



Full wwPDB NMR Structure Validation Report ⓘ

Oct 26, 2020 – 02:17 PM JST

PDB ID : 6L7K
Title : solution structure of hIFABP V60C/Y70C variant.
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Deposited on : 2019-11-01

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 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
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 : 2.14.6
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.14.6

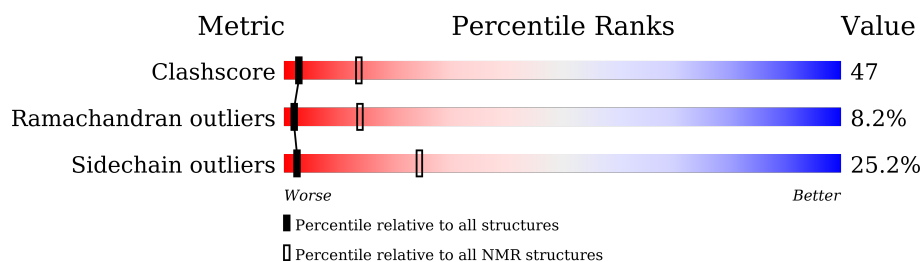
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 79%.

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	131	

2 Ensemble composition and analysis

This entry contains 20 models. Model 4 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:3-A:131 (129)	0.33	4

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 and 1 single-model cluster was found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2109 atoms, of which 1053 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Fatty acid-binding protein, intestinal.

Mol	Chain	Residues	Atoms						Trace
1	A	131	Total	C	H	N	O	S	0
			2109	665	1053	183	204	4	

There are 2 discrepancies between the modelled and reference sequences:

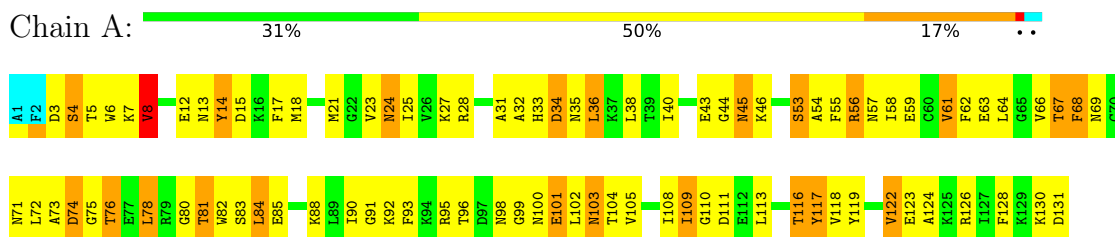
Chain	Residue	Modelled	Actual	Comment	Reference
A	60	CYS	VAL	engineered mutation	UNP P12104
A	70	CYS	TYR	engineered mutation	UNP P12104

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: Fatty acid-binding protein, intestinal

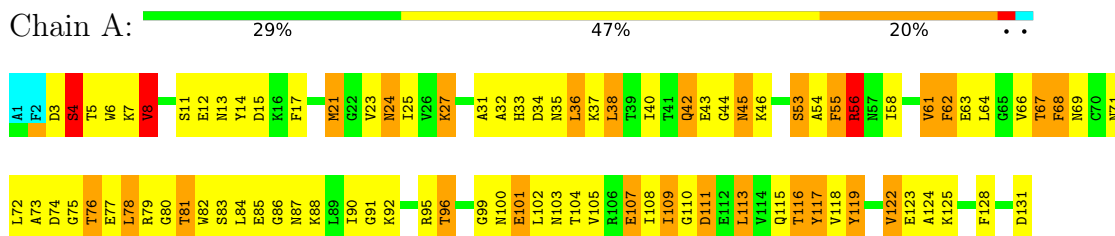


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

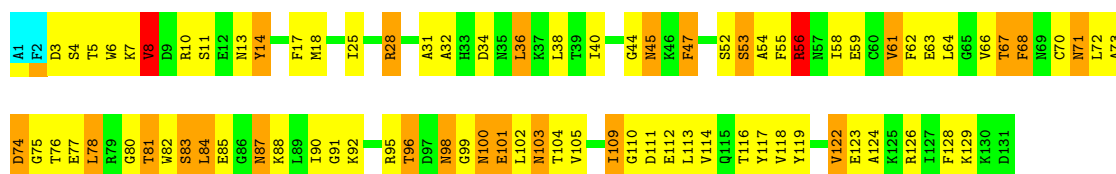
- Molecule 1: Fatty acid-binding protein, intestinal



4.2.2 Score per residue for model 2

- Molecule 1: Fatty acid-binding protein, intestinal

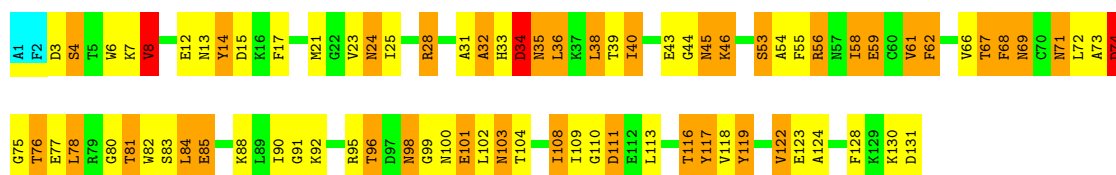




4.2.3 Score per residue for model 3

- Molecule 1: Fatty acid-binding protein, intestinal

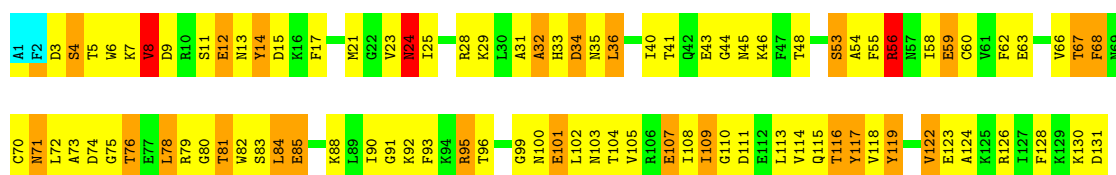
Chain A: 36% 33% 27% ..



4.2.4 Score per residue for model 4 (medoid)

- Molecule 1: Fatty acid-binding protein, intestinal

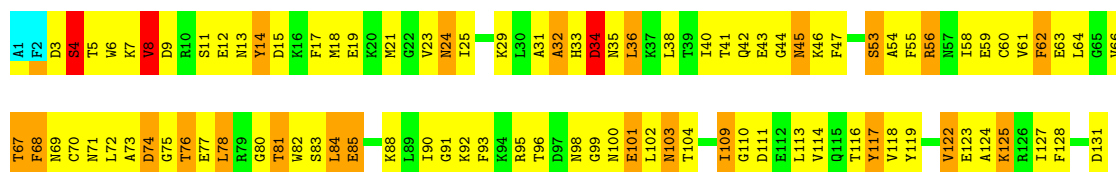
Chain A: 28% 50% 18% ..



4.2.5 Score per residue for model 5

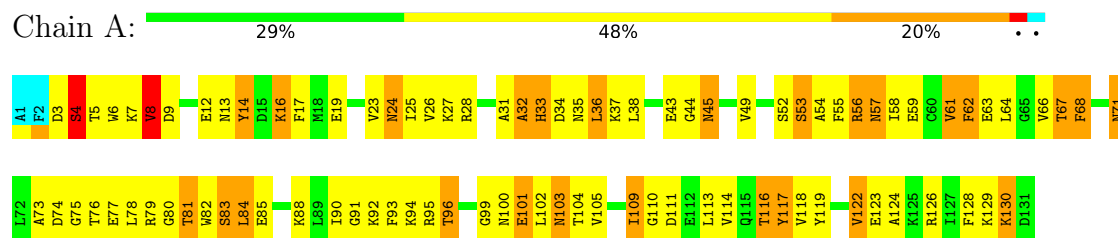
- Molecule 1: Fatty acid-binding protein, intestinal

Chain A: 26% 53% 17% ..



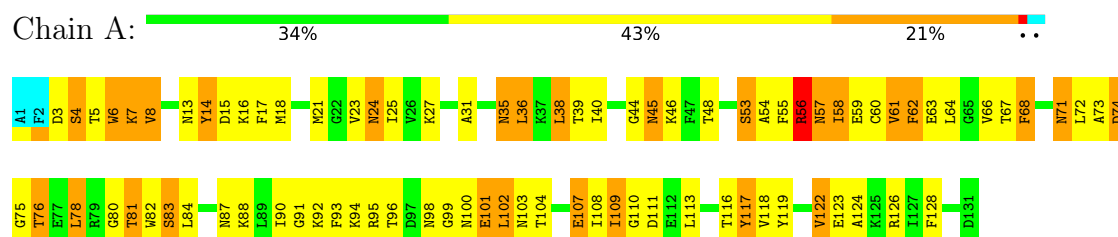
4.2.6 Score per residue for model 6

- Molecule 1: Fatty acid-binding protein, intestinal



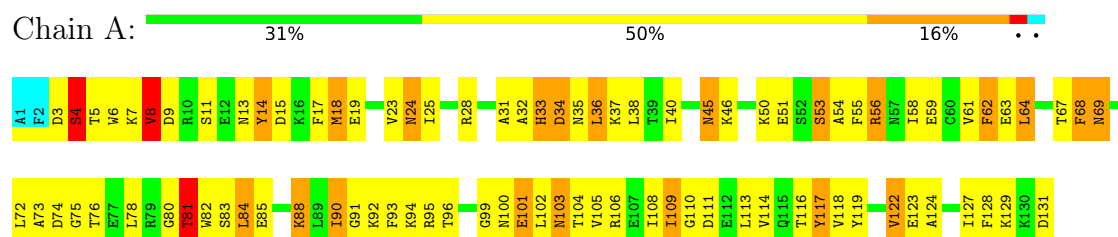
4.2.7 Score per residue for model 7

- Molecule 1: Fatty acid-binding protein, intestinal



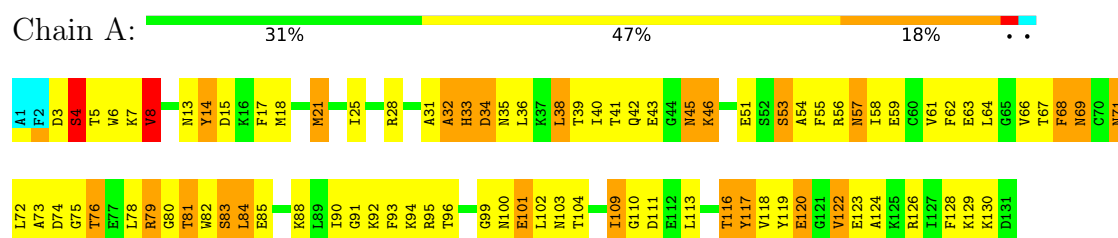
4.2.8 Score per residue for model 8

- Molecule 1: Fatty acid-binding protein, intestinal



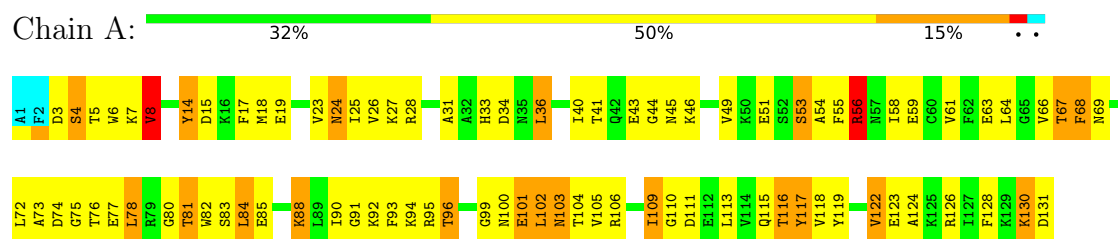
4.2.9 Score per residue for model 9

- Molecule 1: Fatty acid-binding protein, intestinal



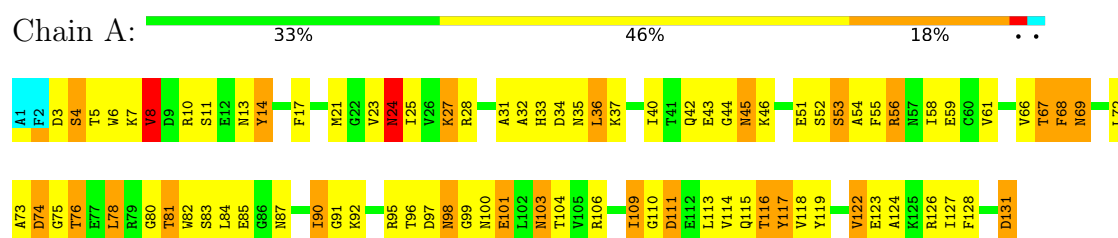
4.2.10 Score per residue for model 10

- Molecule 1: Fatty acid-binding protein, intestinal



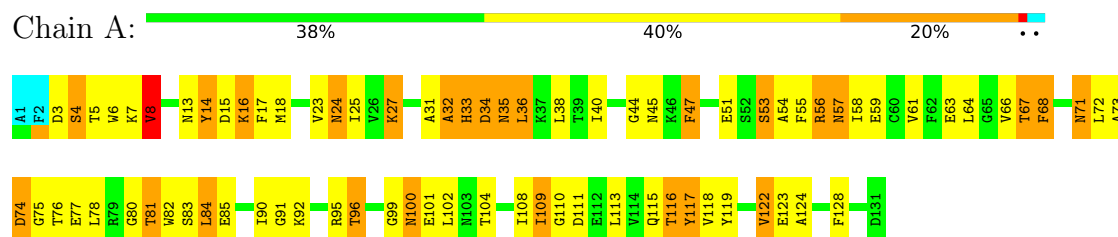
4.2.11 Score per residue for model 11

- Molecule 1: Fatty acid-binding protein, intestinal



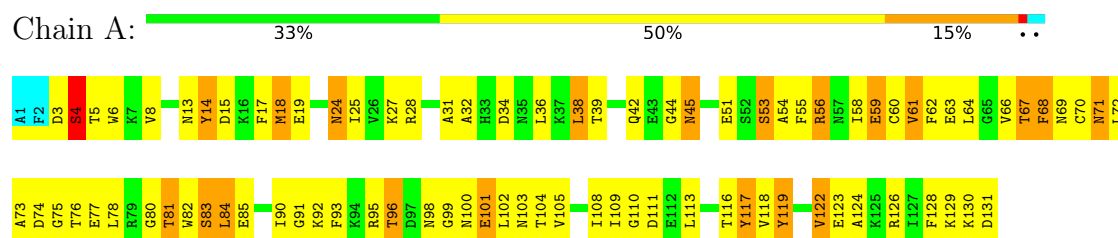
4.2.12 Score per residue for model 12

- Molecule 1: Fatty acid-binding protein, intestinal



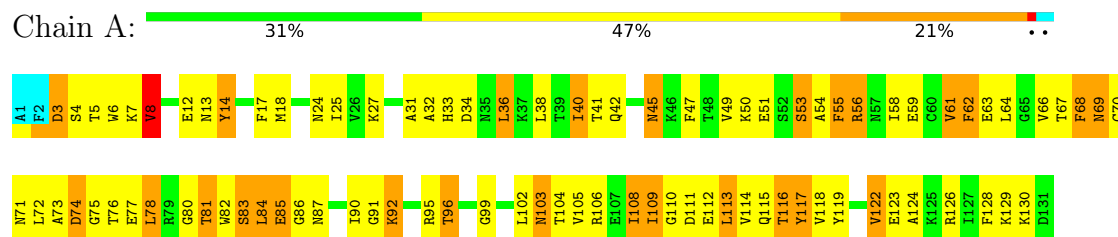
4.2.13 Score per residue for model 13

- Molecule 1: Fatty acid-binding protein, intestinal



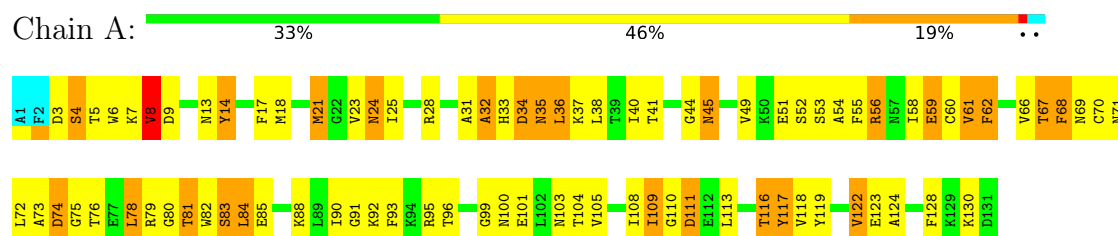
4.2.14 Score per residue for model 14

- Molecule 1: Fatty acid-binding protein, intestinal



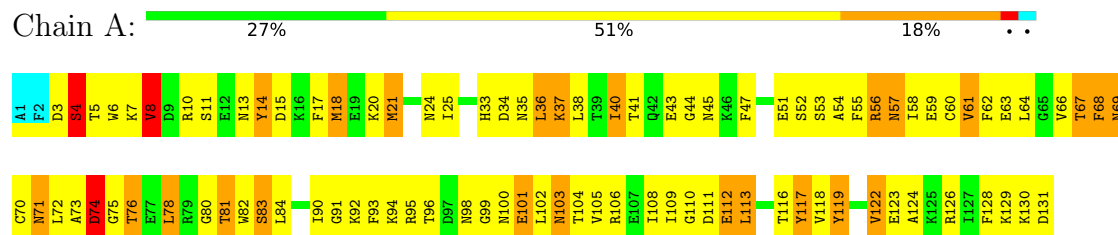
4.2.15 Score per residue for model 15

- Molecule 1: Fatty acid-binding protein, intestinal



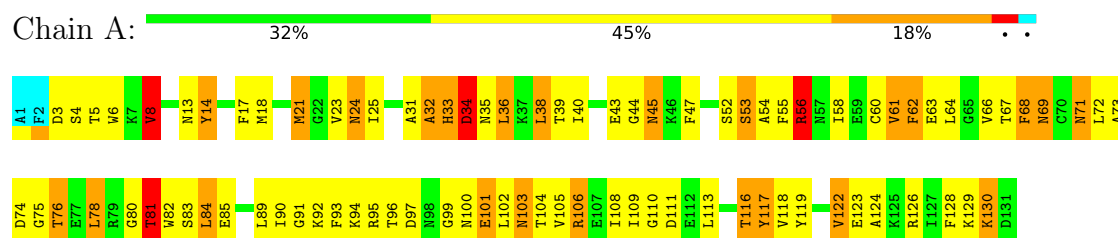
4.2.16 Score per residue for model 16

- Molecule 1: Fatty acid-binding protein, intestinal



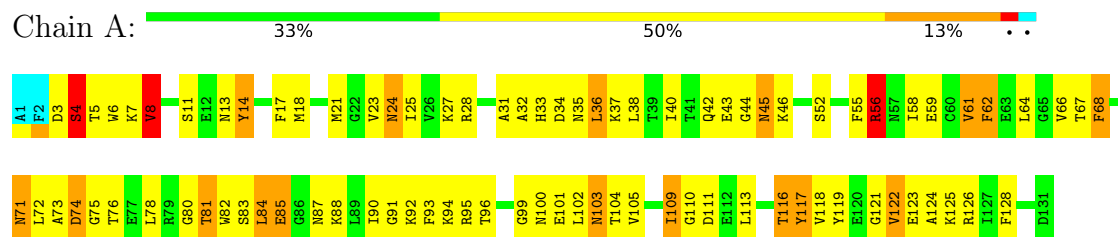
4.2.17 Score per residue for model 17

- Molecule 1: Fatty acid-binding protein, intestinal



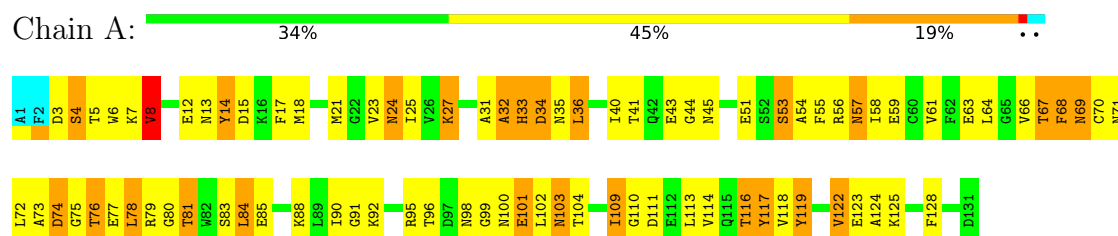
4.2.18 Score per residue for model 18

- Molecule 1: Fatty acid-binding protein, intestinal



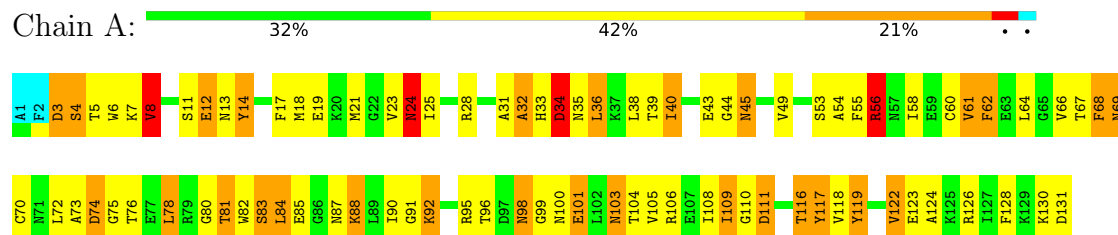
4.2.19 Score per residue for model 19

- Molecule 1: Fatty acid-binding protein, intestinal



4.2.20 Score per residue for model 20

- Molecule 1: Fatty acid-binding protein, intestinal



5 Refinement protocol and experimental data overview

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

Of the 100 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
X-PLOR NIH	structure calculation	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	1378
Number of shifts mapped to atoms	1378
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	79%

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	1040	1037	1035	97±8
All	All	20800	20740	20700	1931

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 47.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:78:LEU:HD22	1:A:78:LEU:H	0.99	1.10	19	2
1:A:78:LEU:HD22	1:A:78:LEU:N	0.87	1.84	5	2
1:A:6:TRP:CD1	1:A:40:ILE:CD1	0.85	2.59	20	2
1:A:40:ILE:HD12	1:A:40:ILE:N	0.84	1.86	7	8
1:A:77:GLU:C	1:A:78:LEU:HD13	0.84	1.94	19	2
1:A:100:ASN:O	1:A:101:GLU:O	0.83	1.95	6	16
1:A:78:LEU:N	1:A:78:LEU:HD12	0.83	1.87	3	7
1:A:84:LEU:HD12	1:A:85:GLU:N	0.83	1.88	8	16
1:A:78:LEU:HD13	1:A:78:LEU:N	0.80	1.92	19	2
1:A:38:LEU:HD23	1:A:38:LEU:N	0.79	1.91	15	2
1:A:17:PHE:HB2	1:A:124:ALA:HB2	0.79	1.55	1	20
1:A:38:LEU:N	1:A:38:LEU:HD23	0.78	1.93	8	2
1:A:78:LEU:HD12	1:A:78:LEU:N	0.78	1.93	4	3
1:A:83:SER:O	1:A:90:ILE:CG1	0.78	2.31	11	19

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:38:LEU:N	1:A:38:LEU:HD12	0.78	1.93	1	5
1:A:27:LYS:O	1:A:31:ALA:HB2	0.75	1.81	18	8
1:A:67:THR:HA	1:A:80:GLY:O	0.74	1.83	20	20
1:A:117:TYR:CD1	1:A:117:TYR:N	0.73	2.56	14	9
1:A:109:ILE:O	1:A:111:ASP:N	0.72	2.22	13	20
1:A:25:ILE:HD13	1:A:28:ARG:HE	0.72	1.43	20	1
1:A:118:VAL:HG13	1:A:122:VAL:O	0.72	1.84	15	20
1:A:117:TYR:N	1:A:117:TYR:CD1	0.72	2.58	16	11
1:A:36:LEU:HD12	1:A:37:LYS:N	0.71	2.01	8	2
1:A:17:PHE:CB	1:A:124:ALA:HB2	0.71	2.15	12	18
1:A:38:LEU:HD13	1:A:128:PHE:CE2	0.70	2.21	13	2
1:A:6:TRP:CZ3	1:A:130:LYS:N	0.69	2.60	13	3
1:A:117:TYR:CZ	1:A:126:ARG:NH1	0.69	2.60	7	1
1:A:33:HIS:O	1:A:35:ASN:N	0.69	2.25	15	10
1:A:55:PHE:CZ	1:A:56:ARG:NH2	0.69	2.60	10	1
1:A:83:SER:O	1:A:90:ILE:HG13	0.69	1.87	11	19
1:A:4:SER:OG	1:A:5:THR:N	0.68	2.25	1	9
1:A:6:TRP:CE3	1:A:130:LYS:N	0.68	2.61	16	4
1:A:17:PHE:CZ	1:A:21:MET:SD	0.68	2.87	18	3
1:A:103:ASN:ND2	1:A:103:ASN:N	0.68	2.41	20	1
1:A:38:LEU:H	1:A:38:LEU:HD23	0.68	1.49	6	2
1:A:14:TYR:CE1	1:A:126:ARG:NH2	0.68	2.61	13	1
1:A:71:ASN:ND2	1:A:71:ASN:H	0.68	1.86	7	4
1:A:45:ASN:N	1:A:45:ASN:ND2	0.68	2.43	13	4
1:A:106:ARG:NE	1:A:115:GLN:NE2	0.68	2.41	14	1
1:A:102:LEU:HD23	1:A:102:LEU:C	0.67	2.09	4	9
1:A:40:ILE:N	1:A:40:ILE:HD12	0.67	2.04	5	4
1:A:66:VAL:O	1:A:68:PHE:CD2	0.67	2.47	9	18
1:A:47:PHE:N	1:A:47:PHE:CD1	0.67	2.61	2	3
1:A:62:PHE:CD1	1:A:62:PHE:C	0.67	2.66	14	4
1:A:102:LEU:HD11	1:A:117:TYR:HB3	0.67	1.65	6	3
1:A:109:ILE:N	1:A:109:ILE:HD12	0.67	2.05	13	1
1:A:78:LEU:CD2	1:A:78:LEU:N	0.66	2.54	5	1
1:A:21:MET:SD	1:A:119:TYR:CE2	0.66	2.88	15	3
1:A:18:MET:SD	1:A:23:VAL:HG21	0.66	2.31	18	1
1:A:24:ASN:ND2	1:A:24:ASN:H	0.66	1.87	20	1
1:A:80:GLY:HA3	1:A:92:LYS:O	0.66	1.90	6	20
1:A:95:ARG:O	1:A:99:GLY:N	0.66	2.29	8	20
1:A:61:VAL:O	1:A:62:PHE:CD2	0.66	2.49	16	3
1:A:58:ILE:HG21	1:A:71:ASN:ND2	0.65	2.06	17	1
1:A:17:PHE:CE2	1:A:21:MET:SD	0.65	2.89	19	7

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:14:TYR:CZ	1:A:126:ARG:NH2	0.65	2.65	13	1
1:A:71:ASN:H	1:A:71:ASN:ND2	0.65	1.89	4	2
1:A:78:LEU:HD12	1:A:78:LEU:H	0.65	1.51	3	1
1:A:71:ASN:ND2	1:A:71:ASN:N	0.65	2.45	7	4
1:A:38:LEU:HD23	1:A:38:LEU:H	0.65	1.51	8	2
1:A:14:TYR:CE2	1:A:126:ARG:NH1	0.64	2.65	2	1
1:A:6:TRP:CD1	1:A:6:TRP:N	0.64	2.65	7	8
1:A:33:HIS:CE1	1:A:35:ASN:ND2	0.64	2.66	6	1
1:A:8:VAL:CG1	1:A:36:LEU:N	0.64	2.61	16	15
1:A:24:ASN:ND2	1:A:24:ASN:N	0.64	2.44	20	2
1:A:61:VAL:O	1:A:62:PHE:CD1	0.64	2.50	13	5
1:A:64:LEU:C	1:A:64:LEU:HD12	0.64	2.12	20	1
1:A:103:ASN:O	1:A:118:VAL:N	0.64	2.31	2	17
1:A:69:ASN:N	1:A:69:ASN:HD22	0.64	1.91	20	2
1:A:102:LEU:HD23	1:A:103:ASN:N	0.64	2.08	1	7
1:A:24:ASN:HD22	1:A:25:ILE:N	0.64	1.91	4	3
1:A:77:GLU:C	1:A:78:LEU:HD23	0.64	2.12	10	1
1:A:76:THR:CG2	1:A:95:ARG:NE	0.63	2.61	5	6
1:A:71:ASN:OD1	1:A:71:ASN:N	0.63	2.31	17	1
1:A:40:ILE:CD1	1:A:40:ILE:N	0.63	2.60	7	5
1:A:33:HIS:CE1	1:A:35:ASN:HD21	0.63	2.12	6	1
1:A:5:THR:C	1:A:6:TRP:CD1	0.62	2.71	7	18
1:A:46:LYS:NZ	1:A:48:THR:OG1	0.62	2.32	4	1
1:A:102:LEU:HD12	1:A:103:ASN:N	0.62	2.08	7	4
1:A:83:SER:O	1:A:90:ILE:CD1	0.62	2.47	8	1
1:A:14:TYR:CE2	1:A:34:ASP:OD2	0.62	2.53	6	1
1:A:38:LEU:N	1:A:38:LEU:CD2	0.62	2.62	15	3
1:A:57:ASN:HD22	1:A:57:ASN:N	0.62	1.92	7	4
1:A:103:ASN:N	1:A:103:ASN:ND2	0.62	2.47	6	2
1:A:70:CYS:O	1:A:78:LEU:HD22	0.61	1.95	19	2
1:A:82:TRP:CH2	1:A:106:ARG:NH1	0.61	2.68	16	3
1:A:78:LEU:N	1:A:78:LEU:CD2	0.61	2.55	19	1
1:A:92:LYS:CE	1:A:94:LYS:NZ	0.61	2.63	16	1
1:A:53:SER:C	1:A:55:PHE:H	0.61	1.99	8	19
1:A:61:VAL:O	1:A:62:PHE:CG	0.61	2.54	13	8
1:A:98:ASN:ND2	1:A:100:ASN:ND2	0.61	2.48	2	1
1:A:64:LEU:HD12	1:A:64:LEU:O	0.61	1.96	7	4
1:A:43:GLU:O	1:A:45:ASN:N	0.61	2.34	16	12
1:A:115:GLN:NE2	1:A:117:TYR:OH	0.61	2.34	12	2
1:A:35:ASN:ND2	1:A:35:ASN:H	0.61	1.92	7	1
1:A:62:PHE:C	1:A:62:PHE:CD2	0.61	2.71	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:47:PHE:CB	1:A:62:PHE:CE2	0.61	2.84	17	1
1:A:102:LEU:HD12	1:A:118:VAL:O	0.61	1.96	6	1
1:A:42:GLN:O	1:A:42:GLN:NE2	0.60	2.34	1	2
1:A:28:ARG:O	1:A:28:ARG:NE	0.60	2.34	2	2
1:A:57:ASN:H	1:A:57:ASN:HD22	0.60	1.39	19	3
1:A:91:GLY:O	1:A:104:THR:HG22	0.60	1.97	15	20
1:A:93:PHE:O	1:A:102:LEU:N	0.60	2.35	9	9
1:A:33:HIS:CG	1:A:33:HIS:O	0.60	2.54	10	4
1:A:24:ASN:ND2	1:A:25:ILE:H	0.60	1.93	16	3
1:A:62:PHE:C	1:A:62:PHE:CD1	0.60	2.74	17	1
1:A:24:ASN:HD22	1:A:25:ILE:H	0.60	1.37	4	3
1:A:49:VAL:HG12	1:A:51:GLU:OE2	0.60	1.96	15	1
1:A:4:SER:HG	1:A:6:TRP:HE1	0.60	1.40	16	1
1:A:100:ASN:OD1	1:A:119:TYR:CE1	0.60	2.55	15	2
1:A:31:ALA:O	1:A:33:HIS:N	0.60	2.35	15	13
1:A:16:LYS:CB	1:A:16:LYS:NZ	0.60	2.64	6	1
1:A:4:SER:OG	1:A:6:TRP:NE1	0.60	2.35	16	2
1:A:38:LEU:N	1:A:38:LEU:CD1	0.59	2.64	1	3
1:A:25:ILE:CD1	1:A:28:ARG:CZ	0.59	2.81	10	2
1:A:14:TYR:CD2	1:A:34:ASP:OD2	0.59	2.56	15	2
1:A:17:PHE:O	1:A:21:MET:SD	0.59	2.60	1	1
1:A:53:SER:O	1:A:55:PHE:N	0.59	2.35	3	19
1:A:88:LYS:CD	1:A:88:LYS:N	0.59	2.65	8	1
1:A:119:TYR:CE1	1:A:120:GLU:OE2	0.59	2.56	9	1
1:A:4:SER:O	1:A:6:TRP:NE1	0.59	2.35	7	2
1:A:14:TYR:OH	1:A:126:ARG:NE	0.59	2.36	10	1
1:A:62:PHE:CE2	1:A:70:CYS:SG	0.59	2.96	2	1
1:A:120:GLU:N	1:A:120:GLU:OE1	0.59	2.36	9	1
1:A:3:ASP:O	1:A:4:SER:CB	0.59	2.51	6	13
1:A:55:PHE:O	1:A:55:PHE:CD1	0.59	2.56	15	1
1:A:76:THR:CG2	1:A:95:ARG:HH21	0.58	2.11	11	2
1:A:56:ARG:NH1	1:A:73:ALA:O	0.58	2.36	8	1
1:A:73:ALA:C	1:A:75:GLY:H	0.58	2.02	8	20
1:A:55:PHE:CD1	1:A:55:PHE:O	0.58	2.56	10	1
1:A:24:ASN:N	1:A:24:ASN:HD22	0.58	1.96	13	1
1:A:23:VAL:O	1:A:28:ARG:NH1	0.58	2.36	20	1
1:A:42:GLN:OE1	1:A:42:GLN:N	0.58	2.36	11	1
1:A:51:GLU:OE1	1:A:51:GLU:N	0.58	2.36	14	1
1:A:95:ARG:NH1	1:A:98:ASN:OD1	0.58	2.37	7	1
1:A:66:VAL:O	1:A:68:PHE:CE2	0.58	2.56	7	15
1:A:103:ASN:O	1:A:118:VAL:HG23	0.58	1.99	16	10

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:115:GLN:O	1:A:117:TYR:CE1	0.58	2.57	14	5
1:A:82:TRP:CD1	1:A:82:TRP:N	0.58	2.71	14	5
1:A:111:ASP:OD2	1:A:129:LYS:NZ	0.58	2.36	8	1
1:A:45:ASN:OD1	1:A:45:ASN:N	0.58	2.36	16	3
1:A:76:THR:CG2	1:A:95:ARG:HE	0.58	2.11	4	2
1:A:82:TRP:N	1:A:82:TRP:CD1	0.58	2.71	2	8
1:A:15:ASP:OD1	1:A:28:ARG:NE	0.58	2.36	4	1
1:A:117:TYR:OH	1:A:126:ARG:NE	0.58	2.36	6	1
1:A:80:GLY:O	1:A:81:THR:OG1	0.58	2.22	17	20
1:A:78:LEU:CD1	1:A:78:LEU:N	0.58	2.61	5	4
1:A:14:TYR:CZ	1:A:34:ASP:OD2	0.58	2.56	6	1
1:A:92:LYS:O	1:A:92:LYS:CG	0.58	2.52	18	6
1:A:81:THR:OG1	1:A:92:LYS:NZ	0.57	2.37	5	2
1:A:33:HIS:O	1:A:33:HIS:CD2	0.57	2.57	10	2
1:A:4:SER:O	1:A:6:TRP:CD1	0.57	2.57	6	6
1:A:45:ASN:H	1:A:45:ASN:HD22	0.57	1.42	11	2
1:A:6:TRP:N	1:A:6:TRP:CD1	0.57	2.73	11	8
1:A:109:ILE:HG22	1:A:109:ILE:O	0.57	1.99	9	8
1:A:38:LEU:HD11	1:A:128:PHE:CE2	0.57	2.34	6	3
1:A:45:ASN:N	1:A:45:ASN:OD1	0.57	2.37	9	1
1:A:24:ASN:HD22	1:A:24:ASN:N	0.57	1.97	20	1
1:A:63:GLU:OE1	1:A:63:GLU:N	0.57	2.37	4	1
1:A:46:LYS:CG	1:A:46:LYS:O	0.57	2.53	8	1
1:A:36:LEU:CD2	1:A:126:ARG:HH12	0.57	2.11	14	1
1:A:12:GLU:OE1	1:A:13:ASN:N	0.57	2.37	20	1
1:A:37:LYS:O	1:A:52:SER:N	0.57	2.38	16	4
1:A:129:LYS:HE2	1:A:130:LYS:HZ2	0.57	1.59	9	1
1:A:78:LEU:N	1:A:78:LEU:CD1	0.57	2.60	19	2
1:A:14:TYR:O	1:A:18:MET:SD	0.57	2.63	15	2
1:A:18:MET:SD	1:A:74:ASP:OD1	0.57	2.63	19	3
1:A:69:ASN:O	1:A:70:CYS:SG	0.57	2.63	13	4
1:A:51:GLU:N	1:A:51:GLU:OE1	0.56	2.38	10	2
1:A:61:VAL:CG2	1:A:62:PHE:N	0.56	2.68	3	4
1:A:98:ASN:ND2	1:A:98:ASN:O	0.56	2.38	13	2
1:A:42:GLN:CD	1:A:42:GLN:H	0.56	2.04	11	1
1:A:14:TYR:CD2	1:A:34:ASP:OD1	0.56	2.58	3	1
1:A:55:PHE:O	1:A:56:ARG:CB	0.56	2.53	8	18
1:A:72:LEU:CD1	1:A:78:LEU:HD11	0.56	2.30	2	1
1:A:77:GLU:O	1:A:96:THR:N	0.56	2.38	10	4
1:A:69:ASN:HD22	1:A:69:ASN:N	0.56	1.98	17	1
1:A:92:LYS:CG	1:A:92:LYS:O	0.56	2.53	9	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:69:ASN:HD22	1:A:69:ASN:H	0.56	1.44	17	3
1:A:18:MET:SD	1:A:74:ASP:OD2	0.56	2.64	7	2
1:A:109:ILE:HD12	1:A:114:VAL:HG21	0.55	1.76	2	5
1:A:14:TYR:OH	1:A:126:ARG:NH2	0.55	2.38	4	2
1:A:31:ALA:O	1:A:34:ASP:N	0.55	2.39	13	1
1:A:13:ASN:CG	1:A:14:TYR:N	0.55	2.59	15	2
1:A:46:LYS:O	1:A:46:LYS:CG	0.55	2.54	7	1
1:A:42:GLN:CD	1:A:42:GLN:N	0.55	2.60	11	1
1:A:42:GLN:NE2	1:A:42:GLN:C	0.55	2.60	1	1
1:A:8:VAL:HG11	1:A:36:LEU:HD23	0.55	1.77	2	6
1:A:45:ASN:N	1:A:45:ASN:HD22	0.55	2.00	3	3
1:A:40:ILE:H	1:A:40:ILE:HD12	0.55	1.62	16	2
1:A:73:ALA:O	1:A:75:GLY:N	0.55	2.40	8	12
1:A:100:ASN:OD1	1:A:101:GLU:N	0.55	2.40	12	3
1:A:7:LYS:O	1:A:8:VAL:C	0.55	2.45	7	18
1:A:25:ILE:O	1:A:25:ILE:CG2	0.55	2.55	11	13
1:A:102:LEU:C	1:A:102:LEU:HD23	0.55	2.23	14	1
1:A:109:ILE:N	1:A:109:ILE:CD1	0.54	2.69	13	1
1:A:82:TRP:CZ3	1:A:106:ARG:NH1	0.54	2.74	16	1
1:A:14:TYR:OH	1:A:126:ARG:NH1	0.54	2.40	20	1
1:A:63:GLU:CG	1:A:64:LEU:N	0.54	2.69	16	9
1:A:40:ILE:HD12	1:A:40:ILE:H	0.54	1.62	20	2
1:A:109:ILE:O	1:A:109:ILE:HG22	0.54	2.03	17	7
1:A:59:GLU:OE2	1:A:59:GLU:N	0.54	2.39	13	1
1:A:117:TYR:O	1:A:123:GLU:HA	0.54	2.01	2	11
1:A:98:ASN:ND2	1:A:100:ASN:OD1	0.54	2.41	5	1
1:A:38:LEU:CD2	1:A:38:LEU:N	0.54	2.69	18	1
1:A:131:ASP:N	1:A:131:ASP:OD1	0.54	2.39	8	2
1:A:25:ILE:CG2	1:A:25:ILE:O	0.54	2.56	2	7
1:A:80:GLY:C	1:A:81:THR:OG1	0.54	2.46	16	20
1:A:72:LEU:HD11	1:A:78:LEU:HD11	0.54	1.79	2	1
1:A:57:ASN:HD22	1:A:57:ASN:H	0.54	1.45	6	3
1:A:102:LEU:HD21	1:A:117:TYR:HB3	0.53	1.80	12	5
1:A:71:ASN:N	1:A:71:ASN:ND2	0.53	2.53	18	2
1:A:123:GLU:CG	1:A:123:GLU:O	0.53	2.56	14	2
1:A:53:SER:C	1:A:55:PHE:N	0.53	2.62	19	19
1:A:45:ASN:ND2	1:A:45:ASN:N	0.53	2.57	3	2
1:A:16:LYS:HZ3	1:A:16:LYS:CB	0.53	2.17	6	1
1:A:87:ASN:OD1	1:A:87:ASN:N	0.53	2.42	18	1
1:A:103:ASN:H	1:A:103:ASN:HD22	0.53	1.46	20	1
1:A:28:ARG:C	1:A:28:ARG:CD	0.53	2.75	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:19:GLU:OE2	1:A:28:ARG:NH2	0.53	2.41	6	1
1:A:55:PHE:O	1:A:56:ARG:CG	0.53	2.57	3	12
1:A:33:HIS:O	1:A:35:ASN:ND2	0.53	2.41	5	1
1:A:49:VAL:O	1:A:49:VAL:HG13	0.53	2.02	10	1
1:A:128:PHE:N	1:A:128:PHE:CD1	0.53	2.75	18	14
1:A:12:GLU:OE1	1:A:125:LYS:NZ	0.53	2.36	5	2
1:A:15:ASP:O	1:A:19:GLU:CG	0.53	2.56	5	1
1:A:83:SER:OG	1:A:90:ILE:CD1	0.52	2.56	14	1
1:A:69:ASN:ND2	1:A:69:ASN:N	0.52	2.56	20	3
1:A:7:LYS:O	1:A:7:LYS:CG	0.52	2.58	8	5
1:A:31:ALA:C	1:A:33:HIS:N	0.52	2.62	15	12
1:A:5:THR:O	1:A:6:TRP:CD1	0.52	2.62	17	2
1:A:73:ALA:C	1:A:75:GLY:N	0.52	2.63	8	19
1:A:33:HIS:ND1	1:A:35:ASN:ND2	0.52	2.58	6	1
1:A:68:PHE:CD1	1:A:68:PHE:C	0.52	2.81	8	2
1:A:19:GLU:OE2	1:A:28:ARG:NH1	0.52	2.43	20	1
1:A:74:ASP:N	1:A:74:ASP:OD2	0.52	2.41	3	1
1:A:117:TYR:CE2	1:A:126:ARG:NH1	0.52	2.78	7	1
1:A:111:ASP:OD2	1:A:130:LYS:NZ	0.52	2.43	15	1
1:A:11:SER:CB	1:A:34:ASP:OD2	0.52	2.57	1	1
1:A:8:VAL:HG22	1:A:8:VAL:O	0.52	2.04	12	10
1:A:62:PHE:CE1	1:A:70:CYS:SG	0.52	3.03	4	1
1:A:98:ASN:HD22	1:A:100:ASN:ND2	0.52	2.02	2	1
1:A:100:ASN:O	1:A:101:GLU:CG	0.52	2.57	5	5
1:A:86:GLY:C	1:A:87:ASN:HD22	0.52	2.09	1	2
1:A:68:PHE:CZ	1:A:81:THR:HG22	0.52	2.39	5	12
1:A:94:LYS:O	1:A:94:LYS:CG	0.52	2.58	10	2
1:A:63:GLU:CD	1:A:64:LEU:H	0.51	2.09	2	1
1:A:43:GLU:OE2	1:A:46:LYS:CD	0.51	2.58	9	1
1:A:6:TRP:CE3	1:A:129:LYS:C	0.51	2.84	17	3
1:A:83:SER:O	1:A:90:ILE:HG12	0.51	2.03	11	19
1:A:131:ASP:N	1:A:131:ASP:OD2	0.51	2.41	5	3
1:A:106:ARG:HE	1:A:115:GLN:NE2	0.51	2.03	11	2
1:A:62:PHE:CD2	1:A:82:TRP:NE1	0.51	2.76	2	1
1:A:55:PHE:N	1:A:55:PHE:CD1	0.51	2.78	1	2
1:A:13:ASN:O	1:A:14:TYR:CB	0.51	2.59	5	15
1:A:35:ASN:O	1:A:36:LEU:O	0.51	2.28	7	1
1:A:66:VAL:HG13	1:A:66:VAL:O	0.51	2.06	1	1
1:A:34:ASP:OD1	1:A:34:ASP:O	0.51	2.29	12	2
1:A:16:LYS:HZ3	1:A:16:LYS:HB3	0.51	1.64	6	1
1:A:69:ASN:ND2	1:A:69:ASN:C	0.51	2.63	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:13:ASN:OD1	1:A:14:TYR:N	0.51	2.44	15	1
1:A:104:THR:OG1	1:A:116:THR:O	0.51	2.25	18	11
1:A:8:VAL:HG11	1:A:36:LEU:H	0.51	1.65	15	12
1:A:68:PHE:CG	1:A:69:ASN:N	0.51	2.77	17	1
1:A:81:THR:CB	1:A:92:LYS:HZ1	0.51	2.17	5	1
1:A:76:THR:CG2	1:A:95:ARG:NH2	0.51	2.74	11	1
1:A:8:VAL:HG12	1:A:36:LEU:O	0.50	2.06	5	11
1:A:14:TYR:OH	1:A:126:ARG:CZ	0.50	2.59	17	3
1:A:8:VAL:CG1	1:A:36:LEU:H	0.50	2.19	17	7
1:A:106:ARG:CZ	1:A:115:GLN:NE2	0.50	2.75	14	1
1:A:33:HIS:CD2	1:A:33:HIS:O	0.50	2.65	17	1
1:A:4:SER:C	1:A:6:TRP:NE1	0.50	2.64	7	1
1:A:94:LYS:CG	1:A:94:LYS:O	0.50	2.59	7	4
1:A:80:GLY:O	1:A:81:THR:HG23	0.50	2.06	8	1
1:A:31:ALA:O	1:A:34:ASP:OD2	0.50	2.30	14	1
1:A:98:ASN:ND2	1:A:100:ASN:HD21	0.50	2.02	2	1
1:A:45:ASN:O	1:A:63:GLU:OE1	0.50	2.30	2	1
1:A:123:GLU:O	1:A:123:GLU:CG	0.50	2.60	15	1
1:A:25:ILE:CD1	1:A:28:ARG:HH11	0.50	2.19	18	1
1:A:12:GLU:OE2	1:A:125:LYS:NZ	0.50	2.42	1	1
1:A:6:TRP:CD1	1:A:40:ILE:HD11	0.50	2.41	3	2
1:A:38:LEU:HD12	1:A:38:LEU:N	0.50	2.21	9	3
1:A:3:ASP:OD1	1:A:42:GLN:OE1	0.50	2.30	13	1
1:A:100:ASN:OD1	1:A:119:TYR:CZ	0.50	2.65	15	2
1:A:77:GLU:O	1:A:96:THR:OG1	0.50	2.30	2	4
1:A:111:ASP:OD1	1:A:111:ASP:N	0.50	2.44	8	1
1:A:36:LEU:HD23	1:A:36:LEU:N	0.50	2.21	13	1
1:A:61:VAL:O	1:A:68:PHE:CE2	0.50	2.65	17	1
1:A:128:PHE:CD1	1:A:128:PHE:N	0.50	2.78	20	6
1:A:19:GLU:N	1:A:28:ARG:NH2	0.50	2.60	20	1
1:A:8:VAL:HG13	1:A:35:ASN:HA	0.49	1.84	11	6
1:A:27:LYS:O	1:A:31:ALA:N	0.49	2.45	7	1
1:A:34:ASP:O	1:A:35:ASN:OD1	0.49	2.30	16	1
1:A:69:ASN:C	1:A:69:ASN:HD22	0.49	2.11	19	1
1:A:23:VAL:O	1:A:24:ASN:O	0.49	2.30	10	11
1:A:80:GLY:O	1:A:81:THR:CB	0.49	2.60	8	8
1:A:95:ARG:CD	1:A:119:TYR:OH	0.49	2.60	12	3
1:A:24:ASN:ND2	1:A:25:ILE:N	0.49	2.60	16	2
1:A:3:ASP:O	1:A:4:SER:OG	0.49	2.30	11	8
1:A:42:GLN:O	1:A:43:GLU:OE1	0.49	2.31	5	1
1:A:81:THR:CB	1:A:92:LYS:NZ	0.49	2.75	5	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:58:ILE:CD1	1:A:71:ASN:O	0.49	2.61	6	1
1:A:9:ASP:OD1	1:A:9:ASP:O	0.49	2.30	4	4
1:A:36:LEU:HD12	1:A:37:LYS:O	0.49	2.07	8	1
1:A:105:VAL:HG12	1:A:106:ARG:N	0.49	2.21	17	5
1:A:60:CYS:O	1:A:60:CYS:SG	0.49	2.71	17	1
1:A:119:TYR:CD1	1:A:120:GLU:OE2	0.49	2.66	9	1
1:A:12:GLU:OE1	1:A:13:ASN:OD1	0.49	2.31	20	1
1:A:10:ARG:O	1:A:11:SER:OG	0.49	2.30	11	3
1:A:7:LYS:CG	1:A:7:LYS:O	0.49	2.60	20	4
1:A:69:ASN:O	1:A:69:ASN:ND2	0.49	2.46	19	1
1:A:18:MET:C	1:A:28:ARG:HH22	0.49	2.11	20	1
1:A:35:ASN:O	1:A:35:ASN:OD1	0.49	2.31	5	1
1:A:40:ILE:N	1:A:40:ILE:CD1	0.49	2.76	5	3
1:A:45:ASN:HD22	1:A:45:ASN:H	0.49	1.51	13	1
1:A:66:VAL:O	1:A:66:VAL:HG13	0.49	2.07	15	1
1:A:61:VAL:O	1:A:68:PHE:CD2	0.49	2.65	17	1
1:A:19:GLU:N	1:A:28:ARG:HH22	0.49	2.05	20	1
1:A:32:ALA:O	1:A:34:ASP:N	0.49	2.46	8	7
1:A:21:MET:SD	1:A:119:TYR:CD2	0.49	3.06	15	1
1:A:49:VAL:O	1:A:51:GLU:OE2	0.49	2.30	15	1
1:A:82:TRP:NE1	1:A:93:PHE:CZ	0.49	2.79	17	1
1:A:34:ASP:O	1:A:35:ASN:ND2	0.49	2.46	18	1
1:A:68:PHE:C	1:A:69:ASN:HD22	0.49	2.10	20	1
1:A:6:TRP:CD1	1:A:40:ILE:HD12	0.49	2.41	20	1
1:A:74:ASP:OD1	1:A:74:ASP:O	0.48	2.31	14	2
1:A:34:ASP:O	1:A:34:ASP:CG	0.48	2.51	8	1
1:A:28:ARG:CD	1:A:28:ARG:C	0.48	2.81	2	1
1:A:85:GLU:O	1:A:85:GLU:CG	0.48	2.61	12	2
1:A:45:ASN:ND2	1:A:45:ASN:H	0.48	2.05	11	2
1:A:17:PHE:CE2	1:A:21:MET:CE	0.48	2.97	7	3
1:A:25:ILE:HD12	1:A:28:ARG:HH11	0.48	1.68	18	1
1:A:69:ASN:N	1:A:69:ASN:ND2	0.48	2.61	8	1
1:A:33:HIS:O	1:A:35:ASN:OD1	0.48	2.31	18	1
1:A:102:LEU:C	1:A:102:LEU:CD2	0.48	2.80	13	3
1:A:84:LEU:HD12	1:A:84:LEU:C	0.48	2.28	8	1
1:A:49:VAL:O	1:A:51:GLU:OE1	0.48	2.31	10	2
1:A:8:VAL:O	1:A:8:VAL:HG22	0.48	2.07	11	7
1:A:122:VAL:HG13	1:A:123:GLU:N	0.48	2.23	8	20
1:A:31:ALA:C	1:A:33:HIS:H	0.48	2.12	11	3
1:A:55:PHE:O	1:A:55:PHE:CG	0.48	2.66	15	1
1:A:68:PHE:CZ	1:A:81:THR:CG2	0.47	2.97	3	14

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:64:LEU:CD1	1:A:64:LEU:O	0.47	2.61	7	1
1:A:105:VAL:CG1	1:A:106:ARG:N	0.47	2.76	17	3
1:A:24:ASN:OD1	1:A:24:ASN:N	0.47	2.46	17	1
1:A:27:LYS:O	1:A:31:ALA:CB	0.47	2.61	6	8
1:A:38:LEU:HD22	1:A:128:PHE:CE2	0.47	2.44	7	4
1:A:55:PHE:C	1:A:56:ARG:CG	0.47	2.82	1	4
1:A:31:ALA:O	1:A:34:ASP:OD1	0.47	2.31	6	2
1:A:129:LYS:CE	1:A:130:LYS:HZ2	0.47	2.21	9	1
1:A:129:LYS:O	1:A:131:ASP:OD2	0.47	2.32	16	1
1:A:58:ILE:HG21	1:A:71:ASN:OD1	0.47	2.09	2	2
1:A:113:LEU:HD23	1:A:128:PHE:CD2	0.47	2.44	18	2
1:A:34:ASP:OD2	1:A:34:ASP:O	0.47	2.32	18	1
1:A:103:ASN:H	1:A:103:ASN:ND2	0.47	2.03	20	1
1:A:58:ILE:HD13	1:A:71:ASN:ND2	0.47	2.23	17	3
1:A:98:ASN:O	1:A:98:ASN:ND2	0.47	2.47	20	2
1:A:12:GLU:CD	1:A:125:LYS:NZ	0.47	2.68	1	1
1:A:58:ILE:HG21	1:A:71:ASN:HD21	0.47	1.70	3	1
1:A:114:VAL:HG22	1:A:127:ILE:HG23	0.47	1.86	5	3
1:A:71:ASN:CB	1:A:76:THR:O	0.47	2.62	17	1
1:A:31:ALA:O	1:A:32:ALA:C	0.47	2.51	9	16
1:A:57:ASN:ND2	1:A:57:ASN:N	0.47	2.62	19	3
1:A:78:LEU:HD12	1:A:93:PHE:CD2	0.47	2.45	10	1
1:A:118:VAL:HG22	1:A:123:GLU:HG2	0.47	1.86	12	1
1:A:69:ASN:C	1:A:69:ASN:ND2	0.47	2.68	19	1
1:A:15:ASP:CG	1:A:28:ARG:NH2	0.47	2.68	9	1
1:A:97:ASP:C	1:A:98:ASN:HD22	0.47	2.12	11	1
1:A:12:GLU:C	1:A:14:TYR:H	0.47	2.14	14	1
1:A:3:ASP:O	1:A:4:SER:HB2	0.47	2.10	20	1
1:A:64:LEU:C	1:A:64:LEU:CD1	0.47	2.81	20	1
1:A:74:ASP:OD1	1:A:76:THR:OG1	0.46	2.30	3	1
1:A:32:ALA:C	1:A:34:ASP:H	0.46	2.13	8	5
1:A:13:ASN:O	1:A:15:ASP:N	0.46	2.48	16	1
1:A:28:ARG:HH21	1:A:28:ARG:CG	0.46	2.23	2	1
1:A:102:LEU:CD2	1:A:102:LEU:C	0.46	2.81	8	2
1:A:117:TYR:OH	1:A:126:ARG:CZ	0.46	2.64	18	1
1:A:32:ALA:O	1:A:34:ASP:OD1	0.46	2.34	5	2
1:A:42:GLN:CB	1:A:47:PHE:CE2	0.46	2.98	5	1
1:A:71:ASN:N	1:A:71:ASN:HD22	0.46	2.07	12	1
1:A:5:THR:C	1:A:6:TRP:CG	0.46	2.88	2	11
1:A:11:SER:OG	1:A:12:GLU:N	0.46	2.49	4	2
1:A:111:ASP:N	1:A:111:ASP:OD2	0.46	2.48	20	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:28:ARG:NH2	1:A:28:ARG:CG	0.46	2.77	2	1
1:A:3:ASP:C	1:A:4:SER:OG	0.46	2.52	5	2
1:A:112:GLU:OE2	1:A:129:LYS:NZ	0.46	2.49	14	1
1:A:55:PHE:O	1:A:56:ARG:HB3	0.46	2.11	11	3
1:A:51:GLU:N	1:A:58:ILE:O	0.46	2.49	13	7
1:A:15:ASP:OD2	1:A:28:ARG:NH2	0.46	2.49	9	1
1:A:14:TYR:CE2	1:A:18:MET:HE1	0.46	2.45	9	1
1:A:25:ILE:CD1	1:A:28:ARG:HE	0.46	2.18	20	1
1:A:120:GLU:N	1:A:120:GLU:CD	0.46	2.69	9	1
1:A:23:VAL:HG11	1:A:74:ASP:OD1	0.46	2.10	11	1
1:A:56:ARG:HE	1:A:73:ALA:HB1	0.46	1.70	14	1
1:A:14:TYR:CZ	1:A:18:MET:CE	0.46	2.98	17	1
1:A:119:TYR:CB	1:A:122:VAL:HG12	0.46	2.41	18	16
1:A:109:ILE:N	1:A:112:GLU:O	0.46	2.49	16	1
1:A:23:VAL:O	1:A:24:ASN:C	0.46	2.54	8	11
1:A:130:LYS:O	1:A:131:ASP:C	0.46	2.54	20	2
1:A:93:PHE:HB2	1:A:102:LEU:HD23	0.46	1.87	5	1
1:A:84:LEU:O	1:A:85:GLU:CG	0.46	2.64	8	1
1:A:85:GLU:O	1:A:85:GLU:CD	0.46	2.55	10	1
1:A:72:LEU:O	1:A:73:ALA:C	0.45	2.54	8	19
1:A:63:GLU:CD	1:A:64:LEU:N	0.45	2.70	2	1
1:A:98:ASN:O	1:A:99:GLY:C	0.45	2.54	20	7
1:A:3:ASP:O	1:A:3:ASP:OD1	0.45	2.34	3	1
1:A:43:GLU:OE1	1:A:46:LYS:CD	0.45	2.63	3	1
1:A:82:TRP:CZ2	1:A:93:PHE:CZ	0.45	3.04	6	8
1:A:15:ASP:CG	1:A:28:ARG:HH21	0.45	2.14	9	1
1:A:119:TYR:N	1:A:122:VAL:HG12	0.45	2.26	2	18
1:A:76:THR:CG2	1:A:95:ARG:CZ	0.45	2.94	5	1
1:A:12:GLU:OE1	1:A:13:ASN:CG	0.45	2.54	20	1
1:A:19:GLU:CA	1:A:28:ARG:NH2	0.45	2.79	20	1
1:A:72:LEU:O	1:A:75:GLY:N	0.45	2.50	17	10
1:A:72:LEU:O	1:A:74:ASP:N	0.45	2.49	16	2
1:A:62:PHE:O	1:A:62:PHE:CD1	0.45	2.70	17	1
1:A:25:ILE:O	1:A:25:ILE:HG22	0.45	2.12	3	8
1:A:61:VAL:HG22	1:A:62:PHE:N	0.45	2.25	3	3
1:A:94:LYS:O	1:A:95:ARG:C	0.45	2.55	17	2
1:A:15:ASP:O	1:A:19:GLU:N	0.45	2.50	10	1
1:A:74:ASP:CG	1:A:74:ASP:O	0.45	2.55	20	1
1:A:25:ILE:HG22	1:A:25:ILE:O	0.45	2.12	12	12
1:A:4:SER:N	1:A:40:ILE:O	0.45	2.49	3	2
1:A:36:LEU:H	1:A:36:LEU:HD23	0.45	1.70	9	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:102:LEU:HD11	1:A:117:TYR:CB	0.45	2.38	6	2
1:A:80:GLY:C	1:A:81:THR:HG1	0.45	2.12	7	2
1:A:78:LEU:HD23	1:A:94:LYS:C	0.45	2.32	6	1
1:A:92:LYS:HE3	1:A:94:LYS:HZ1	0.45	1.72	16	1
1:A:15:ASP:O	1:A:19:GLU:CB	0.45	2.65	13	2
1:A:100:ASN:CG	1:A:119:TYR:OH	0.45	2.55	15	1
1:A:64:LEU:HD23	1:A:64:LEU:H	0.45	1.72	8	1
1:A:85:GLU:C	1:A:85:GLU:OE2	0.45	2.55	10	1
1:A:62:PHE:CE1	1:A:68:PHE:CB	0.45	3.00	13	1
1:A:58:ILE:CG2	1:A:71:ASN:ND2	0.45	2.79	17	1
1:A:82:TRP:HA	1:A:90:ILE:O	0.45	2.11	11	2
1:A:58:ILE:HG22	1:A:59:GLU:H	0.45	1.72	8	16
1:A:66:VAL:O	1:A:81:THR:CG2	0.45	2.65	17	5
1:A:48:THR:HG23	1:A:61:VAL:HG22	0.45	1.89	7	1
1:A:3:ASP:OD2	1:A:42:GLN:CD	0.45	2.56	9	1
1:A:115:GLN:CD	1:A:117:TYR:OH	0.45	2.56	1	1
1:A:70:CYS:SG	1:A:71:ASN:N	0.45	2.89	19	3
1:A:83:SER:O	1:A:90:ILE:HD12	0.45	2.11	8	1
1:A:120:GLU:CA	1:A:120:GLU:OE1	0.45	2.65	9	1
1:A:106:ARG:NE	1:A:115:GLN:OE1	0.45	2.47	10	1
1:A:62:PHE:CD1	1:A:82:TRP:CD1	0.45	3.05	14	1
1:A:45:ASN:O	1:A:63:GLU:CG	0.44	2.65	7	2
1:A:42:GLN:CD	1:A:47:PHE:CE2	0.44	2.90	14	1
1:A:31:ALA:O	1:A:34:ASP:CB	0.44	2.65	2	1
1:A:18:MET:N	1:A:18:MET:SD	0.44	2.90	8	1
1:A:62:PHE:CE2	1:A:68:PHE:CB	0.44	3.00	15	1
1:A:25:ILE:HD13	1:A:28:ARG:NE	0.44	2.22	20	1
1:A:62:PHE:CD1	1:A:63:GLU:N	0.44	2.85	8	2
1:A:13:ASN:CG	1:A:14:TYR:H	0.44	2.15	15	1
1:A:66:VAL:O	1:A:66:VAL:CG1	0.44	2.65	15	1
1:A:62:PHE:CD2	1:A:68:PHE:CB	0.44	3.01	15	1
1:A:92:LYS:CE	1:A:94:LYS:HZ1	0.44	2.24	16	1
1:A:19:GLU:CA	1:A:28:ARG:HH22	0.44	2.25	20	1
1:A:6:TRP:NE1	1:A:40:ILE:HD13	0.44	2.28	20	1
1:A:6:TRP:NE1	1:A:40:ILE:CD1	0.44	2.81	20	1
1:A:118:VAL:CG1	1:A:122:VAL:O	0.44	2.62	15	12
1:A:129:LYS:NZ	1:A:130:LYS:NZ	0.44	2.66	9	1
1:A:69:ASN:C	1:A:70:CYS:SG	0.44	2.95	16	3
1:A:42:GLN:CD	1:A:47:PHE:CZ	0.44	2.91	14	1
1:A:87:ASN:ND2	1:A:87:ASN:O	0.44	2.51	2	1
1:A:14:TYR:CE2	1:A:18:MET:CE	0.44	3.00	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:34:ASP:O	1:A:36:LEU:HD23	0.44	2.13	13	1
1:A:76:THR:HG22	1:A:95:ARG:NE	0.44	2.28	5	1
1:A:33:HIS:O	1:A:34:ASP:C	0.44	2.56	8	3
1:A:131:ASP:OD2	1:A:131:ASP:O	0.44	2.35	13	1
1:A:77:GLU:C	1:A:96:THR:OG1	0.44	2.57	10	1
1:A:13:ASN:O	1:A:14:TYR:C	0.44	2.56	14	1
1:A:14:TYR:CE2	1:A:34:ASP:OD1	0.43	2.70	3	2
1:A:130:LYS:O	1:A:131:ASP:O	0.43	2.36	10	2
1:A:71:ASN:H	1:A:71:ASN:HD22	0.43	1.51	4	1
1:A:14:TYR:O	1:A:15:ASP:C	0.43	2.56	10	2
1:A:34:ASP:O	1:A:126:ARG:NH1	0.43	2.51	13	1
1:A:92:LYS:NZ	1:A:92:LYS:CB	0.43	2.82	20	1
1:A:24:ASN:OD1	1:A:26:VAL:HG23	0.43	2.13	6	1
1:A:64:LEU:CG	1:A:64:LEU:O	0.43	2.66	7	1
1:A:8:VAL:HG21	1:A:34:ASP:O	0.43	2.14	12	1
1:A:57:ASN:N	1:A:57:ASN:ND2	0.43	2.65	16	1
1:A:14:TYR:CZ	1:A:18:MET:HE2	0.43	2.48	17	1
1:A:129:LYS:CG	1:A:130:LYS:N	0.43	2.82	6	1
1:A:62:PHE:CG	1:A:68:PHE:CD2	0.43	3.06	13	1
1:A:28:ARG:C	1:A:28:ARG:NE	0.43	2.72	2	1
1:A:83:SER:H	1:A:90:ILE:HD12	0.43	1.73	8	1
1:A:13:ASN:C	1:A:13:ASN:OD1	0.43	2.56	15	1
1:A:35:ASN:N	1:A:35:ASN:ND2	0.43	2.65	7	1
1:A:34:ASP:OD2	1:A:126:ARG:NH1	0.43	2.52	10	1
1:A:85:GLU:O	1:A:88:LYS:CE	0.43	2.67	20	1
1:A:36:LEU:HD11	1:A:38:LEU:HD21	0.42	1.91	9	1
1:A:15:ASP:OD2	1:A:15:ASP:N	0.42	2.51	3	1
1:A:36:LEU:CD2	1:A:126:ARG:NH1	0.42	2.82	14	1
1:A:109:ILE:CD1	1:A:114:VAL:HG21	0.42	2.44	2	1
1:A:3:ASP:C	1:A:3:ASP:OD2	0.42	2.57	4	1
1:A:51:GLU:CG	1:A:52:SER:N	0.42	2.81	11	1
1:A:69:ASN:ND2	1:A:69:ASN:O	0.42	2.53	3	2
1:A:118:VAL:HA	1:A:122:VAL:O	0.42	2.13	12	4
1:A:64:LEU:HD12	1:A:64:LEU:C	0.42	2.35	18	1
1:A:85:GLU:CG	1:A:85:GLU:O	0.42	2.66	9	1
1:A:28:ARG:O	1:A:28:ARG:CD	0.42	2.67	3	1
1:A:116:THR:CG2	1:A:124:ALA:O	0.42	2.68	19	11
1:A:47:PHE:HB2	1:A:62:PHE:CE2	0.42	2.48	17	1
1:A:103:ASN:HD22	1:A:103:ASN:N	0.42	2.08	20	1
1:A:34:ASP:CG	1:A:34:ASP:O	0.42	2.58	13	1
1:A:62:PHE:CZ	1:A:70:CYS:SG	0.42	3.13	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:67:THR:HG22	1:A:79:ARG:HG3	0.42	1.91	9	1
1:A:59:GLU:OE1	1:A:59:GLU:O	0.42	2.37	13	1
1:A:99:GLY:C	1:A:101:GLU:H	0.42	2.18	20	2
1:A:91:GLY:O	1:A:104:THR:CG2	0.42	2.67	14	5
1:A:11:SER:OG	1:A:125:LYS:O	0.42	2.30	18	1
1:A:100:ASN:O	1:A:101:GLU:HG2	0.41	2.15	20	3
1:A:111:ASP:O	1:A:129:LYS:CD	0.41	2.68	17	1
1:A:40:ILE:HG23	1:A:49:VAL:HG22	0.41	1.92	20	1
1:A:38:LEU:HD21	1:A:128:PHE:CD2	0.41	2.51	3	1
1:A:100:ASN:CB	1:A:119:TYR:OH	0.41	2.69	15	2
1:A:59:GLU:CD	1:A:59:GLU:O	0.41	2.59	13	1
1:A:31:ALA:O	1:A:34:ASP:CG	0.41	2.58	14	1
1:A:89:LEU:O	1:A:106:ARG:N	0.41	2.52	17	1
1:A:84:LEU:C	1:A:84:LEU:HD12	0.41	2.34	5	1
1:A:12:GLU:CD	1:A:125:LYS:HZ1	0.41	2.18	1	1
1:A:79:ARG:NH2	1:A:79:ARG:CB	0.41	2.84	1	1
1:A:87:ASN:CG	1:A:87:ASN:O	0.41	2.58	7	1
1:A:130:LYS:O	1:A:130:LYS:CG	0.41	2.68	13	1
1:A:69:ASN:OD1	1:A:69:ASN:O	0.41	2.37	5	1
1:A:95:ARG:NH2	1:A:100:ASN:OD1	0.41	2.53	8	1
1:A:34:ASP:C	1:A:35:ASN:OD1	0.41	2.59	9	1
1:A:18:MET:SD	1:A:18:MET:N	0.41	2.94	13	1
1:A:36:LEU:HD23	1:A:36:LEU:H	0.41	1.74	19	2
1:A:63:GLU:N	1:A:68:PHE:CE2	0.41	2.87	19	1
1:A:104:THR:OG1	1:A:105:VAL:N	0.41	2.54	15	10
1:A:9:ASP:OD1	1:A:9:ASP:C	0.41	2.58	4	1
1:A:68:PHE:C	1:A:69:ASN:OD1	0.41	2.58	11	1
1:A:28:ARG:O	1:A:31:ALA:N	0.41	2.53	13	1
1:A:59:GLU:O	1:A:60:CYS:SG	0.41	2.78	5	1
1:A:78:LEU:N	1:A:78:LEU:HD23	0.41	2.30	10	1
1:A:98:ASN:O	1:A:100:ASN:N	0.41	2.54	3	1
1:A:35:ASN:O	1:A:36:LEU:C	0.41	2.57	7	1
1:A:49:VAL:CG1	1:A:49:VAL:O	0.41	2.68	10	1
1:A:93:PHE:CB	1:A:102:LEU:HD23	0.41	2.46	5	1
1:A:117:TYR:CZ	1:A:126:ARG:CZ	0.41	3.03	7	1
1:A:39:THR:C	1:A:40:ILE:HD12	0.41	2.34	7	1
1:A:15:ASP:CG	1:A:16:LYS:N	0.41	2.74	12	2
1:A:33:HIS:CD2	1:A:33:HIS:N	0.41	2.89	14	1
1:A:130:LYS:O	1:A:131:ASP:CG	0.41	2.59	16	1
1:A:68:PHE:C	1:A:69:ASN:ND2	0.41	2.74	20	1
1:A:109:ILE:HD12	1:A:114:VAL:CG2	0.40	2.46	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:38:LEU:CD1	1:A:38:LEU:N	0.40	2.84	9	1
1:A:47:PHE:CD2	1:A:47:PHE:C	0.40	2.94	16	1
1:A:18:MET:O	1:A:23:VAL:HG23	0.40	2.16	19	1
1:A:87:ASN:O	1:A:87:ASN:CG	0.40	2.60	20	1
1:A:24:ASN:ND2	1:A:26:VAL:HG23	0.40	2.32	10	1
1:A:85:GLU:OE1	1:A:88:LYS:CE	0.40	2.69	10	1
1:A:119:TYR:O	1:A:121:GLY:N	0.40	2.54	18	1
1:A:3:ASP:N	1:A:3:ASP:OD2	0.40	2.51	19	1
1:A:107:GLU:HG3	1:A:108:ILE:N	0.40	2.31	7	3
1:A:71:ASN:HA	1:A:76:THR:O	0.40	2.16	19	2
1:A:36:LEU:CB	1:A:53:SER:OG	0.40	2.69	11	1
1:A:62:PHE:CB	1:A:68:PHE:CZ	0.40	3.05	17	1
1:A:37:LYS:C	1:A:38:LEU:HD12	0.40	2.36	1	1
1:A:95:ARG:O	1:A:99:GLY:CA	0.40	2.69	16	1
1:A:112:GLU:OE1	1:A:129:LYS:NZ	0.40	2.53	2	1
1:A:34:ASP:O	1:A:36:LEU:N	0.40	2.53	11	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	128/131 (98%)	100±2 (78±1%)	18±2 (14±2%)	11±2 (8±1%)	2	13
All	All	2560/2620 (98%)	1990 (78%)	359 (14%)	211 (8%)	2	13

All 17 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	110	GLY	20
1	A	8	VAL	20
1	A	56	ARG	20
1	A	54	ALA	19
1	A	74	ASP	19
1	A	24	ASN	17

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Mol	Chain	Res	Type	Models (Total)
1	A	44	GLY	17
1	A	109	ILE	16
1	A	101	GLU	16
1	A	4	SER	16
1	A	32	ALA	11
1	A	34	ASP	10
1	A	33	HIS	5
1	A	81	THR	2
1	A	100	ASN	1
1	A	3	ASP	1
1	A	36	LEU	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	114/115 (99%)	85±4 (75±3%)	29±4 (25±3%)	2	24
All	All	2280/2300 (99%)	1706 (75%)	574 (25%)	2	24

All 84 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	122	VAL	20
1	A	14	TYR	20
1	A	81	THR	20
1	A	84	LEU	20
1	A	96	THR	20
1	A	68	PHE	20
1	A	76	THR	20
1	A	61	VAL	19
1	A	116	THR	19
1	A	78	LEU	19
1	A	117	TYR	19
1	A	8	VAL	18
1	A	36	LEU	17
1	A	53	SER	16

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Mol	Chain	Res	Type	Models (Total)
1	A	45	ASN	16
1	A	88	LYS	14
1	A	103	ASN	14
1	A	67	THR	13
1	A	71	ASN	12
1	A	69	ASN	11
1	A	62	PHE	11
1	A	4	SER	10
1	A	83	SER	9
1	A	41	THR	8
1	A	56	ARG	8
1	A	38	LEU	7
1	A	46	LYS	7
1	A	85	GLU	7
1	A	119	TYR	7
1	A	57	ASN	6
1	A	21	MET	6
1	A	108	ILE	6
1	A	60	CYS	6
1	A	79	ARG	5
1	A	113	LEU	5
1	A	39	THR	5
1	A	34	ASP	5
1	A	58	ILE	5
1	A	74	ASP	5
1	A	27	LYS	5
1	A	111	ASP	5
1	A	18	MET	5
1	A	59	GLU	5
1	A	98	ASN	4
1	A	40	ILE	4
1	A	28	ARG	4
1	A	12	GLU	4
1	A	35	ASN	4
1	A	24	ASN	3
1	A	107	GLU	3
1	A	130	LYS	3
1	A	87	ASN	2
1	A	15	ASP	2
1	A	3	ASP	2
1	A	13	ASN	2
1	A	50	LYS	2

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Mol	Chain	Res	Type	Models (Total)
1	A	55	PHE	2
1	A	126	ARG	2
1	A	16	LYS	2
1	A	11	SER	2
1	A	37	LYS	2
1	A	33	HIS	2
1	A	90	ILE	2
1	A	47	PHE	2
1	A	29	LYS	2
1	A	92	LYS	2
1	A	102	LEU	2
1	A	52	SER	2
1	A	106	ARG	1
1	A	120	GLU	1
1	A	7	LYS	1
1	A	131	ASP	1
1	A	125	LYS	1
1	A	95	ARG	1
1	A	94	LYS	1
1	A	42	GLN	1
1	A	20	LYS	1
1	A	97	ASP	1
1	A	112	GLU	1
1	A	49	VAL	1
1	A	100	ASN	1
1	A	64	LEU	1
1	A	6	TRP	1
1	A	9	ASP	1

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 monosaccharides in this entry.

6.6 Ligand geometry

There are no ligands in this entry.

6.7 Other polymers

There are no such molecules in this entry.

6.8 Polymer linkage issues

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 79% for the well-defined parts and 78% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *fabp6070c.str*

7.1.1 Bookkeeping

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	1378
Number of shifts mapped to atoms	1378
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	5

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	131	-0.08 ± 0.12	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	121	-0.34 ± 0.13	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	130	-1.07 ± 0.28	Should be applied

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 79%, i.e. 1283 atoms were assigned a chemical shift out of a possible 1630. 1 out of 20 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	514/645 (80%)	257/258 (100%)	129/258 (50%)	128/129 (99%)
Sidechain	689/867 (79%)	425/503 (84%)	251/316 (79%)	13/48 (27%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	80/118 (68%)	51/63 (81%)	27/52 (52%)	2/3 (67%)
Overall	1283/1630 (79%)	733/824 (89%)	407/626 (65%)	143/180 (79%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 78%, i.e. 1298 atoms were assigned a chemical shift out of a possible 1654. 1 out of 20 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	521/655 (80%)	260/262 (99%)	131/262 (50%)	130/131 (99%)
Sidechain	694/872 (80%)	428/506 (85%)	253/318 (80%)	13/48 (27%)
Aromatic	83/127 (65%)	53/68 (78%)	28/56 (50%)	2/3 (67%)
Overall	1298/1654 (78%)	741/836 (89%)	412/636 (65%)	145/182 (80%)

7.1.4 Statistically unusual chemical shifts [i](#)

The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	120	GLU	HG2	0.74	3.33 – 1.23	-7.3
1	A	113	LEU	HB2	-0.73	3.32 – -0.08	-6.9
1	A	82	TRP	HD1	5.22	8.95 – 5.35	-5.4
1	A	91	GLY	HA2	2.05	5.87 – 2.07	-5.1
1	A	47	PHE	HB2	1.14	4.85 – 1.15	-5.0

7.1.5 Random Coil Index (RCI) plots [i](#)

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.

Random coil index (RCI) for chain A:

