



# Full wwPDB NMR Structure Validation Report ⓘ

May 28, 2020 – 10:31 pm BST

PDB ID : 2JNP  
Title : Solution structure of matrix metalloproteinase 3 (MMP-3) in the presence of N-isobutyl-N-[4-methoxyphenylsulfonyl]glycyl hydroxamic acid (NNGH)  
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Deposited on : 2007-01-30

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A user guide is available at

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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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	:	1.8.5 (274361), CSD as541be (2020)
buster-report	:	1.1.7 (2018)
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	:	2.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

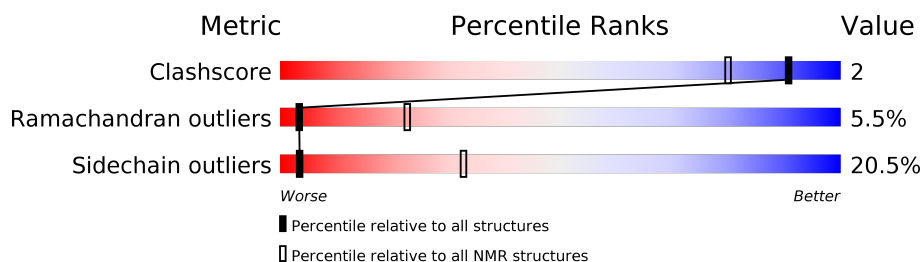
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*


The overall completeness of chemical shifts assignment is 61%.

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  $\geq 3$ , 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	161	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA and RNA chains that are outliers for geometric criteria:

Mol	Chain	Compound	Res	Total models with violations	
				Chirality	Geometry
4	A	NGH	253	9	-

## 2 Ensemble composition and analysis

This entry contains 25 models. Model 14 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:89-A:247 (159)	0.61	14

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	1, 2, 3, 4, 5, 6, 7, 9, 10, 11, 12, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 25
2	8, 13
Single-model clusters	24

### 3 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2533 atoms, of which 1230 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Matrix metalloproteinase-3.

Mol	Chain	Residues	Atoms						Trace
1	A	161	Total	C	H	N	O	S	0
			2489	818	1211	213	245	2	

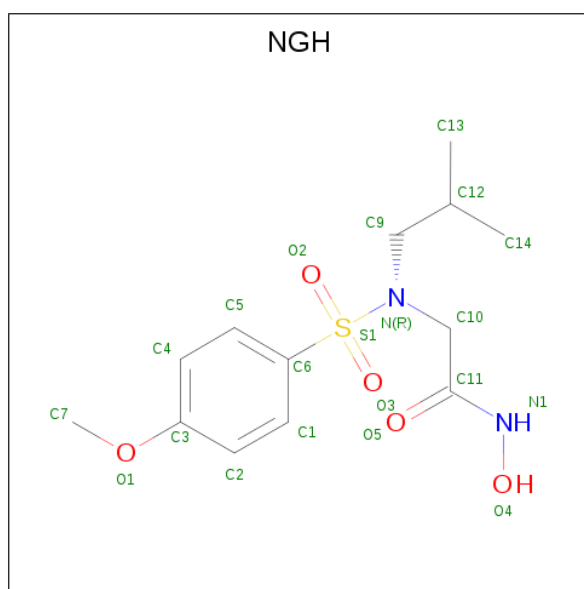
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	
2	A	2	Total	Zn
			2	2

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	
3	A	2	Total	Ca
			2	2

- Molecule 4 is N-ISOBUTYL-N-[4-METHOXYPHENYLSULFONYL]GLYCYL HYDROX-AMIC ACID (three-letter code: NGH) (formula: C<sub>13</sub>H<sub>20</sub>N<sub>2</sub>O<sub>5</sub>S).



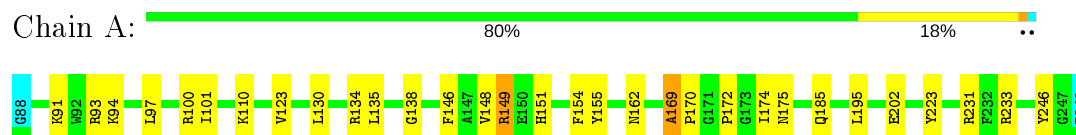
Mol	Chain	Residues	Atoms					
4	A	1	Total	C	H	N	O	S
			40	13	19	2	5	1

## 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: Matrix metalloproteinase-3

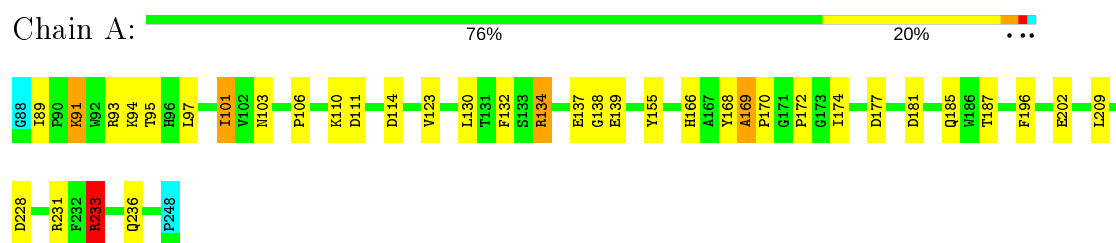


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

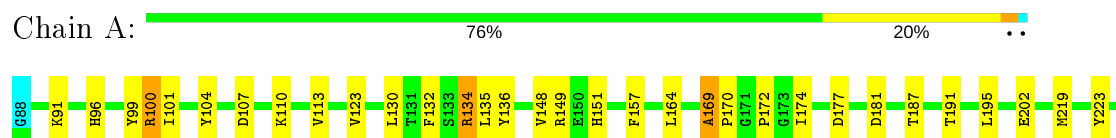
#### 4.2.1 Score per residue for model 1

- Molecule 1: Matrix metalloproteinase-3



#### 4.2.2 Score per residue for model 2

- Molecule 1: Matrix metalloproteinase-3

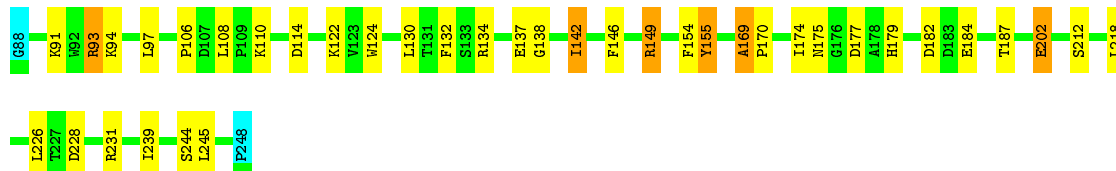




### 4.2.3 Score per residue for model 3

- Molecule 1: Matrix metalloproteinase-3

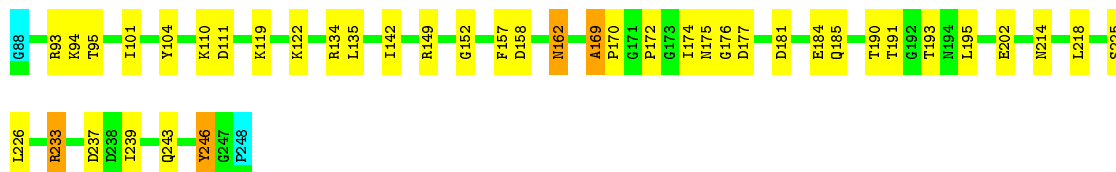
Chain A: 75% 20% ..



### 4.2.4 Score per residue for model 4

- Molecule 1: Matrix metalloproteinase-3

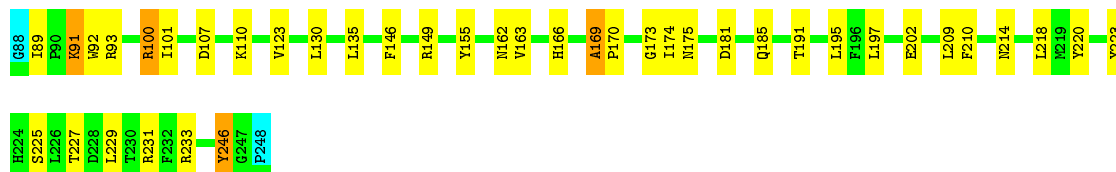
Chain A: 73% 23% ..



### 4.2.5 Score per residue for model 5

- Molecule 1: Matrix metalloproteinase-3

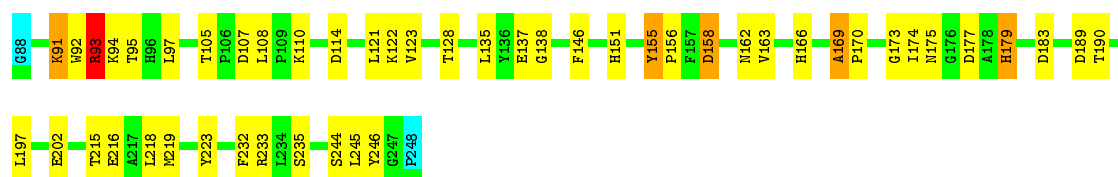
Chain A: 74% 22% ..



### 4.2.6 Score per residue for model 6

- Molecule 1: Matrix metalloproteinase-3

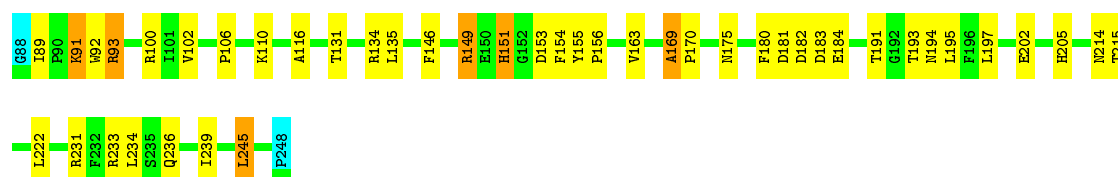
Chain A: 68% 27% ..



#### 4.2.7 Score per residue for model 7

- Molecule 1: Matrix metalloproteinase-3

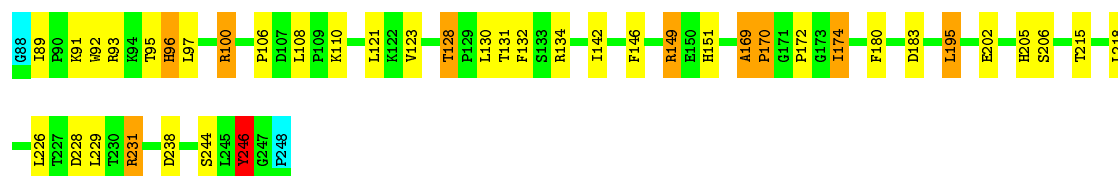
Chain A: 71% 24% ..



#### 4.2.8 Score per residue for model 8

- Molecule 1: Matrix metalloproteinase-3

Chain A: 73% 19% 6% ..



#### 4.2.9 Score per residue for model 9

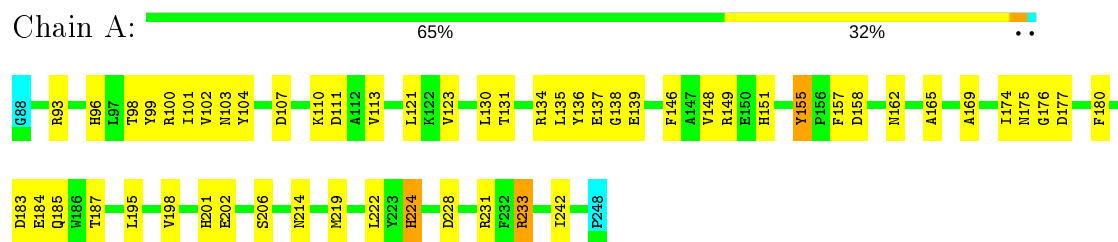
- Molecule 1: Matrix metalloproteinase-3

Chain A: 74% 22% ..



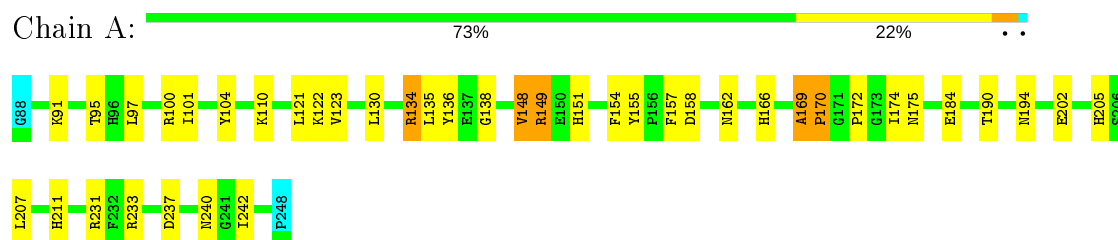
#### 4.2.10 Score per residue for model 10

- Molecule 1: Matrix metalloproteinase-3



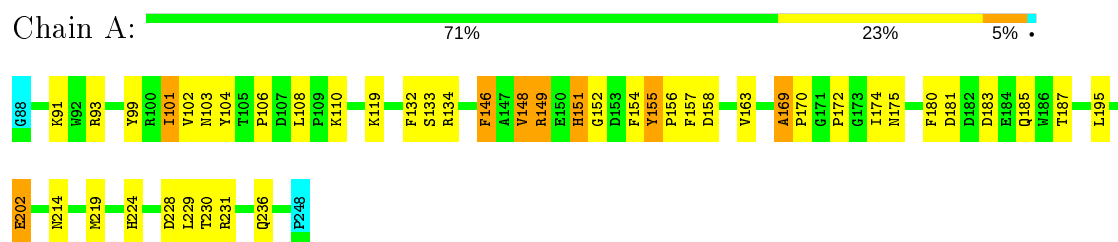
#### 4.2.11 Score per residue for model 11

- Molecule 1: Matrix metalloproteinase-3



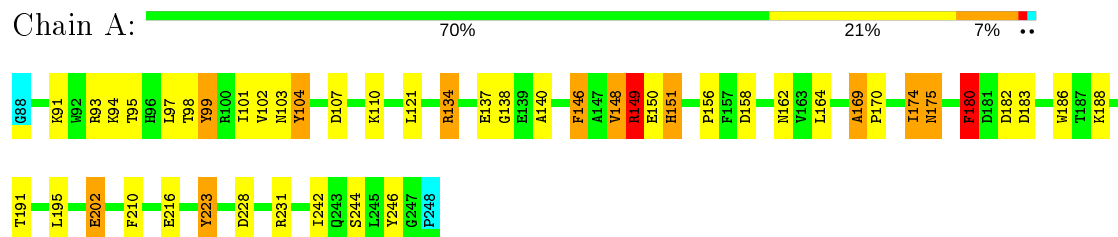
#### 4.2.12 Score per residue for model 12

- Molecule 1: Matrix metalloproteinase-3



#### 4.2.13 Score per residue for model 13

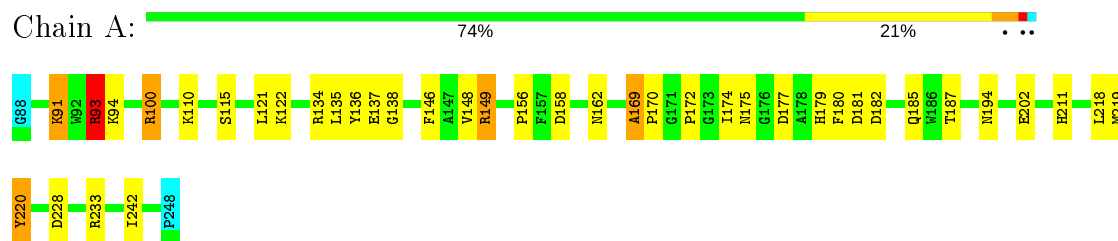
- Molecule 1: Matrix metalloproteinase-3





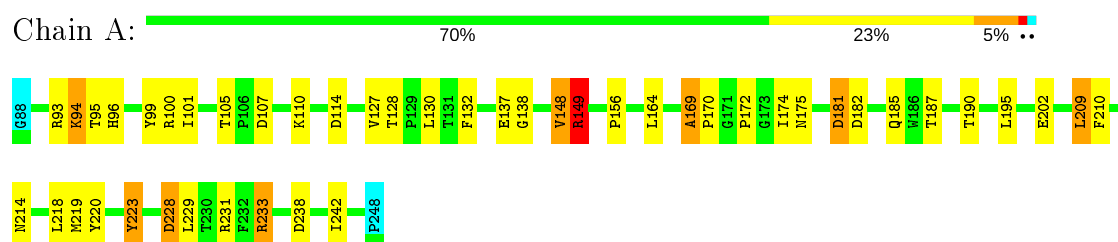
## 4.2.14 Score per residue for model 14 (medoid)

- Molecule 1: Matrix metalloproteinase-3



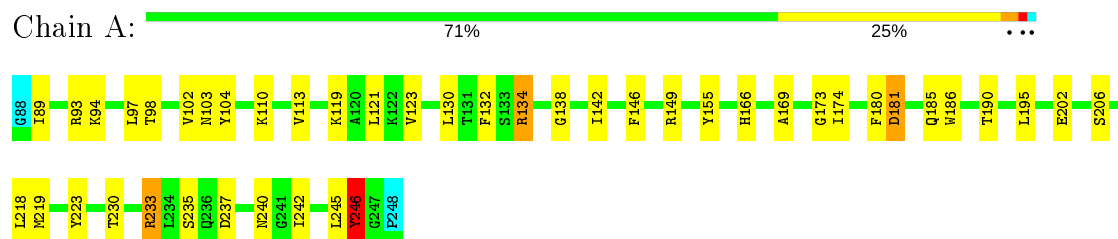
## 4.2.15 Score per residue for model 15

- Molecule 1: Matrix metalloproteinase-3



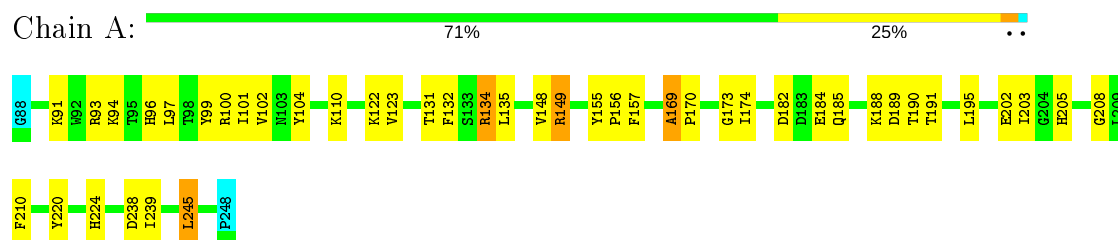
## 4.2.16 Score per residue for model 16

- Molecule 1: Matrix metalloproteinase-3



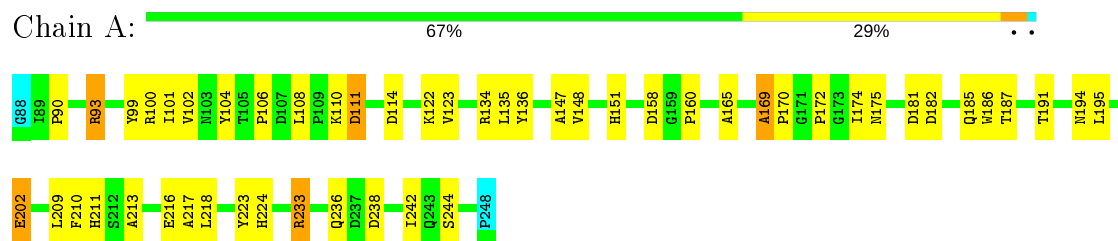
## 4.2.17 Score per residue for model 17

- Molecule 1: Matrix metalloproteinase-3



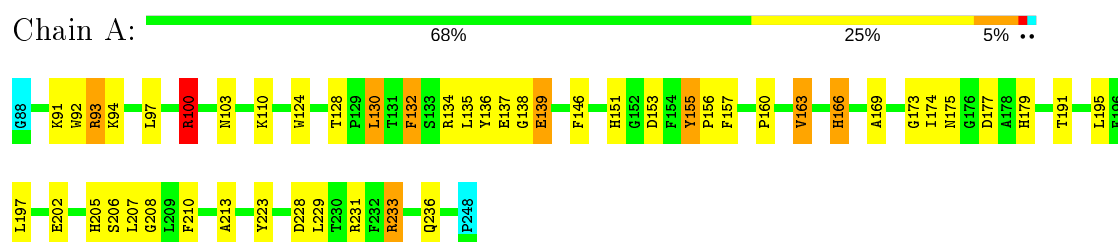
## 4.2.18 Score per residue for model 18

- Molecule 1: Matrix metalloproteinase-3



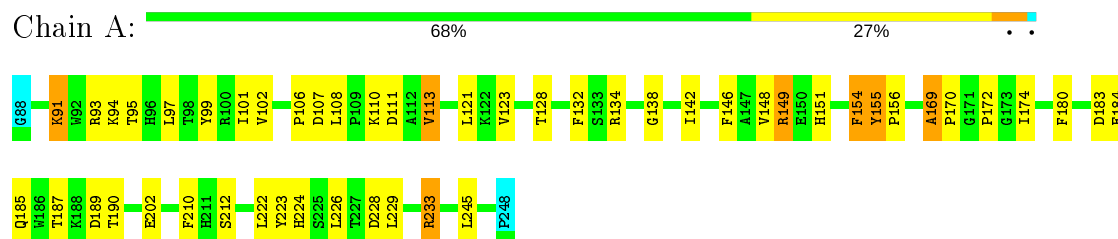
## 4.2.19 Score per residue for model 19

- Molecule 1: Matrix metalloproteinase-3



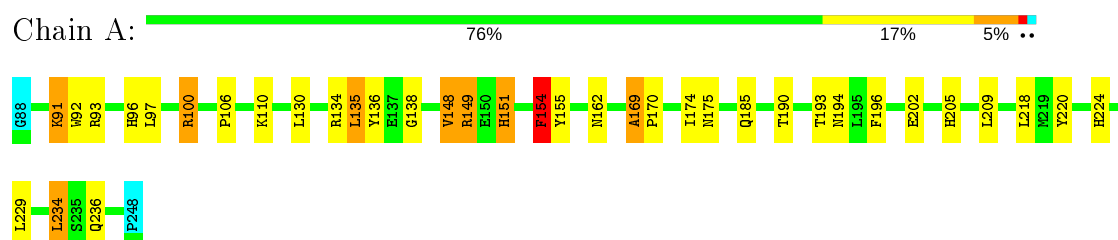
## 4.2.20 Score per residue for model 20

- Molecule 1: Matrix metalloproteinase-3



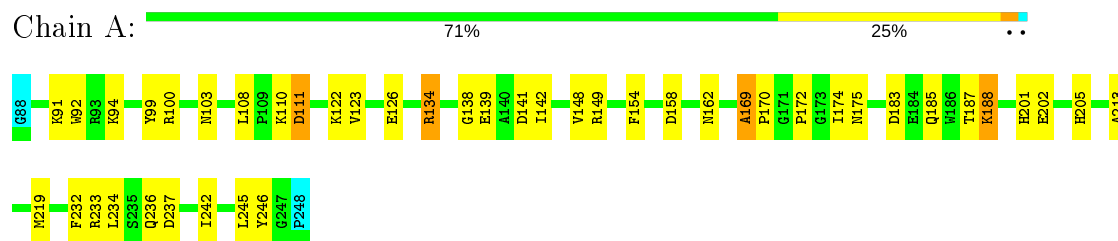
## 4.2.21 Score per residue for model 21

- Molecule 1: Matrix metalloproteinase-3



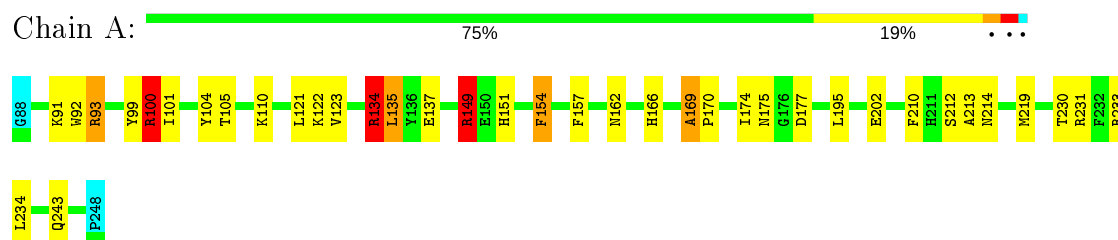
### 4.2.22 Score per residue for model 22

- Molecule 1: Matrix metalloproteinase-3



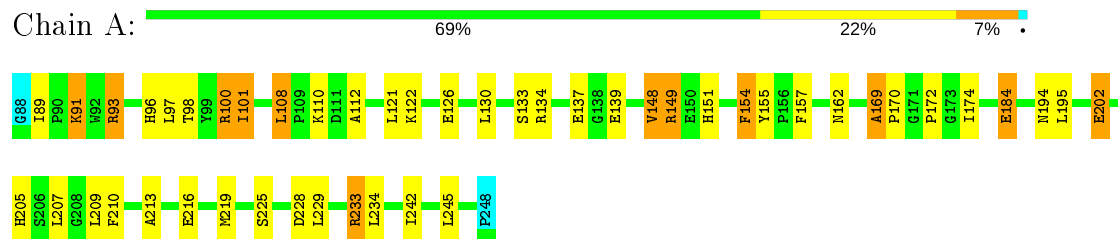
### 4.2.23 Score per residue for model 23

- Molecule 1: Matrix metalloproteinase-3



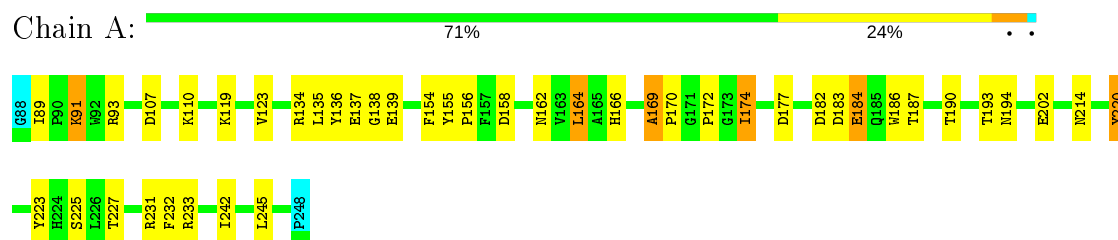
### 4.2.24 Score per residue for model 24

- Molecule 1: Matrix metalloproteinase-3



### 4.2.25 Score per residue for model 25

- Molecule 1: Matrix metalloproteinase-3



## 5 Refinement protocol and experimental data overview

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

Of the 400 calculated structures, 25 were deposited, based on the following criterion: *target function*.

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

Software name	Classification	Version
CYANA	structure solution	
Amber	refinement	8
CSI	structure solution	2.0

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 6 of this report.

Chemical shift file(s)	input_cs.cif
Number of chemical shift lists	1
Total number of shifts	1374
Number of shifts mapped to atoms	1374
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	61%

No validations of the models with respect to experimental NMR restraints is performed at this time.

COVALENT-GEOMETRY INFOmissingINFO

### 5.1 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	1266	1199	1198	4±2
4	A	21	19	20	0±0
All	All	32275	30450	30447	101

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 2.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:169:ALA:HB3	1:A:170:PRO:HD3	0.59	1.74	9	20
1:A:91:LYS:HE2	1:A:169:ALA:HB1	0.56	1.77	20	3
1:A:100:ARG:NH2	1:A:135:LEU:HD12	0.56	2.14	21	1
1:A:91:LYS:CE	1:A:169:ALA:HB1	0.56	2.31	20	2
1:A:176:GLY:HA2	1:A:206:SER:HB2	0.53	1.80	10	1
1:A:169:ALA:HB3	1:A:170:PRO:CD	0.53	2.34	14	11
1:A:164:LEU:HD21	1:A:193:THR:HG23	0.53	1.81	25	1
1:A:130:LEU:HD21	1:A:132:PHE:CD2	0.52	2.39	19	1
1:A:146:PHE:CZ	1:A:180:PHE:CD2	0.52	2.97	13	1
1:A:165:ALA:HB1	1:A:202:GLU:CD	0.52	2.25	18	1
1:A:148:VAL:HG22	1:A:149:ARG:H	0.51	1.66	11	5
1:A:234:LEU:H	1:A:234:LEU:HD23	0.51	1.66	23	1
1:A:101:ILE:H	1:A:101:ILE:HD12	0.50	1.66	4	6
1:A:209:LEU:HD11	1:A:238:ASP:HA	0.47	1.85	9	1
1:A:100:ARG:HH22	1:A:135:LEU:HD12	0.47	1.69	21	1
1:A:101:ILE:HD12	1:A:101:ILE:H	0.47	1.69	1	2
1:A:146:PHE:CD1	1:A:180:PHE:HB2	0.47	2.45	13	1
1:A:108:LEU:HD13	1:A:112:ALA:CB	0.46	2.40	24	1
1:A:104:TYR:HA	1:A:113:VAL:HG11	0.46	1.88	2	2
1:A:128:THR:HB	1:A:246:TYR:CE1	0.46	2.46	8	1
1:A:116:ALA:HB2	1:A:195:LEU:HD13	0.46	1.88	7	1
1:A:208:GLY:HA3	1:A:245:LEU:HD11	0.46	1.88	17	1
4:A:253:NGH:H133	4:A:253:NGH:H102	0.46	1.88	20	1
1:A:100:ARG:HH21	1:A:135:LEU:C	0.45	2.15	21	1
1:A:99:TYR:CE2	1:A:121:LEU:HD22	0.44	2.48	13	1
1:A:134:ARG:C	1:A:135:LEU:HD23	0.44	2.32	23	1
1:A:146:PHE:CD2	1:A:186:TRP:CH2	0.44	3.06	13	1
1:A:234:LEU:CD2	1:A:234:LEU:H	0.44	2.26	24	1
1:A:94:LYS:HE3	1:A:96:HIS:O	0.43	2.13	15	1
1:A:116:ALA:HB2	1:A:195:LEU:CD1	0.43	2.44	7	1
1:A:213:ALA:HA	1:A:217:ALA:HB3	0.43	1.90	18	1
1:A:103:ASN:HB2	1:A:146:PHE:CD1	0.43	2.48	16	1
1:A:101:ILE:N	1:A:101:ILE:HD12	0.43	2.29	17	2
1:A:146:PHE:CE1	1:A:180:PHE:CG	0.42	3.06	13	1
1:A:103:ASN:HB2	1:A:146:PHE:CD2	0.42	2.49	12	1
1:A:169:ALA:HB2	1:A:205:HIS:O	0.42	2.14	17	2
1:A:169:ALA:CB	1:A:170:PRO:CD	0.42	2.98	23	3
1:A:234:LEU:H	1:A:234:LEU:HD22	0.42	1.74	21	1
1:A:197:LEU:CD2	4:A:253:NGH:H71	0.42	2.44	6	1
1:A:98:THR:HG22	1:A:133:SER:HB3	0.42	1.92	24	1
1:A:165:ALA:HB3	1:A:198:VAL:CG1	0.42	2.44	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:188:LYS:HA	1:A:188:LYS:HE2	0.42	1.90	22	1
1:A:174:ILE:O	1:A:175:ASN:C	0.42	2.58	13	1
1:A:216:GLU:H	1:A:216:GLU:CD	0.42	2.18	24	1
1:A:211:HIS:CD2	1:A:211:HIS:N	0.41	2.88	18	1
1:A:147:ALA:HB1	1:A:151:HIS:CG	0.41	2.51	18	1
1:A:108:LEU:HD12	1:A:195:LEU:CD2	0.41	2.46	8	1
1:A:100:ARG:HH21	1:A:139:GLU:C	0.40	2.19	19	1
1:A:103:ASN:HB2	1:A:146:PHE:CG	0.40	2.52	13	1
1:A:216:GLU:CD	1:A:216:GLU:N	0.40	2.75	6	1
1:A:96:HIS:HA	1:A:131:THR:O	0.40	2.17	8	1
1:A:169:ALA:HB2	1:A:206:SER:HA	0.40	1.94	8	1
1:A:99:TYR:CE2	1:A:132:PHE:CG	0.40	3.09	12	1
1:A:142:ILE:HG23	1:A:176:GLY:O	0.40	2.16	4	1

## 5.2 Torsion angles ⓘ

### 5.2.1 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	159/161 (99%)	126±4 (79±3%)	24±4 (15±3%)	9±2 (6±1%)	3	23
All	All	3975/4025 (99%)	3146 (79%)	609 (15%)	220 (6%)	3	23

All 45 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	169	ALA	25
1	A	175	ASN	16
1	A	149	ARG	15
1	A	148	VAL	14
1	A	91	LYS	14
1	A	138	GLY	14
1	A	172	PRO	13
1	A	156	PRO	10
1	A	154	PHE	9

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Mol	Chain	Res	Type	Models (Total)
1	A	106	PRO	8
1	A	190	THR	7
1	A	173	GLY	6
1	A	137	GLU	6
1	A	162	ASN	6
1	A	163	VAL	5
1	A	213	ALA	4
1	A	139	GLU	4
1	A	224	HIS	3
1	A	245	LEU	3
1	A	194	ASN	3
1	A	228	ASP	3
1	A	89	ILE	3
1	A	93	ARG	3
1	A	152	GLY	2
1	A	229	LEU	2
1	A	225	SER	2
1	A	210	PHE	2
1	A	182	ASP	1
1	A	183	ASP	1
1	A	195	LEU	1
1	A	174	ILE	1
1	A	212	SER	1
1	A	157	PHE	1
1	A	208	GLY	1
1	A	223	TYR	1
1	A	129	PRO	1
1	A	216	GLU	1
1	A	160	PRO	1
1	A	185	GLN	1
1	A	90	PRO	1
1	A	186	TRP	1
1	A	191	THR	1
1	A	218	LEU	1
1	A	219	MET	1
1	A	140	ALA	1

### 5.2.2 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	134/135 (99%)	107±4 (79±3%)	27±4 (21±3%)	3	33
All	All	3350/3375 (99%)	2663 (79%)	687 (21%)	3	33

All 116 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	110	LYS	25
1	A	174	ILE	24
1	A	123	VAL	15
1	A	155	TYR	14
1	A	195	LEU	14
1	A	135	LEU	14
1	A	151	HIS	14
1	A	94	LYS	13
1	A	185	GLN	13
1	A	97	LEU	13
1	A	93	ARG	12
1	A	130	LEU	12
1	A	187	THR	12
1	A	146	PHE	11
1	A	233	ARG	11
1	A	242	ILE	11
1	A	132	PHE	10
1	A	122	LYS	10
1	A	121	LEU	10
1	A	134	ARG	10
1	A	218	LEU	10
1	A	91	LYS	10
1	A	166	HIS	9
1	A	210	PHE	9
1	A	219	MET	9
1	A	102	VAL	8
1	A	136	TYR	8
1	A	157	PHE	8
1	A	101	ILE	8
1	A	107	ASP	8
1	A	214	ASN	8
1	A	95	THR	8
1	A	245	LEU	8
1	A	92	TRP	8
1	A	183	ASP	7
1	A	182	ASP	7

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Mol	Chain	Res	Type	Models (Total)
1	A	108	LEU	7
1	A	236	GLN	7
1	A	158	ASP	7
1	A	162	ASN	7
1	A	180	PHE	7
1	A	191	THR	7
1	A	205	HIS	7
1	A	149	ARG	6
1	A	209	LEU	6
1	A	229	LEU	6
1	A	96	HIS	6
1	A	184	GLU	6
1	A	104	TYR	6
1	A	246	TYR	6
1	A	137	GLU	5
1	A	114	ASP	5
1	A	128	THR	5
1	A	111	ASP	5
1	A	179	HIS	5
1	A	181	ASP	5
1	A	100	ARG	5
1	A	224	HIS	5
1	A	142	ILE	5
1	A	228	ASP	5
1	A	194	ASN	5
1	A	223	TYR	5
1	A	99	TYR	5
1	A	154	PHE	5
1	A	89	ILE	4
1	A	237	ASP	4
1	A	202	GLU	4
1	A	119	LYS	4
1	A	239	ILE	4
1	A	164	LEU	4
1	A	244	SER	4
1	A	226	LEU	4
1	A	103	ASN	4
1	A	201	HIS	3
1	A	222	LEU	3
1	A	197	LEU	3
1	A	234	LEU	3
1	A	189	ASP	3

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Mol	Chain	Res	Type	Models (Total)
1	A	230	THR	3
1	A	193	THR	3
1	A	207	LEU	3
1	A	105	THR	3
1	A	124	TRP	3
1	A	243	GLN	3
1	A	98	THR	3
1	A	131	THR	3
1	A	220	TYR	3
1	A	188	LYS	3
1	A	215	THR	3
1	A	212	SER	2
1	A	113	VAL	2
1	A	206	SER	2
1	A	190	THR	2
1	A	225	SER	2
1	A	196	PHE	2
1	A	238	ASP	2
1	A	186	TRP	2
1	A	235	SER	2
1	A	227	THR	2
1	A	126	GLU	2
1	A	177	ASP	2
1	A	153	ASP	2
1	A	240	ASN	2
1	A	133	SER	1
1	A	163	VAL	1
1	A	150	GLU	1
1	A	170	PRO	1
1	A	115	SER	1
1	A	203	ILE	1
1	A	141	ASP	1
1	A	231	ARG	1
1	A	232	PHE	1
1	A	216	GLU	1
1	A	139	GLU	1
1	A	175	ASN	1
1	A	127	VAL	1

### 5.2.3 RNA ⓘ

There are no RNA molecules in this entry.

### 5.3 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 5.4 Carbohydrates [i](#)

There are no carbohydrates in this entry.

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### 5.5 Other polymers [i](#)

There are no such molecules in this entry.

### 5.6 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 61% for the well-defined parts and 61% for the entire structure.

### 6.1 Chemical shift list 1

File name: input\_cs.cif

Chemical shift list name: *assigned\_chem\_shift\_list\_1*

#### 6.1.1 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	1374
Number of shifts mapped to atoms	1374
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	9

#### 6.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	121	$2.58 \pm 0.25$	Should be applied
$^{13}\text{C}_\beta$	110	$2.77 \pm 0.22$	Should be applied
$^{13}\text{C}'$	0	—	None (insufficient data)
$^{15}\text{N}$	146	$0.17 \pm 0.39$	None needed ( $< 0.5$ ppm)

#### 6.1.3 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 61%, i.e. 1173 atoms were assigned a chemical shift out of a possible 1922. 12 out of 24 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	558/777 (72%)	291/309 (94%)	121/318 (38%)	146/150 (97%)
Sidechain	578/917 (63%)	366/535 (68%)	206/349 (59%)	6/33 (18%)

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	<b>Total</b>	<b><sup>1</sup>H</b>	<b><sup>13</sup>C</b>	<b><sup>15</sup>N</b>
Aromatic	37/228 (16%)	34/122 (28%)	0/95 (0%)	3/11 (27%)
Overall	1173/1922 (61%)	691/966 (72%)	327/762 (43%)	155/194 (80%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 61%, i.e. 1174 atoms were assigned a chemical shift out of a possible 1939. 12 out of 24 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	<b>Total</b>	<b><sup>1</sup>H</b>	<b><sup>13</sup>C</b>	<b><sup>15</sup>N</b>
Backbone	558/785 (71%)	291/312 (93%)	121/322 (38%)	146/151 (97%)
Sidechain	579/926 (63%)	367/541 (68%)	206/352 (59%)	6/33 (18%)
Aromatic	37/228 (16%)	34/122 (28%)	0/95 (0%)	3/11 (27%)
Overall	1174/1939 (61%)	692/975 (71%)	327/769 (43%)	155/195 (79%)

#### 6.1.4 Statistically unusual chemical shifts ⓘ

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	208	GLY	CA	55.80	51.81 – 38.91	8.1
1	A	105	THR	HB	1.94	5.82 – 2.52	-6.8
1	A	93	ARG	CD	37.30	47.57 – 38.77	-6.7
1	A	91	LYS	CE	47.07	46.00 – 37.80	6.3
1	A	152	GLY	CA	53.30	51.81 – 38.91	6.2
1	A	122	LYS	CE	37.48	46.00 – 37.80	-5.4
1	A	94	LYS	CG	18.85	30.67 – 19.17	-5.3
1	A	91	LYS	CG	19.06	30.67 – 19.17	-5.1
1	A	202	GLU	HB2	0.96	3.08 – 0.98	-5.1

#### 6.1.5 Random Coil Index (RCI) plots ⓘ

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:

