43% 24% • 29%



4.2.5 Score per residue for model 5

- Molecule 1: Basic fibroblast growth factor receptor 1

Chain A: 46% 22% • 29%



4.2.6 Score per residue for model 6

- Molecule 1: Basic fibroblast growth factor receptor 1

Chain A: 38% 28% • 29%

G1 S2 S3 G4 S5 S6 G7 V8 E9 F13 L14 V15 H16 P17 L20 R24 L27 R28 D29 D30 V31 Q32 S33 I34 N35 W36 L37 R38 V41 S46 N47 R48 T49 R50 I51 T52 G53 E57 D60 S61 V62 S66 C71 V72 T73 S74 S75 P76 S77 G78 S79 T82 Y83 F84 S85 V86 N87 V88 S89 D90 A91 L92 P93 S94 G95 P96 S97 S98 G99

4.2.7 Score per residue for model 7

- Molecule 1: Basic fibroblast growth factor receptor 1

Chain A: 34% 32% • 29%

G1 S2 S3 G4 S5 S6 G7 V8 E9 F13 L14 V15 H16 P17 L20 R24 L27 R28 D29 D30 V31 Q32 S33 I34 N35 W36 L37 R38 V41 Q42 E45 S46 N47 R48 T49 R50 I51 T52 G53 E54 E57 V58 Q59 D60 S61 V62 D65 S66 Y69 A70 C71 S75 P76 S77 G78 S79 T82 Y83 F84 S85 V86 N87 V88 A91 L92 P93 S94 G95 P96 S97 S98 G99

4.2.8 Score per residue for model 8

- Molecule 1: Basic fibroblast growth factor receptor 1

Chain A: 38% 28% • 29%

G1 S2 S3 G4 S5 S6 G7 V8 E9 L14 V15 H16 P17 L20 R24 C25 R26 L27 R28 D29 D30 V31 Q32 N35 W36 L37 R38 V41 E45 T49 R50 I51 T52 G53 E54 E55 V56 E57 V58 Q59 D60 S61 V62 S66 Y69 A70 C71 V72 S75 P76 S77 G78 S79 D80 T81 T82 Y83 F84 V88 A91 L92 P93 S94 G95 P96 S97 S98 G99

4.2.9 Score per residue for model 9

- Molecule 1: Basic fibroblast growth factor receptor 1

Chain A: 44% 23% • 29%

G1 S2 S3 G4 S5 S6 G7 V8 E9 L14 V15 H16 P17 L20 R24 L27 R28 D29 D30 V31 Q32 S33 I34 N35 W36 L37 R38 V41 Q42 S46 R50 I51 T52 G53 E54 E57 S61 V62 S66 Y69 A70 C71 S75 P76 S77 G78 S79 T82 Y83 F84 V88 S89 D90 A91 L92 P93 S94 G95 P96 S97 S98 G99

4.2.10 Score per residue for model 10

- Molecule 1: Basic fibroblast growth factor receptor 1

Chain A: 37% 30% • 29%

G1 S2 S3 G4 S5 S6 G7 V8 E9 F13 L14 V15 H16 P17 R24 C25 R26 L27 R28 D29 D30 V31 Q32 S33 I34 N35 W36 L37 R38 V41 Q42 S46 N47 R48 T49 R50 I51 V56 E57 V58 Q59 D60 S61 V62 S66 Y69 A70 C71 S75 P76 S77 G78

S79 T82 Y83 F84 S85 V88 S89 D90 A91 L92 P93 S94 G95 P96 S97 S98 G99

4.2.11 Score per residue for model 11

- Molecule 1: Basic fibroblast growth factor receptor 1

Chain A: 46% 20% • 29%

G1 S2 S3 G4 S5 S6 G7 V8 E9 F13 L14 V15 H16 P17 L27 R28 D29 D30 V31 Q32 N35 R38 V41 N47 R50 E57 D60 S61 V62 D65 S66 Y69 V72 T73 S74 S75 P76 S77 G78 S79 T82 Y83 F84 S85 V88 S89

D90 A91 L92 P93 S94 G95 P96 S97 S98 G99

4.2.12 Score per residue for model 12

- Molecule 1: Basic fibroblast growth factor receptor 1

Chain A: 42% 25% • 29%

G1 S2 S3 G4 S5 S6 G7 V8 E9 F13 L14 V15 H16 P17 L20 R24 L27 R28 D29 D30 V31 Q32 N35 W36 L37 R38 V41 Q42 T49 R50 I51 T52 G53 E57 V58 Q59 D60 S61 V62 S66 C71 V72 S75 P76 S77 G78 S79 T82

Y83 F84 S85 V88 A91 L92 P93 S94 G95 P96 S97 S98 G99

4.2.13 Score per residue for model 13

- Molecule 1: Basic fibroblast growth factor receptor 1

Chain A: 41% 27% • 29%

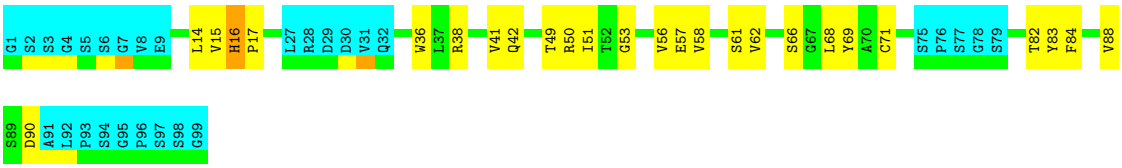
G1 S2 S3 G4 S5 S6 G7 V8 E9 F13 L14 V15 H16 P17 L20 R24 L27 R28 D29 D30 V31 Q32 N35 W36 L37 R38 V41 E45 T49 R50 I51 T52 G53 V56 E57 V58 Q59 D60 S61 V62 S66 V72 S75 P76 S77 G78 S79

T82 Y83 F84 S85 V88 S89 D90 A91 L92 P93 S94 G95 P96 S97 S98 G99

4.2.14 Score per residue for model 14

- Molecule 1: Basic fibroblast growth factor receptor 1

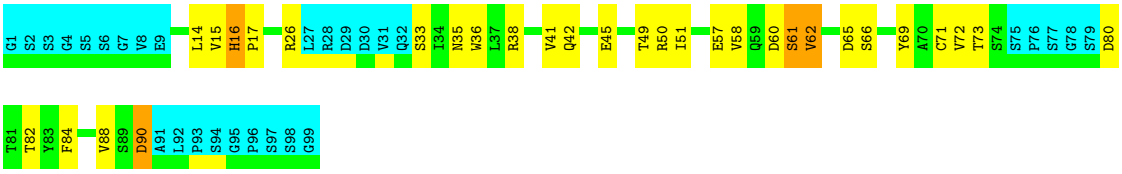
Chain A: 44% 25% • 29%



4.2.15 Score per residue for model 15

- Molecule 1: Basic fibroblast growth factor receptor 1

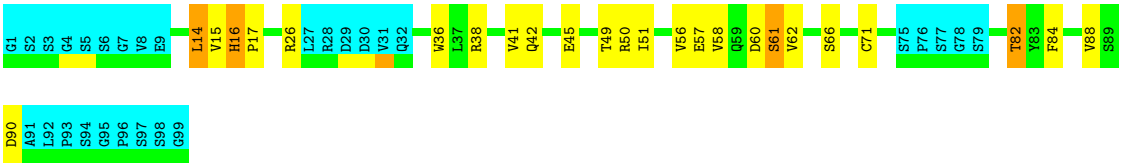
Chain A: 39% 27% • 29%



4.2.16 Score per residue for model 16

- Molecule 1: Basic fibroblast growth factor receptor 1

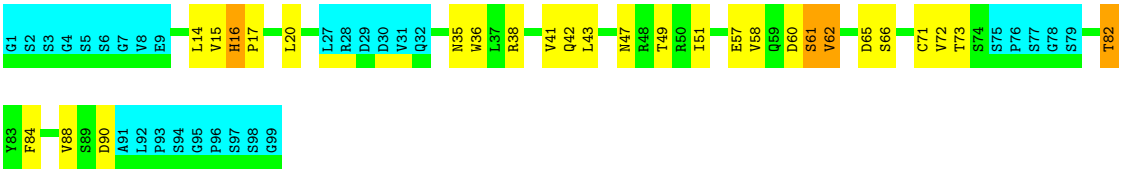
Chain A: 45% 21% • 29%



4.2.17 Score per residue for model 17

- Molecule 1: Basic fibroblast growth factor receptor 1

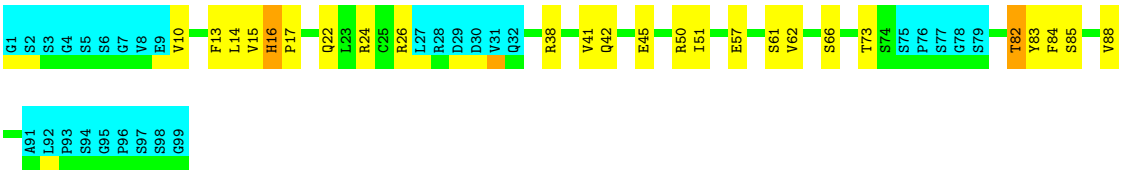
Chain A: 42% 24% • 29%



4.2.18 Score per residue for model 18

- Molecule 1: Basic fibroblast growth factor receptor 1

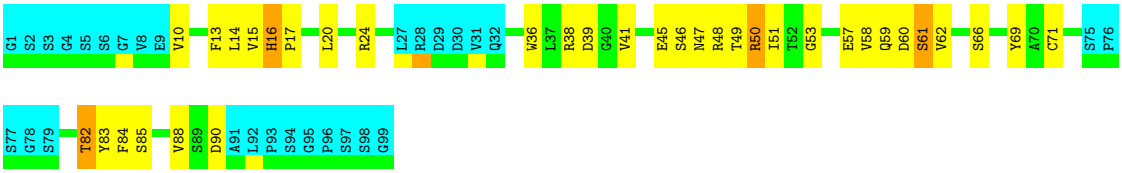
Chain A: 45% 23% • 29%



4.2.19 Score per residue for model 19

- Molecule 1: Basic fibroblast growth factor receptor 1

Chain A: 35% 31% • 29%



4.2.20 Score per residue for model 20

- Molecule 1: Basic fibroblast growth factor receptor 1

Chain A: 37% 28% 5% 29%

5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *torsion angle dynamics*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *target function,structures with the lowest energy,structures with the least restraint violations*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
CYANA	structure solution	2.0.17
CYANA	refinement	2.0.17

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	544	519	518	21±3
All	All	10880	10380	10360	413

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:15:VAL:CG2	1:A:88:VAL:HG22	0.89	1.97	12	20
1:A:20:LEU:HD11	1:A:57:GLU:CG	0.82	2.04	7	11
1:A:38:ARG:O	1:A:41:VAL:HG12	0.75	1.80	17	18
1:A:20:LEU:HD11	1:A:57:GLU:HG2	0.71	1.61	7	3
1:A:14:LEU:HD13	1:A:15:VAL:N	0.70	2.00	10	20
1:A:15:VAL:HG23	1:A:88:VAL:HG22	0.70	1.64	4	20
1:A:14:LEU:HD13	1:A:14:LEU:C	0.64	2.13	19	19
1:A:14:LEU:C	1:A:14:LEU:HD13	0.61	2.17	18	1
1:A:16:HIS:CD2	1:A:16:HIS:C	0.59	2.75	1	16
1:A:36:TRP:CD1	1:A:51:ILE:CG2	0.58	2.87	5	18
1:A:24:ARG:O	1:A:84:PHE:CE2	0.56	2.58	19	9
1:A:36:TRP:CD1	1:A:51:ILE:HG23	0.56	2.35	13	14
1:A:16:HIS:C	1:A:16:HIS:CD2	0.56	2.78	11	3
1:A:20:LEU:HD11	1:A:57:GLU:HG3	0.56	1.74	7	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:82:THR:O	1:A:84:PHE:CE1	0.55	2.60	18	20
1:A:68:LEU:HD11	1:A:83:TYR:HD2	0.55	1.62	14	1
1:A:14:LEU:C	1:A:14:LEU:CD1	0.54	2.75	19	19
1:A:36:TRP:CZ2	1:A:56:VAL:HG23	0.53	2.39	8	6
1:A:45:GLU:CG	1:A:51:ILE:HD12	0.52	2.34	8	9
1:A:26:ARG:CG	1:A:26:ARG:O	0.52	2.58	10	3
1:A:49:THR:HG23	1:A:58:VAL:HG22	0.51	1.81	20	13
1:A:10:VAL:HG22	1:A:83:TYR:HB2	0.50	1.81	2	3
1:A:38:ARG:HD3	1:A:69:TYR:CE2	0.50	2.41	7	13
1:A:50:ARG:N	1:A:57:GLU:O	0.50	2.45	8	17
1:A:48:ARG:CD	1:A:59:GLN:O	0.50	2.59	19	2
1:A:46:SER:O	1:A:48:ARG:N	0.50	2.45	10	4
1:A:10:VAL:HG22	1:A:83:TYR:CB	0.49	2.37	2	1
1:A:62:VAL:CG2	1:A:65:ASP:OD2	0.48	2.61	17	5
1:A:36:TRP:NE1	1:A:53:GLY:O	0.48	2.45	9	10
1:A:38:ARG:CD	1:A:69:TYR:CZ	0.48	2.96	8	2
1:A:35:ASN:N	1:A:72:VAL:O	0.48	2.47	8	7
1:A:24:ARG:O	1:A:84:PHE:CZ	0.47	2.67	19	2
1:A:25:CYS:N	1:A:54:GLU:O	0.46	2.48	8	1
1:A:13:PHE:N	1:A:85:SER:O	0.46	2.49	18	12
1:A:68:LEU:O	1:A:68:LEU:HD13	0.45	2.11	14	1
1:A:68:LEU:HD11	1:A:83:TYR:CD2	0.45	2.45	14	1
1:A:46:SER:O	1:A:47:ASN:C	0.45	2.55	10	5
1:A:16:HIS:CB	1:A:17:PRO:HD2	0.44	2.42	10	20
1:A:26:ARG:NH2	1:A:80:ASP:OD2	0.43	2.51	15	1
1:A:71:CYS:SG	1:A:71:CYS:O	0.42	2.77	8	2
1:A:16:HIS:CG	1:A:17:PRO:HD2	0.42	2.49	12	3
1:A:45:GLU:HG2	1:A:51:ILE:HD12	0.42	1.91	18	4
1:A:10:VAL:O	1:A:10:VAL:HG12	0.42	2.14	2	1
1:A:36:TRP:CE2	1:A:56:VAL:HG23	0.42	2.50	5	3
1:A:34:ILE:CG2	1:A:71:CYS:SG	0.42	3.07	20	1
1:A:86:VAL:CG1	1:A:87:ASN:N	0.42	2.83	1	1
1:A:47:ASN:OD1	1:A:47:ASN:N	0.42	2.53	2	1
1:A:71:CYS:O	1:A:71:CYS:SG	0.42	2.77	2	14
1:A:22:GLN:NE2	1:A:57:GLU:OE2	0.42	2.53	18	1
1:A:60:ASP:O	1:A:61:SER:O	0.42	2.38	16	15
1:A:47:ASN:C	1:A:47:ASN:ND2	0.42	2.73	20	1
1:A:11:GLU:O	1:A:85:SER:N	0.41	2.54	2	1
1:A:46:SER:C	1:A:48:ARG:N	0.41	2.74	10	2
1:A:35:ASN:ND2	1:A:42:GLN:HE22	0.41	2.13	7	1
1:A:80:ASP:CG	1:A:81:THR:N	0.41	2.74	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:90:ASP:OD1	1:A:90:ASP:C	0.41	2.60	15	1
1:A:83:TYR:C	1:A:84:PHE:CG	0.41	2.94	7	1
1:A:43:LEU:HG	1:A:51:ILE:HD11	0.41	1.92	17	1
1:A:26:ARG:CZ	1:A:26:ARG:CB	0.40	2.99	16	1
1:A:60:ASP:O	1:A:61:SER:C	0.40	2.59	13	1
1:A:24:ARG:HB2	1:A:24:ARG:CZ	0.40	2.47	9	2
1:A:38:ARG:HD2	1:A:69:TYR:CZ	0.40	2.52	8	2

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	70/99 (71%)	62±1 (89±2%)	5±1 (8±2%)	2±0 (3±1%)	7	40
All	All	1400/1980 (71%)	1249 (89%)	109 (8%)	42 (3%)	7	40

All 3 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	61	SER	20
1	A	66	SER	19
1	A	47	ASN	3

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	63/85 (74%)	58±2 (92±3%)	5±2 (8±3%)	16	64
All	All	1260/1700 (74%)	1162 (92%)	98 (8%)	16	64

All 16 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	16	HIS	20
1	A	62	VAL	20
1	A	90	ASP	14
1	A	42	GLN	11
1	A	82	THR	7
1	A	14	LEU	6
1	A	33	SER	4
1	A	87	ASN	4
1	A	41	VAL	3
1	A	47	ASN	3
1	A	80	ASP	1
1	A	46	SER	1
1	A	39	ASP	1
1	A	50	ARG	1
1	A	71	CYS	1
1	A	74	SER	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 monosaccharides 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 (i)

No chemical shift data were provided