



Full wwPDB NMR Structure Validation Report ⓘ

Aug 10, 2020 – 08:48 AM BST

PDB ID : 6R0J
Title : The N-terminal domain of rhomboid protease YqgP
Authors : Began, J.; Strisovsky, K.; Veverka, V.
Deposited on : 2019-03-13

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:

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 : 2.13.1
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

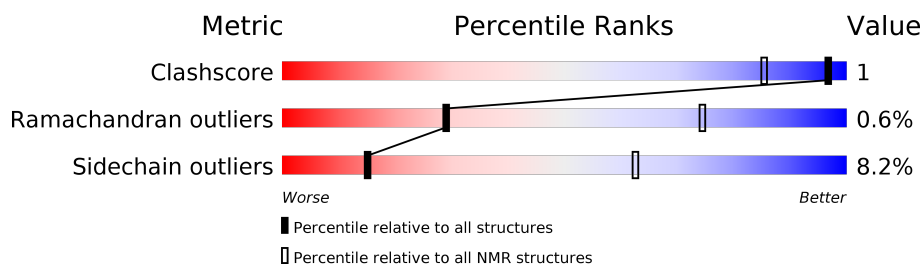
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 84%.

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	185	 73% . . 23%

2 Ensemble composition and analysis ⓘ

This entry contains 30 models. Model 27 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *fewest violations*.

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:25, A:29-A:133, A:146-A:159 (142)	0.43	27

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 3 clusters and 5 single-model clusters were found.

Cluster number	Models
1	1, 2, 3, 5, 8, 9, 10, 13, 14, 19, 20, 25, 27, 29
2	4, 11, 15, 18, 24, 26, 28
3	7, 16, 17, 22
Single-model clusters	6; 12; 21; 23; 30

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3031 atoms, of which 1494 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Rhomboid family serine protease.

Mol	Chain	Residues	Atoms						Trace
1	A	185	Total	C	H	N	O	S	0
			3031	967	1494	271	293	6	

There are 9 discrepancies between the modelled and reference sequences:

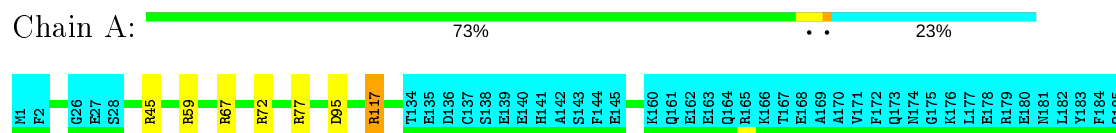
Chain	Residue	Modelled	Actual	Comment	Reference
A	177	LEU	-	expression tag	UNP A0A162T8T3
A	178	GLU	-	expression tag	UNP A0A162T8T3
A	179	ARG	-	expression tag	UNP A0A162T8T3
A	180	GLU	-	expression tag	UNP A0A162T8T3
A	181	ASN	-	expression tag	UNP A0A162T8T3
A	182	LEU	-	expression tag	UNP A0A162T8T3
A	183	TYR	-	expression tag	UNP A0A162T8T3
A	184	PHE	-	expression tag	UNP A0A162T8T3
A	185	GLN	-	expression tag	UNP A0A162T8T3

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: Rhomboid family serine protease

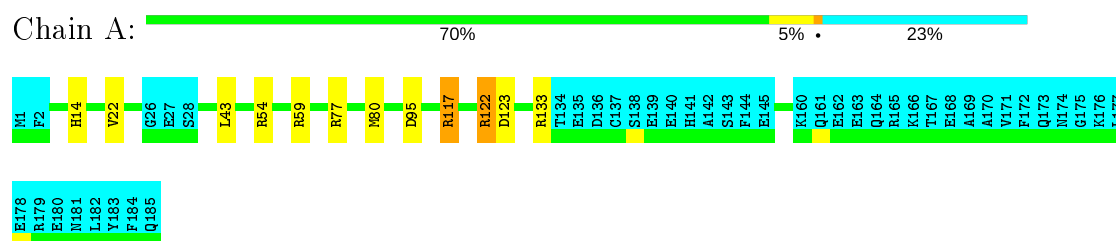


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

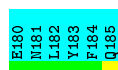
- Molecule 1: Rhomboid family serine protease



4.2.2 Score per residue for model 2

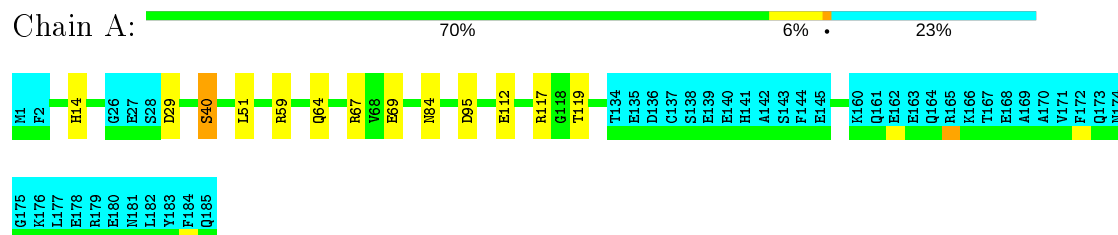
- Molecule 1: Rhomboid family serine protease





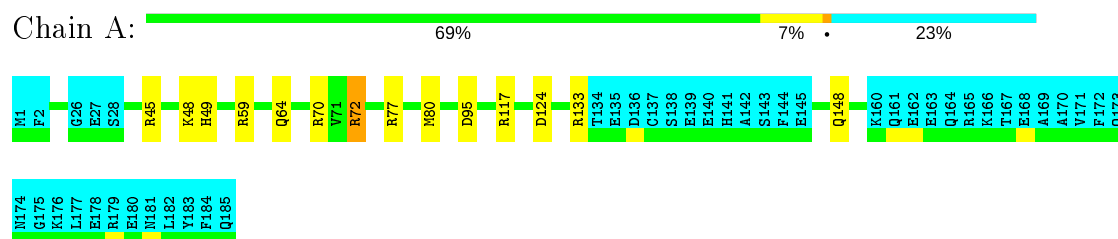
4.2.3 Score per residue for model 3

- Molecule 1: Rhomboid family serine protease



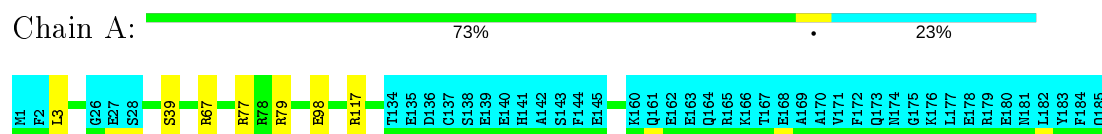
4.2.4 Score per residue for model 4

- Molecule 1: Rhomboid family serine protease



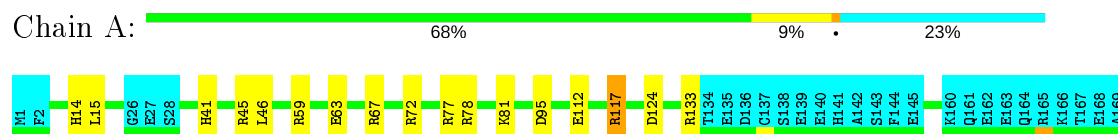
4.2.5 Score per residue for model 5

- Molecule 1: Rhomboid family serine protease



4.2.6 Score per residue for model 6

- Molecule 1: Rhomboid family serine protease



A170
V171
F172
Q173
M174
G175
K176
L177
E178
E180
M181
L182
Y183
F184
Q185

4.2.7 Score per residue for model 7

- Molecule 1: Rhomboid family serine protease

Chain A:  72% 23%

M1 F2 G26 E27 S28 R45 R48 H49 D50 E66 R77 P80 D85 R117 T134 E135 D136 C137 S138 E139 E140 H141 A142 S143 F144 E145 Q148 K160 Q161 E162 Q164 R165 K166 T167 E168 A169 A170 V171 F172 Q173 M174 G175 K176 L177 E178 R179 M181

L182 Y183 F184 Q185

4.2.8 Score per residue for model 8

- Molecule 1: Rhomboid family serine protease

Chain A:  71% 23%

M1 F2 G26 E27 S28 L33 R54 R67 R72 R77 R78 R79 P80 K81 T99 R117 L121 T134 E135 D136 C137 S138 E139 E140 H141 A142 S143 F144 E145 K160 Q161 E162 E163 Q164 M165 K166 T167 E168 A169 A170 V171 F172 Q173 M174 G175 K176 L177 R179

E180 M181 L182 Y183 F184 Q185

4.2.9 Score per residue for model 9

- Molecule 1: Rhomboid family serine protease

Chain A:  70% 5% 23%

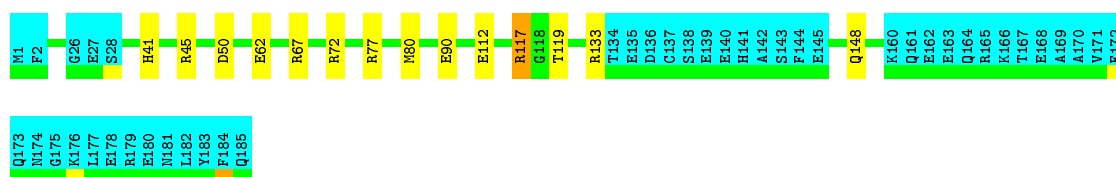
M1 F2 G26 E27 S28 L43 V44 R45 L51 R59 R70 V71 R72 R77 E97 E98 E112 R117 T134 E135 D136 C137 S138 E139 E140 H141 A142 S143 F144 E145 N146 K160 Q161 E162 E163 Q164 R165 K166 T167 E168 A169 A170 V171 F172 Q173 M174 G175 K176 L177

E178 R179 E180 M181 L182 Y183 F184 Q185

4.2.10 Score per residue for model 10

- Molecule 1: Rhomboid family serine protease

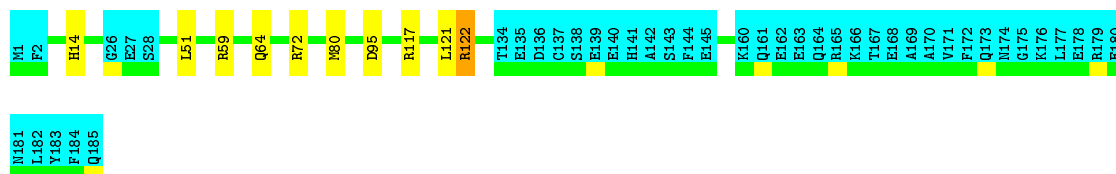
Chain A:  69% 7% 23%



4.2.11 Score per residue for model 11

- Molecule 1: Rhomboid family serine protease

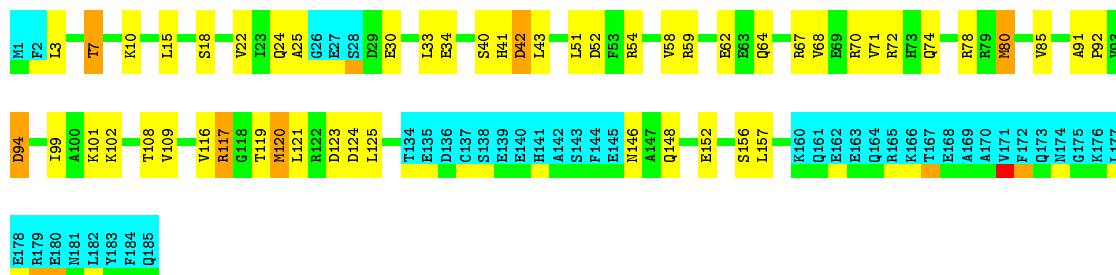
Chain A: 71% 5% 23%



4.2.12 Score per residue for model 12

- Molecule 1: Rhomboid family serine protease

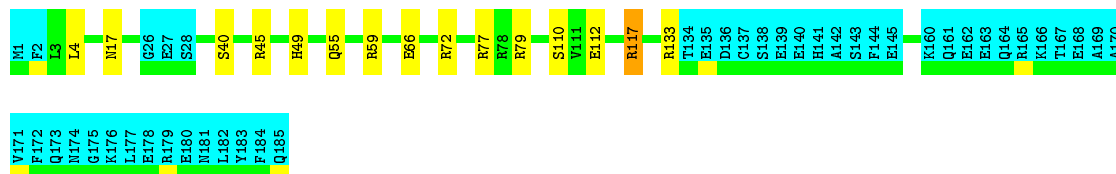
Chain A: 49% 25% 23%



4.2.13 Score per residue for model 13

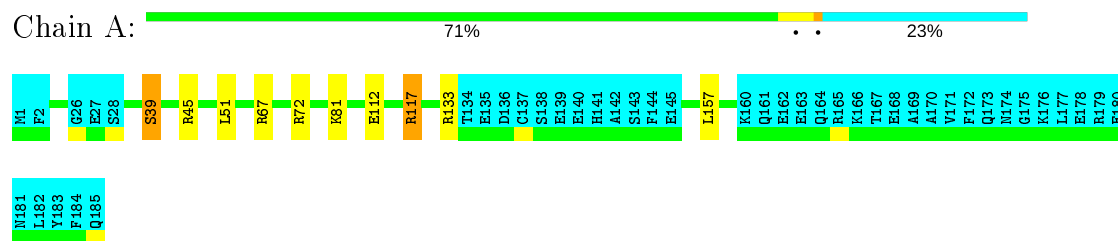
- Molecule 1: Rhomboid family serine protease

Chain A: 69% 8% 23%



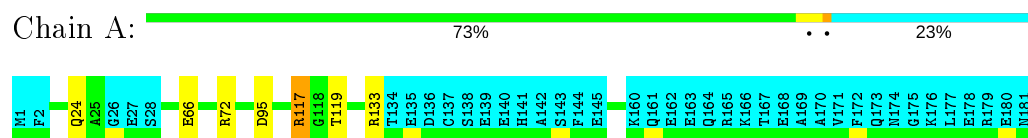
4.2.14 Score per residue for model 14

- Molecule 1: Rhomboid family serine protease



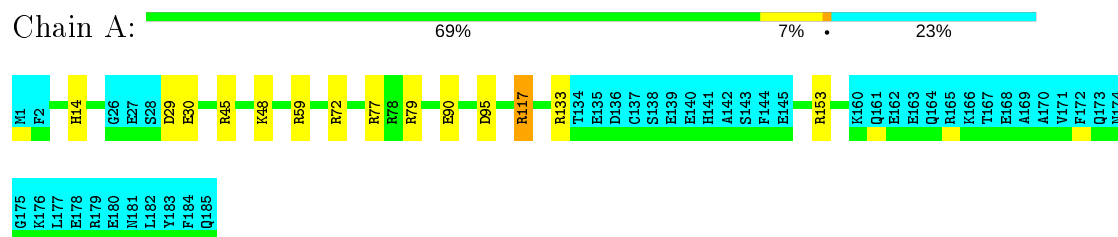
4.2.15 Score per residue for model 15

- Molecule 1: Rhomboid family serine protease



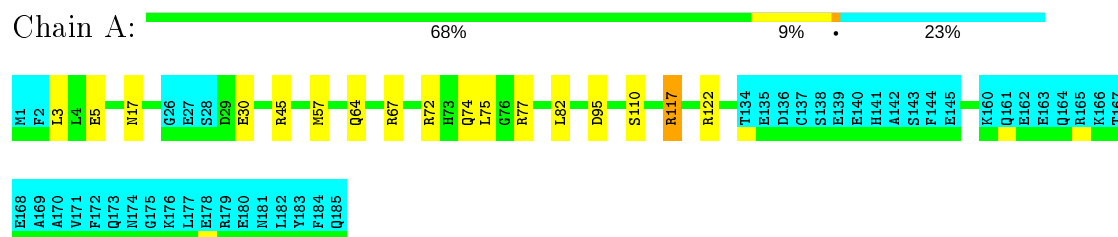
4.2.16 Score per residue for model 16

- Molecule 1: Rhomboid family serine protease



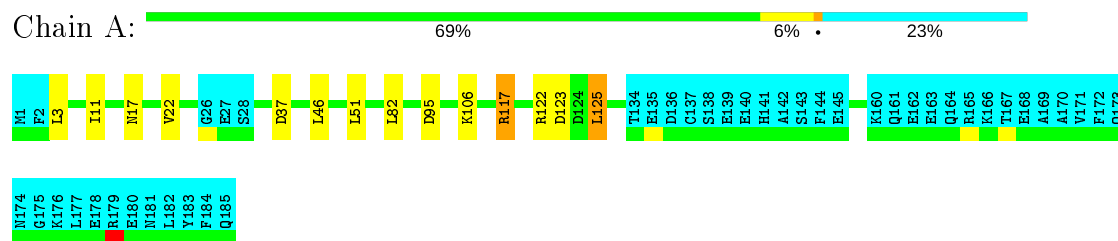
4.2.17 Score per residue for model 17

- Molecule 1: Rhomboid family serine protease



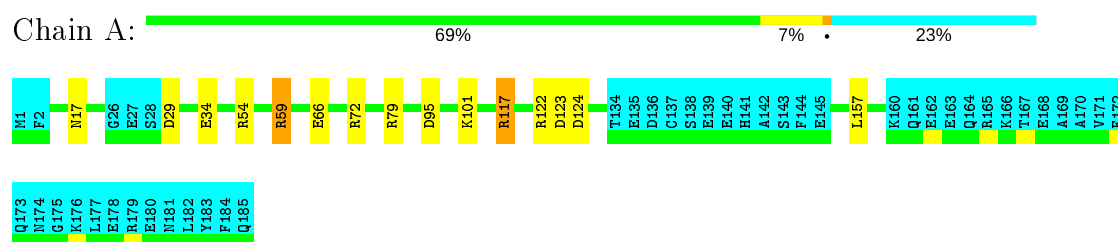
4.2.18 Score per residue for model 18

- Molecule 1: Rhomboid family serine protease



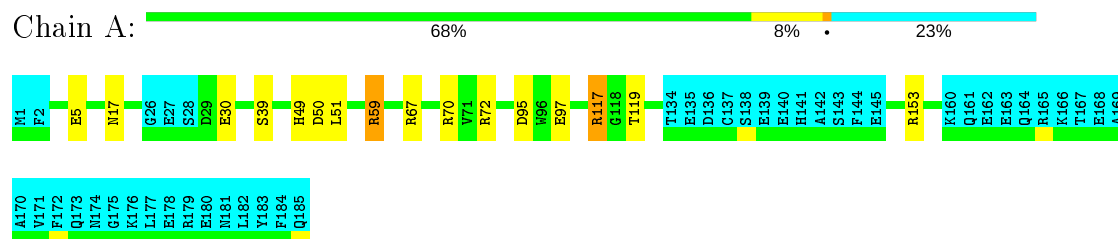
4.2.19 Score per residue for model 19

- Molecule 1: Rhomboid family serine protease



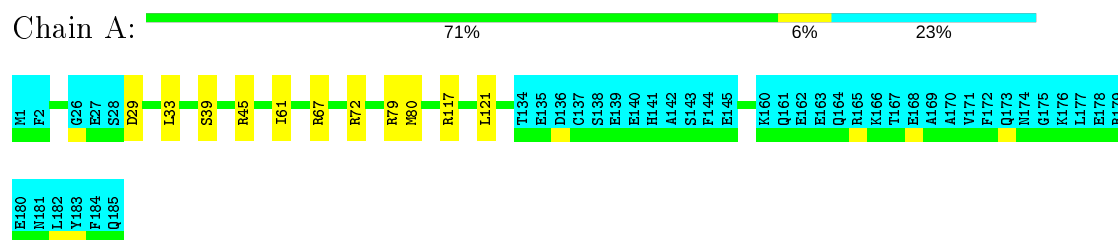
4.2.20 Score per residue for model 20

- Molecule 1: Rhomboid family serine protease



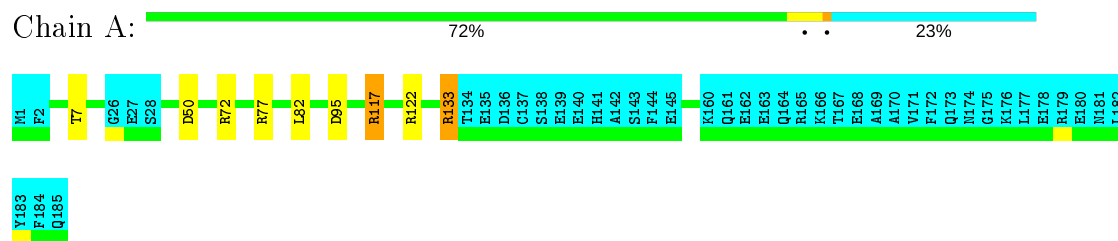
4.2.21 Score per residue for model 21

- Molecule 1: Rhomboid family serine protease



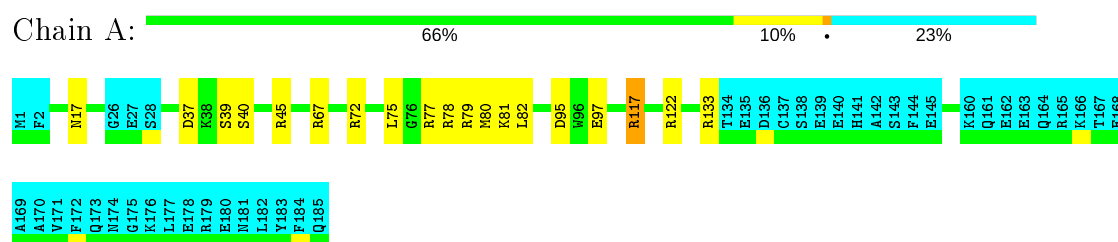
4.2.22 Score per residue for model 22

- Molecule 1: Rhomboid family serine protease



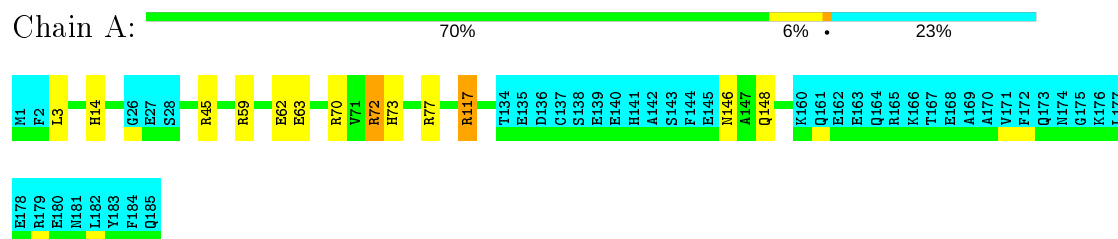
4.2.23 Score per residue for model 23

- Molecule 1: Rhomboid family serine protease



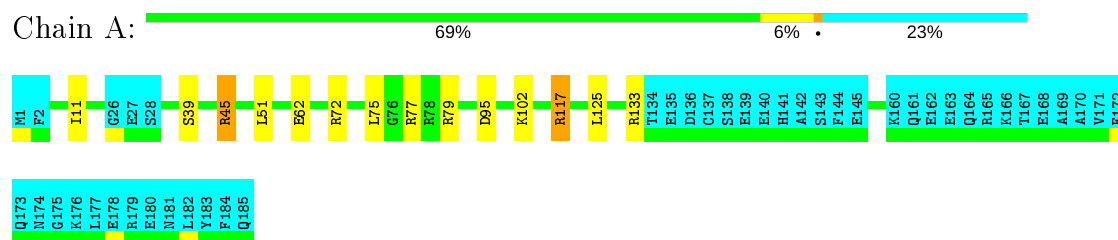
4.2.24 Score per residue for model 24

- Molecule 1: Rhomboid family serine protease



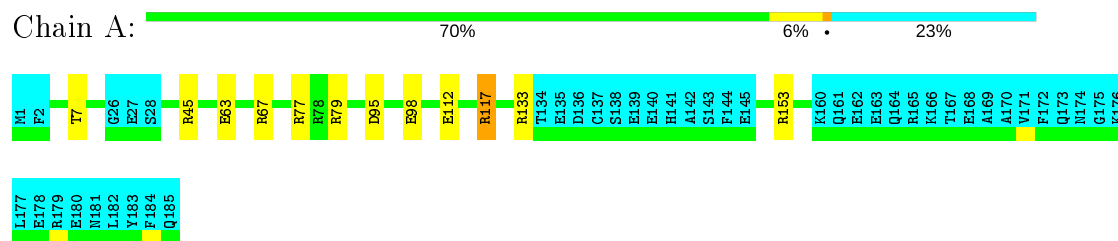
4.2.25 Score per residue for model 25

- Molecule 1: Rhomboid family serine protease



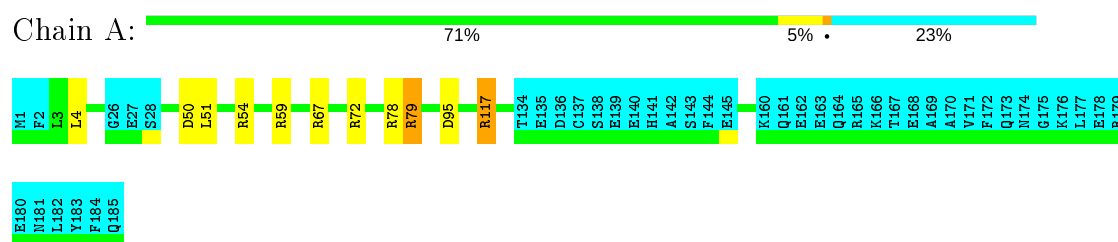
4.2.26 Score per residue for model 26

- Molecule 1: Rhomboid family serine protease



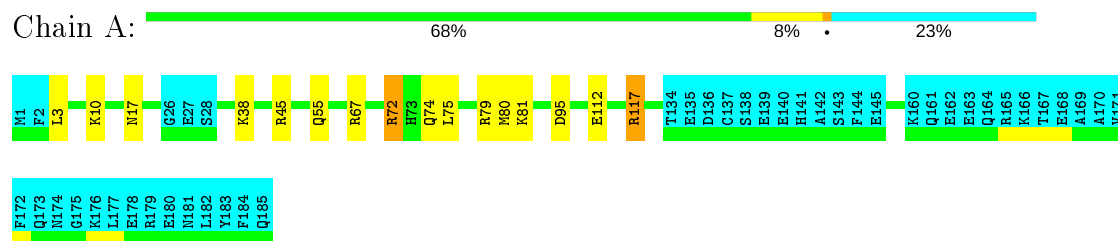
4.2.27 Score per residue for model 27 (medoid)

- Molecule 1: Rhomboid family serine protease



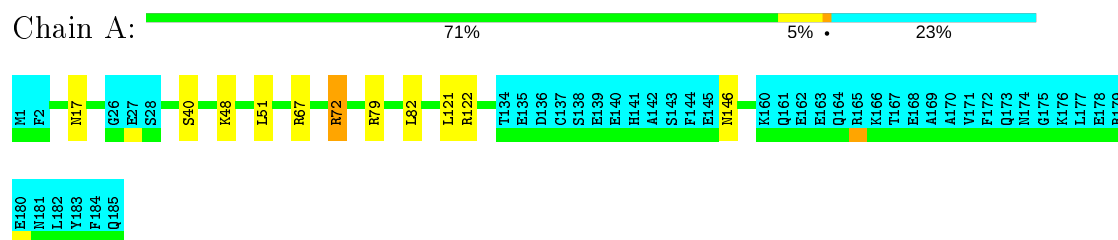
4.2.28 Score per residue for model 28

- Molecule 1: Rhomboid family serine protease



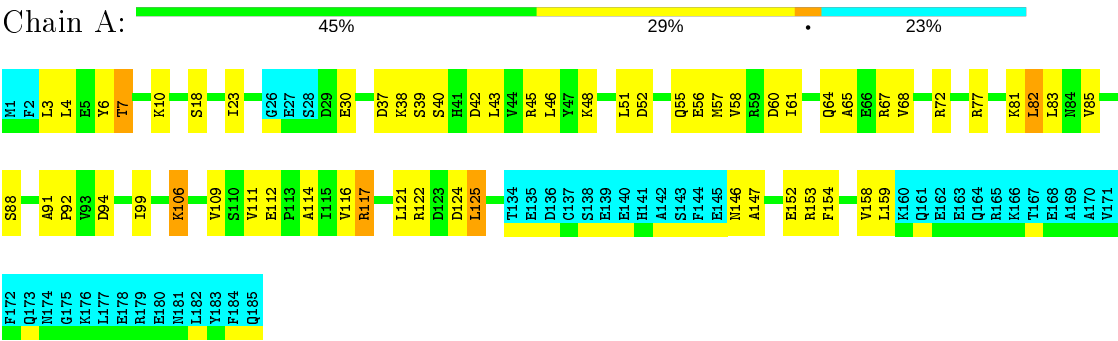
4.2.29 Score per residue for model 29

- Molecule 1: Rhomboid family serine protease



4.2.30 Score per residue for model 30

● Molecule 1: Rhomboid family serine protease



5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 30 were deposited, based on the following criterion: *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 calculation	
YASARA	refinement	

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	2244
Number of shifts mapped to atoms	2244
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	84%

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

6 Model quality [i](#)

6.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	0.64±0.12	0±0/1204 (0.0± 0.0%)	0.81±0.14	4±2/1626 (0.2± 0.1%)
All	All	0.65	0/36120 (0.0%)	0.82	118/48780 (0.2%)

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	77	ARG	NE-CZ-NH1	6.89	123.74	120.30	16	16
1	A	45	ARG	NE-CZ-NH1	6.88	123.74	120.30	25	10
1	A	133	ARG	NE-CZ-NH1	6.61	123.60	120.30	6	13
1	A	72	ARG	NE-CZ-NH1	6.49	123.54	120.30	13	11
1	A	59	ARG	NE-CZ-NH1	6.33	123.46	120.30	19	11
1	A	79	ARG	NE-CZ-NH1	6.12	123.36	120.30	5	10
1	A	122	ARG	NE-CZ-NH1	6.11	123.36	120.30	17	7
1	A	67	ARG	NE-CZ-NH1	5.95	123.27	120.30	10	6
1	A	70	ARG	NE-CZ-NH1	5.76	123.18	120.30	24	4
1	A	117	ARG	NE-CZ-NH1	5.74	123.17	120.30	9	21
1	A	78	ARG	NE-CZ-NH1	5.64	123.12	120.30	27	2
1	A	54	ARG	NE-CZ-NH1	5.57	123.08	120.30	19	3
1	A	54	ARG	NE-CZ-NH2	-5.46	117.57	120.30	1	2
1	A	153	ARG	NE-CZ-NH1	5.26	122.93	120.30	26	1
1	A	122	ARG	NE-CZ-NH2	-5.08	117.76	120.30	29	1

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	1179	1172	1172	2±5
All	All	35370	35160	35160	46

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 1.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:68:VAL:HG11	1:A:109:VAL:HG13	0.76	1.55	12	2
1:A:7:THR:HG21	1:A:121:LEU:HD21	0.74	1.57	12	1
1:A:116:VAL:HG13	1:A:124:ASP:CB	0.63	2.24	12	1
1:A:64:GLN:O	1:A:68:VAL:HG23	0.63	1.93	12	2
1:A:7:THR:CG2	1:A:121:LEU:HD21	0.59	2.26	12	1
1:A:119:THR:HG23	1:A:120:MET:HG2	0.58	1.75	12	1
1:A:42:ASP:O	1:A:43:LEU:HD23	0.58	1.99	12	1
1:A:116:VAL:HG12	1:A:124:ASP:HB3	0.57	1.76	30	1
1:A:116:VAL:HG12	1:A:124:ASP:CB	0.57	2.29	30	1
1:A:91:ALA:HB2	1:A:117:ARG:HD2	0.56	1.77	30	2
1:A:82:LEU:O	1:A:111:VAL:HG13	0.55	2.02	30	1
1:A:159:LEU:O	1:A:159:LEU:HD13	0.54	2.01	30	1
1:A:116:VAL:HG13	1:A:124:ASP:HB2	0.53	1.80	12	1
1:A:82:LEU:HD13	1:A:83:LEU:N	0.53	2.19	30	1
1:A:6:TYR:HB2	1:A:147:ALA:HB2	0.52	1.81	30	1
1:A:45:ARG:CG	1:A:82:LEU:HD11	0.51	2.36	30	1
1:A:22:VAL:HG11	1:A:25:ALA:HB2	0.50	1.84	12	1
1:A:45:ARG:HG3	1:A:82:LEU:HD11	0.49	1.82	30	1
1:A:4:LEU:HD11	1:A:88:SER:O	0.49	2.08	30	1
1:A:119:THR:HG23	1:A:120:MET:CG	0.48	2.38	12	1
1:A:85:VAL:CG1	1:A:116:VAL:HG23	0.47	2.39	12	1
1:A:57:MET:O	1:A:61:ILE:HD12	0.47	2.08	30	1
1:A:154:PHE:O	1:A:158:VAL:HG23	0.47	2.09	30	1
1:A:91:ALA:HB1	1:A:92:PRO:HD2	0.45	1.87	12	2
1:A:85:VAL:HG23	1:A:114:ALA:CB	0.45	2.42	30	1
1:A:23:ILE:HD11	1:A:43:LEU:HD22	0.45	1.89	30	1
1:A:22:VAL:CG1	1:A:25:ALA:HB2	0.44	2.42	12	1
1:A:54:ARG:HD2	1:A:99:ILE:HD11	0.44	1.89	8	1
1:A:68:VAL:CG1	1:A:109:VAL:HG13	0.44	2.34	12	1
1:A:11:ILE:HD11	1:A:125:LEU:HD11	0.44	1.89	25	2
1:A:15:LEU:HG	1:A:33:LEU:HD13	0.44	1.89	12	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:58:VAL:HG13	1:A:99:ILE:HG12	0.44	1.90	12	1
1:A:43:LEU:HD11	1:A:71:VAL:HG11	0.44	1.90	12	1
1:A:15:LEU:HB3	1:A:33:LEU:HD22	0.43	1.89	12	1
1:A:65:ALA:HB1	1:A:106:LYS:CB	0.42	2.44	30	1
1:A:159:LEU:C	1:A:159:LEU:HD13	0.42	2.36	30	1
1:A:68:VAL:HG13	1:A:80:MET:HB3	0.41	1.91	12	1
1:A:7:THR:CG2	1:A:125:LEU:HD11	0.41	2.46	30	1
1:A:58:VAL:CG1	1:A:99:ILE:HD12	0.41	2.44	30	1
1:A:45:ARG:O	1:A:46:LEU:HD12	0.40	2.15	30	1
1:A:3:LEU:HD12	1:A:3:LEU:O	0.40	2.17	30	1

6.3 Torsion angles [i](#)

6.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the backbone conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	142/185 (77%)	138±2 (97±1%)	3±2 (2±1%)	1±1 (1±0%)	29	74
All	All	4260/5550 (77%)	4138 (97%)	97 (2%)	25 (1%)	29	74

All 4 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	95	ASP	19
1	A	39	SER	2
1	A	94	ASP	2
1	A	40	SER	2

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	126/164 (77%)	116±6 (92±5%)	10±6 (8±5%)	15	62
All	All	3780/4920 (77%)	3470 (92%)	310 (8%)	15	62

All 79 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	117	ARG	29
1	A	72	ARG	19
1	A	51	LEU	11
1	A	67	ARG	10
1	A	80	MET	9
1	A	112	GLU	9
1	A	17	ASN	8
1	A	3	LEU	6
1	A	14	HIS	6
1	A	45	ARG	6
1	A	59	ARG	6
1	A	82	LEU	6
1	A	39	SER	6
1	A	81	LYS	6
1	A	66	GLU	5
1	A	48	LYS	5
1	A	148	GLN	5
1	A	30	GLU	5
1	A	146	ASN	5
1	A	121	LEU	5
1	A	50	ASP	5
1	A	40	SER	5
1	A	119	THR	4
1	A	64	GLN	4
1	A	29	ASP	4
1	A	62	GLU	4
1	A	74	GLN	4
1	A	122	ARG	4
1	A	7	THR	4
1	A	75	LEU	4
1	A	123	ASP	4
1	A	49	HIS	3
1	A	157	LEU	3
1	A	124	ASP	3
1	A	98	GLU	3
1	A	125	LEU	3

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Mol	Chain	Res	Type	Models (Total)
1	A	46	LEU	3
1	A	37	ASP	3
1	A	79	ARG	3
1	A	63	GLU	3
1	A	55	GLN	3
1	A	97	GLU	3
1	A	10	LYS	3
1	A	22	VAL	3
1	A	41	HIS	3
1	A	153	ARG	3
1	A	90	GLU	2
1	A	101	LYS	2
1	A	38	LYS	2
1	A	33	LEU	2
1	A	78	ARG	2
1	A	152	GLU	2
1	A	34	GLU	2
1	A	5	GLU	2
1	A	42	ASP	2
1	A	102	LYS	2
1	A	52	ASP	2
1	A	43	LEU	2
1	A	110	SER	2
1	A	60	ASP	2
1	A	4	LEU	2
1	A	18	SER	2
1	A	70	ARG	2
1	A	24	GLN	2
1	A	106	LYS	2
1	A	108	THR	1
1	A	15	LEU	1
1	A	120	MET	1
1	A	61	ILE	1
1	A	69	GLU	1
1	A	94	ASP	1
1	A	156	SER	1
1	A	84	ASN	1
1	A	57	MET	1
1	A	73	HIS	1
1	A	133	ARG	1
1	A	56	GLU	1
1	A	54	ARG	1

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Mol	Chain	Res	Type	Models (Total)
1	A	77	ARG	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

The completeness of assignment taking into account all chemical shift lists is 84% for the well-defined parts and 84% for the entire structure.

7.1 Chemical shift list 1

File name: `working_cs.cif`

Chemical shift list name: *starch_output*

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	2244
Number of shifts mapped to atoms	2244
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	8

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	184	-0.52 ± 0.14	Should be applied
$^{13}\text{C}_\beta$	177	0.04 ± 0.09	None needed (< 0.5 ppm)
$^{13}\text{C}'$	183	-0.11 ± 0.14	None needed (< 0.5 ppm)
^{15}N	176	-0.20 ± 0.24	None needed (< 0.5 ppm)

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 84%, i.e. 1580 atoms were assigned a chemical shift out of a possible 1875. 27 out of 28 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	697/702 (99%)	278/280 (99%)	283/284 (100%)	136/138 (99%)
Sidechain	767/1014 (76%)	481/593 (81%)	277/363 (76%)	9/58 (16%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	116/159 (73%)	72/85 (85%)	41/67 (61%)	3/7 (43%)
Overall	1580/1875 (84%)	831/958 (87%)	601/714 (84%)	148/203 (73%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 84%, i.e. 2021 atoms were assigned a chemical shift out of a possible 2420. 30 out of 31 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	903/917 (98%)	360/366 (98%)	367/370 (99%)	176/181 (97%)
Sidechain	975/1293 (75%)	617/758 (81%)	345/462 (75%)	13/73 (18%)
Aromatic	143/210 (68%)	90/113 (80%)	50/89 (56%)	3/8 (38%)
Overall	2021/2420 (84%)	1067/1237 (86%)	762/921 (83%)	192/262 (73%)

7.1.4 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	151	ARG	HG3	-0.48	3.00 – 0.10	-7.0
1	A	38	LYS	HD3	3.11	2.75 – 0.45	6.6
1	A	38	LYS	HD2	3.11	2.76 – 0.46	6.5
1	A	45	ARG	HB3	-0.02	3.17 – 0.37	-6.4
1	A	97	GLU	HG3	0.97	3.31 – 1.21	-6.1
1	A	151	ARG	HB3	0.06	3.17 – 0.37	-6.1
1	A	48	LYS	HB3	0.23	3.10 – 0.40	-5.6
1	A	48	LYS	HD3	0.35	2.75 – 0.45	-5.4

7.1.5 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:

