



Full wwPDB NMR Structure Validation Report ⓘ

May 19, 2016 – 08:00 PM EDT

PDB ID : 4B2S
Title : Solution structure of CCP modules 11-12 of complement factor H
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Deposited on : 2012-07-17

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/NMRValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20027457
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

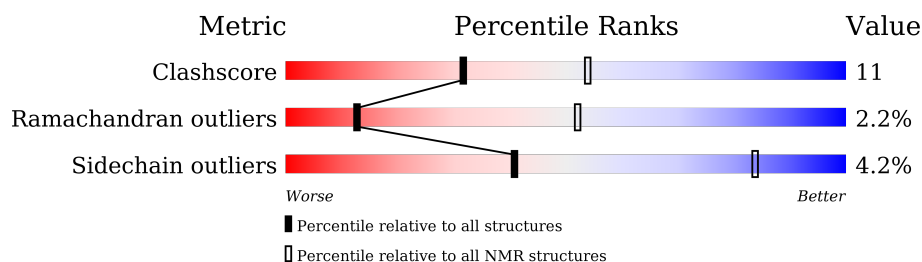
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 93%.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	127	

2 Ensemble composition and analysis

This entry contains 20 models. Model 6 is the overall representative, medoid model (most similar to other models). The authors have identified model 12 as representative.

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:629-A:686 (58)	0.25	6
2	A:690-A:747 (58)	0.25	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 3 clusters and 3 single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1911 atoms, of which 924 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called COMPLEMENT FACTOR H.

Mol	Chain	Residues	Atoms						Trace
1	A	127	Total	C	H	N	O	S	0
			1911	622	924	159	196	10	

There are 6 discrepancies between the modelled and reference sequences:

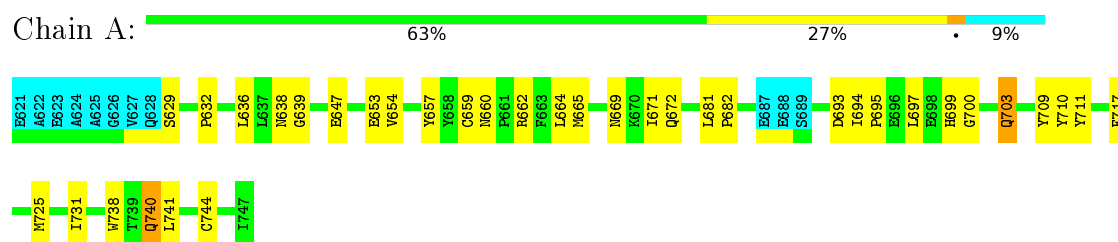
Chain	Residue	Modelled	Actual	Comment	Reference
A	621	GLU	-	EXPRESSION TAG	UNP P08603
A	622	ALA	-	EXPRESSION TAG	UNP P08603
A	623	GLU	-	EXPRESSION TAG	UNP P08603
A	624	ALA	-	EXPRESSION TAG	UNP P08603
A	625	ALA	-	EXPRESSION TAG	UNP P08603
A	626	GLY	-	EXPRESSION TAG	UNP P08603

4 Residue-property plots [i](#)

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: COMPLEMENT FACTOR H

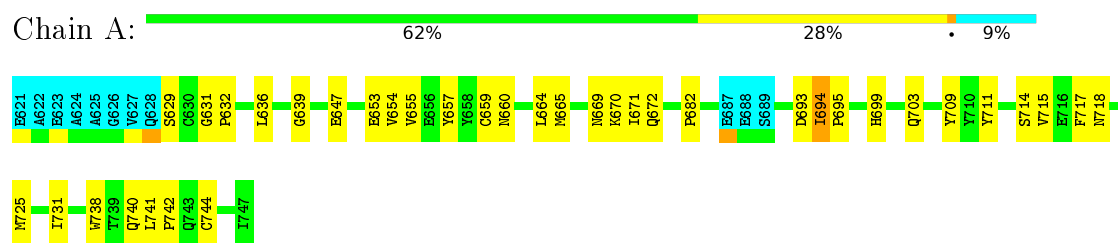


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

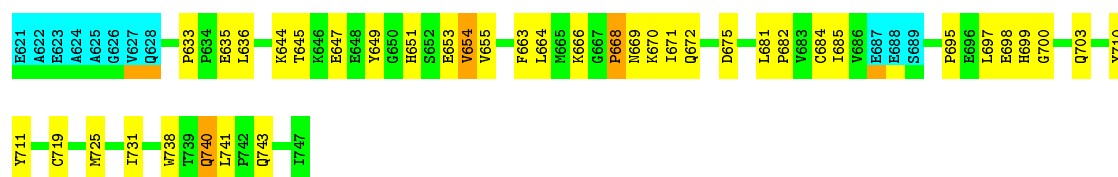
- Molecule 1: COMPLEMENT FACTOR H



4.2.2 Score per residue for model 2

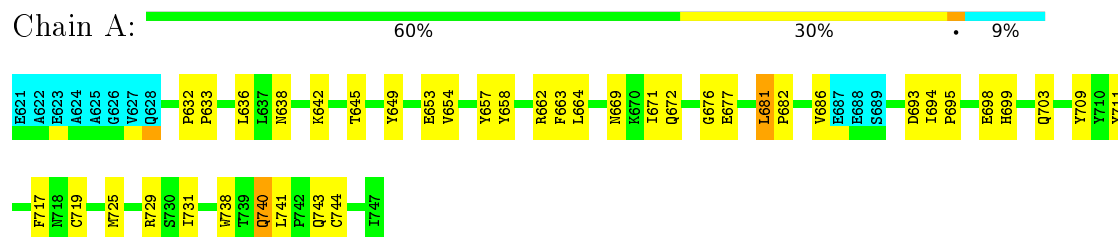
- Molecule 1: COMPLEMENT FACTOR H





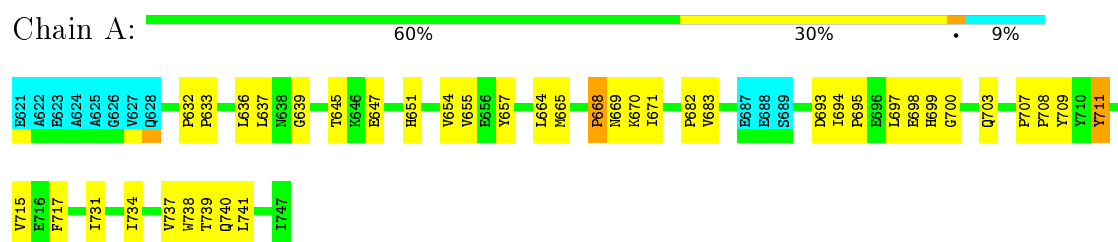
4.2.3 Score per residue for model 3

- Molecule 1: COMPLEMENT FACTOR H



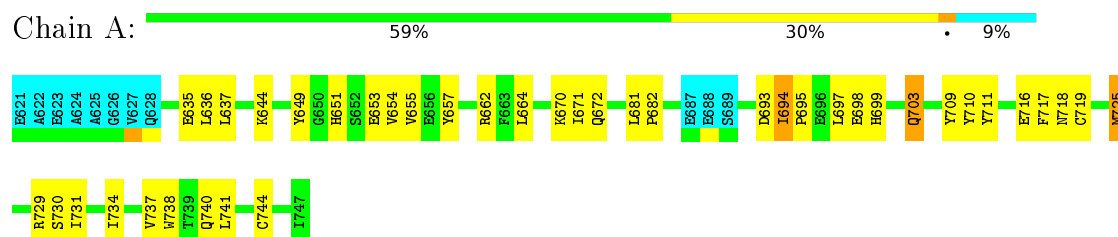
4.2.4 Score per residue for model 4

- Molecule 1: COMPLEMENT FACTOR H



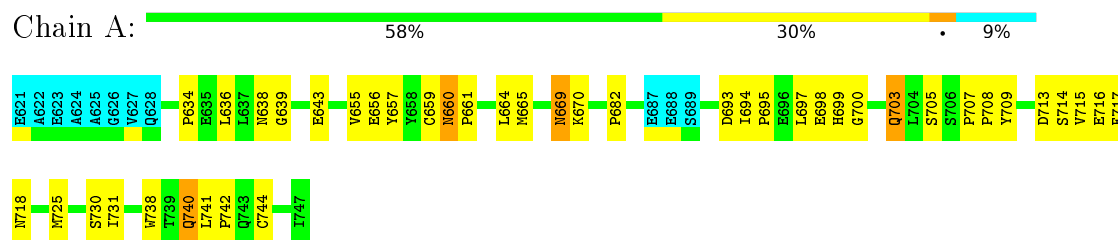
4.2.5 Score per residue for model 5

- Molecule 1: COMPLEMENT FACTOR H



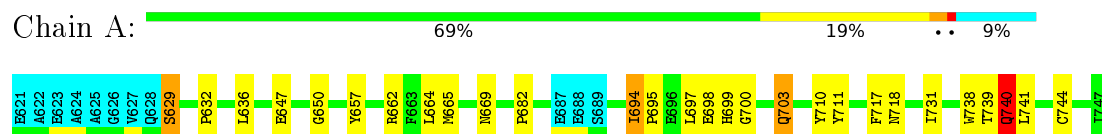
4.2.6 Score per residue for model 6 (medoid)

- Molecule 1: COMPLEMENT FACTOR H



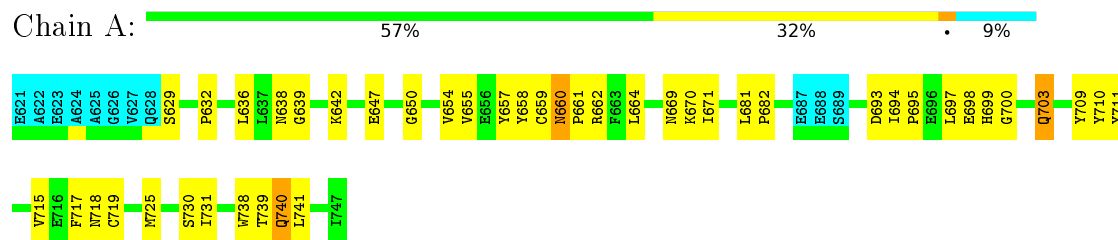
4.2.7 Score per residue for model 7

- Molecule 1: COMPLEMENT FACTOR H



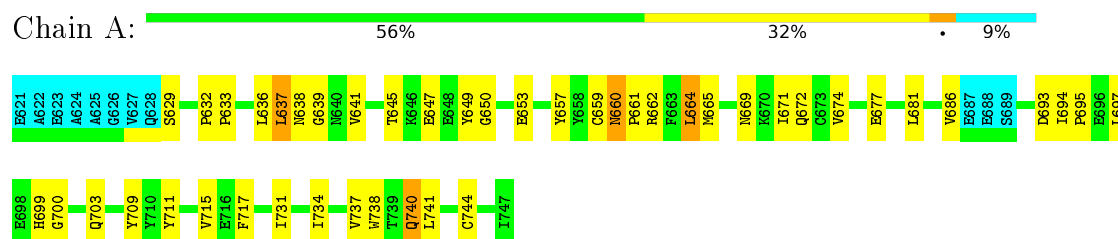
4.2.8 Score per residue for model 8

- Molecule 1: COMPLEMENT FACTOR H



4.2.9 Score per residue for model 9

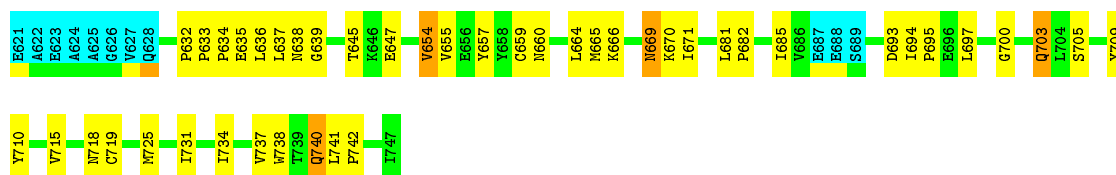
- Molecule 1: COMPLEMENT FACTOR H



4.2.10 Score per residue for model 10

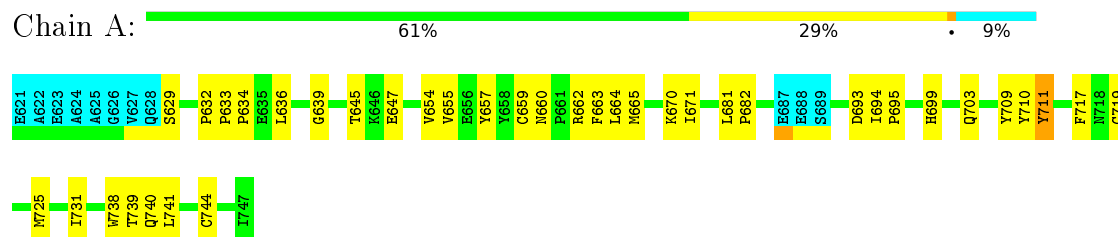
- Molecule 1: COMPLEMENT FACTOR H





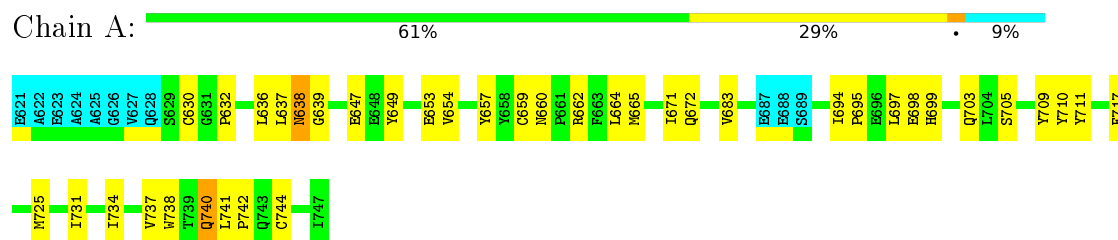
4.2.11 Score per residue for model 11

- Molecule 1: COMPLEMENT FACTOR H



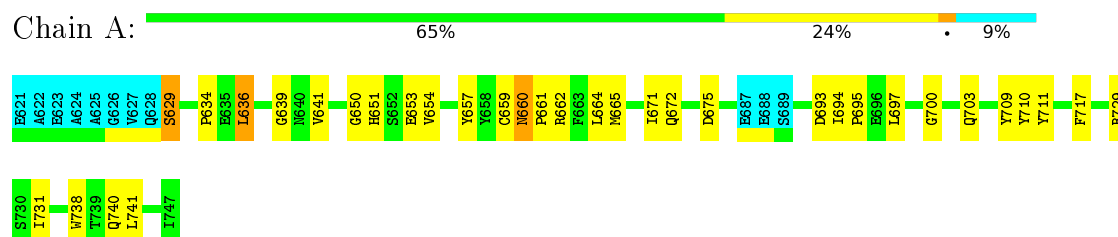
4.2.12 Score per residue for model 12

- Molecule 1: COMPLEMENT FACTOR H



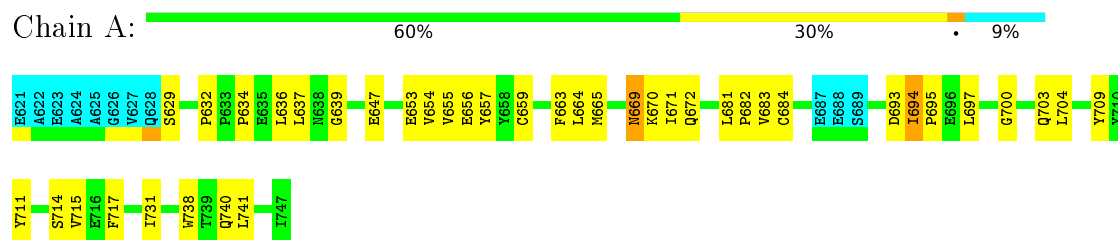
4.2.13 Score per residue for model 13

- Molecule 1: COMPLEMENT FACTOR H



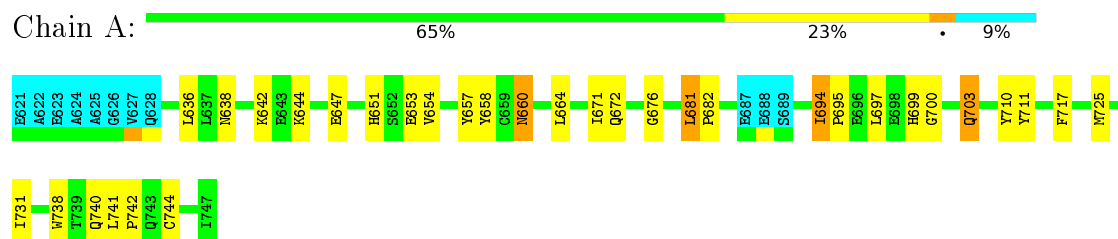
4.2.14 Score per residue for model 14

- Molecule 1: COMPLEMENT FACTOR H



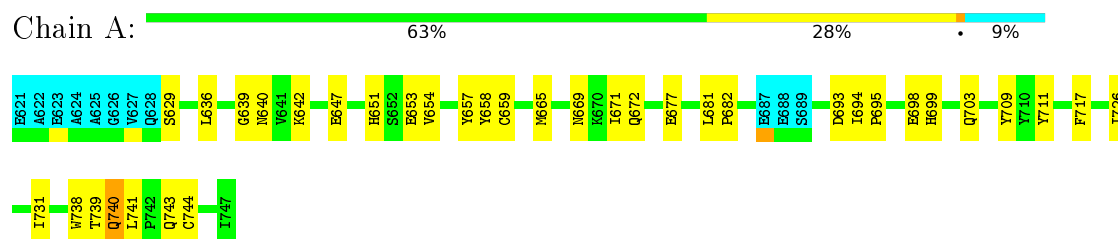
4.2.15 Score per residue for model 15

- Molecule 1: COMPLEMENT FACTOR H



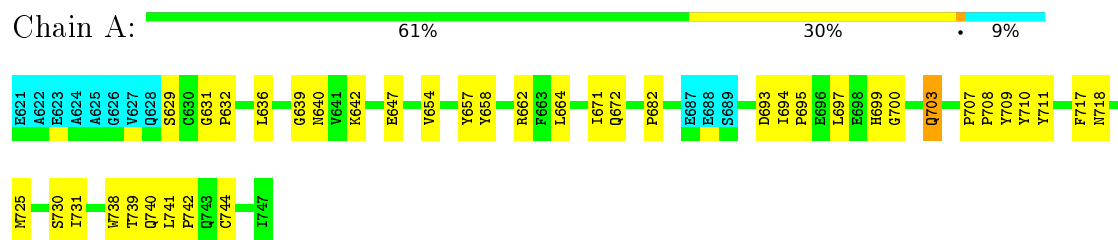
4.2.16 Score per residue for model 16

- Molecule 1: COMPLEMENT FACTOR H



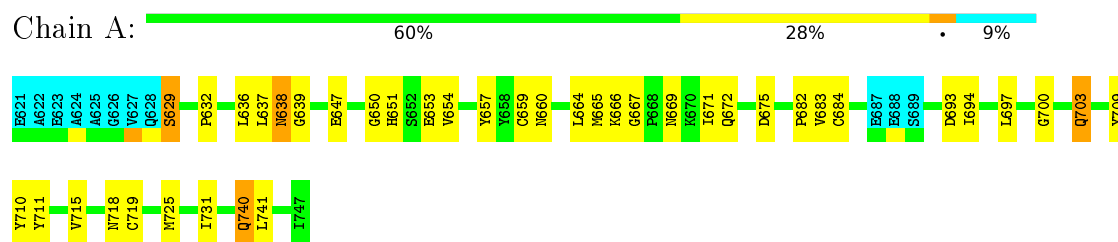
4.2.17 Score per residue for model 17

- Molecule 1: COMPLEMENT FACTOR H



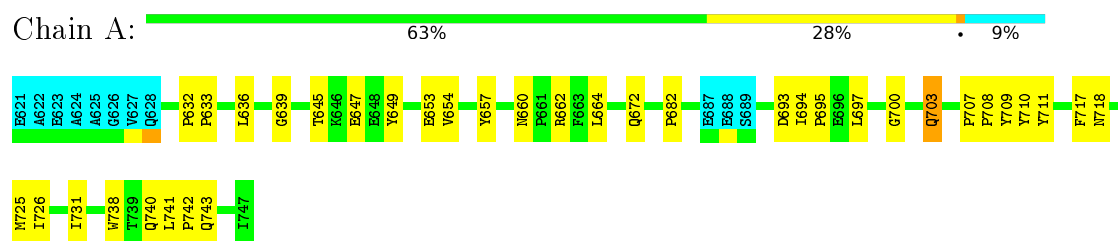
4.2.18 Score per residue for model 18

- Molecule 1: COMPLEMENT FACTOR H



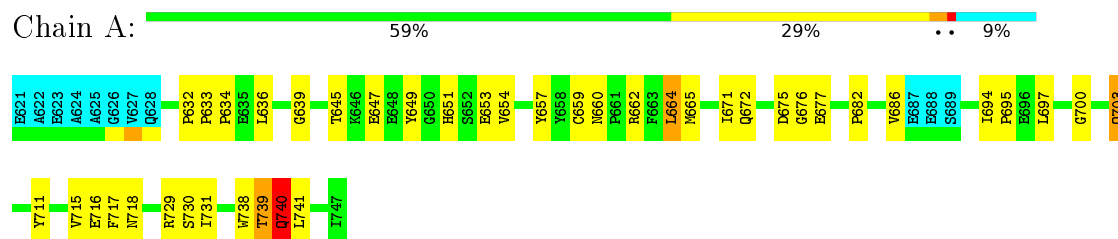
4.2.19 Score per residue for model 19

- Molecule 1: COMPLEMENT FACTOR H



4.2.20 Score per residue for model 20

- Molecule 1: COMPLEMENT FACTOR H



5 Refinement protocol and experimental data overview

The models were refined using the following method: *SIMULATED ANNEALING*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *LOWEST ENERGY*.

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

Software name	Classification	Version
CNS 1.2	refinement	
AZARA 2.0	structure solution	
CCPNMR ANALYSIS 2.0	structure solution	
CCPNMR ANALYSIS 2.1	structure solution	
CCPNMR ANALYSIS 2.2	structure solution	
MOLMOL 2	structure solution	
CNS 1.2	structure solution	
TOPSPIN 1.3	structure solution	
PROCHECKNMR 3. 4.3	structure solution	

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)	4b2s_cs.cif
Number of chemical shift lists	1
Total number of shifts	1519
Number of shifts mapped to atoms	1514
Number of unparsed shifts	5
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	93%

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

6 Model quality

6.1 Standard geometry

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	0.95±0.03	0±1/938 (0.0±0.1%)	0.69±0.02	0±0/1279 (0.0±0.0%)
All	All	0.95	5/18760 (0.0%)	0.69	0/25580 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	0.1±0.4
All	All	0	3

All unique bond 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(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	683	VAL	N-CA	-5.36	1.35	1.46	4	2
1	A	638	ASN	C-N	-5.14	1.23	1.33	9	3

There are no bond-angle outliers.

There are no chirality outliers.

All unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	729	ARG	Sidechain	2
1	A	662	ARG	Sidechain	1

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	910	858	854	20±2
All	All	18200	17160	17080	402

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 11.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:629:SER:HA	1:A:650:GLY:HA2	0.82	1.51	7	4
1:A:697:LEU:HD23	1:A:700:GLY:HA3	0.80	1.54	7	13
1:A:664:LEU:HD11	1:A:711:TYR:HB3	0.78	1.53	13	6
1:A:632:PRO:HG3	1:A:647:GLU:HG2	0.78	1.54	7	13
1:A:699:HIS:HB2	1:A:744:CYS:HB2	0.74	1.59	5	11
1:A:641:VAL:HG22	1:A:657:TYR:CE2	0.72	2.20	9	1
1:A:649:TYR:HB3	1:A:653:GLU:HG3	0.69	1.64	2	5
1:A:630:CYS:HB2	1:A:649:TYR:HB2	0.67	1.64	12	1
1:A:693:ASP:HA	1:A:709:TYR:CE1	0.66	2.25	13	13
1:A:636:LEU:HD12	1:A:657:TYR:HB3	0.65	1.68	9	8
1:A:664:LEU:HG	1:A:711:TYR:CD1	0.64	2.27	20	7
1:A:641:VAL:HG22	1:A:657:TYR:CE1	0.64	2.28	13	1
1:A:633:PRO:HD2	1:A:645:THR:HG22	0.63	1.68	11	8
1:A:636:LEU:HG	1:A:682:PRO:HG2	0.63	1.70	17	4
1:A:671:ILE:HG21	1:A:681:LEU:HD12	0.62	1.71	15	3
1:A:719:CYS:HB2	1:A:725:MET:HB3	0.61	1.70	2	6
1:A:662:ARG:HA	1:A:710:TYR:CB	0.61	2.26	5	6
1:A:693:ASP:HA	1:A:709:TYR:CE2	0.59	2.32	11	2
1:A:695:PRO:HD3	1:A:738:TRP:CD1	0.59	2.32	8	19
1:A:731:ILE:HG21	1:A:741:LEU:HD23	0.59	1.73	20	20
1:A:636:LEU:HD13	1:A:639:GLY:HA3	0.58	1.75	18	9
1:A:639:GLY:HA3	1:A:659:CYS:HA	0.57	1.77	6	5
1:A:664:LEU:HD22	1:A:711:TYR:CD1	0.57	2.35	4	4
1:A:636:LEU:HD13	1:A:682:PRO:HG2	0.56	1.78	3	11
1:A:694:ILE:HG23	1:A:717:PHE:CZ	0.56	2.34	17	17
1:A:636:LEU:HD23	1:A:637:LEU:N	0.55	2.17	9	4
1:A:671:ILE:HG21	1:A:681:LEU:HG	0.55	1.79	14	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:636:LEU:HB2	1:A:657:TYR:CD2	0.55	2.36	17	13
1:A:698:GLU:HG3	1:A:699:HIS:N	0.54	2.18	2	7
1:A:725:MET:HE2	1:A:742:PRO:HG3	0.54	1.78	15	7
1:A:663:PHE:HB3	1:A:684:CYS:HB3	0.53	1.80	2	2
1:A:642:LYS:HE2	1:A:658:TYR:HB3	0.52	1.82	15	4
1:A:654:VAL:HA	1:A:671:ILE:O	0.52	2.04	18	16
1:A:662:ARG:HA	1:A:710:TYR:HB2	0.51	1.82	19	3
1:A:717:PHE:O	1:A:729:ARG:HB2	0.51	2.06	13	2
1:A:653:GLU:O	1:A:672:GLN:HA	0.51	2.05	14	13
1:A:703:GLN:NE2	1:A:718:ASN:HB2	0.50	2.22	7	3
1:A:734:ILE:O	1:A:737:VAL:HG22	0.50	2.06	9	5
1:A:660:ASN:OD1	1:A:661:PRO:HD2	0.50	2.07	13	3
1:A:631:GLY:HA2	1:A:647:GLU:O	0.50	2.07	1	2
1:A:638:ASN:ND2	1:A:660:ASN:HB2	0.49	2.22	6	2
1:A:645:THR:HA	1:A:649:TYR:OH	0.49	2.07	3	1
1:A:659:CYS:SG	1:A:665:MET:HA	0.49	2.47	18	7
1:A:637:LEU:HD13	1:A:683:VAL:HG23	0.49	1.84	14	1
1:A:662:ARG:O	1:A:686:VAL:HG23	0.49	2.08	9	2
1:A:636:LEU:HB2	1:A:657:TYR:CD1	0.49	2.43	20	5
1:A:655:VAL:O	1:A:670:LYS:HA	0.48	2.08	2	9
1:A:668:PRO:HD2	1:A:682:PRO:HA	0.48	1.84	2	2
1:A:740:GLN:HE21	1:A:741:LEU:N	0.48	2.07	7	1
1:A:654:VAL:HG12	1:A:672:GLN:HB2	0.48	1.86	17	1
1:A:698:GLU:OE2	1:A:743:GLN:HB2	0.48	2.09	3	1
1:A:671:ILE:HG21	1:A:681:LEU:HD23	0.48	1.85	2	3
1:A:666:LYS:HD2	1:A:685:ILE:HD13	0.48	1.85	2	2
1:A:665:MET:HG2	1:A:669:ASN:HB3	0.47	1.87	14	5
1:A:694:ILE:HG12	1:A:715:VAL:HG11	0.47	1.87	18	6
1:A:707:PRO:HA	1:A:708:PRO:C	0.47	2.30	17	4
1:A:664:LEU:HD21	1:A:711:TYR:HB3	0.47	1.85	4	1
1:A:662:ARG:HB2	1:A:710:TYR:CD2	0.47	2.44	19	1
1:A:636:LEU:HB3	1:A:639:GLY:C	0.47	2.30	18	3
1:A:634:PRO:HG2	1:A:681:LEU:HD21	0.46	1.88	14	1
1:A:644:LYS:HE2	1:A:644:LYS:HA	0.45	1.88	2	1
1:A:662:ARG:HG3	1:A:663:PHE:CD1	0.45	2.47	3	2
1:A:694:ILE:CG1	1:A:715:VAL:HG11	0.45	2.42	10	1
1:A:668:PRO:O	1:A:682:PRO:HB3	0.45	2.12	2	1
1:A:719:CYS:SG	1:A:725:MET:HB2	0.45	2.52	5	1
1:A:656:GLU:OE1	1:A:670:LYS:HE3	0.45	2.12	14	1
1:A:697:LEU:HD11	1:A:742:PRO:O	0.44	2.12	12	2
1:A:703:GLN:CD	1:A:718:ASN:HB2	0.44	2.32	6	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:663:PHE:CE2	1:A:686:VAL:HB	0.44	2.47	3	1
1:A:716:GLU:HG2	1:A:730:SER:HB3	0.44	1.89	20	3
1:A:715:VAL:O	1:A:730:SER:HA	0.44	2.13	8	2
1:A:638:ASN:HB3	1:A:684:CYS:HB2	0.44	1.90	18	1
1:A:669:ASN:HA	1:A:682:PRO:HG3	0.44	1.90	6	1
1:A:639:GLY:HA2	1:A:660:ASN:OD1	0.43	2.13	19	1
1:A:659:CYS:SG	1:A:665:MET:HE2	0.42	2.54	20	1
1:A:731:ILE:HD12	1:A:738:TRP:CG	0.42	2.49	15	1
1:A:656:GLU:HG3	1:A:669:ASN:ND2	0.42	2.29	14	1
1:A:703:GLN:N	1:A:703:GLN:HE21	0.42	2.12	15	1
1:A:666:LYS:HB3	1:A:683:VAL:HB	0.42	1.89	18	1
1:A:642:LYS:HB3	1:A:658:TYR:CD1	0.42	2.49	3	1
1:A:705:SER:O	1:A:707:PRO:HD3	0.42	2.15	6	1
1:A:629:SER:HA	1:A:650:GLY:O	0.42	2.15	9	1
1:A:665:MET:SD	1:A:669:ASN:HB3	0.42	2.54	4	1
1:A:661:PRO:HB2	1:A:713:ASP:OD2	0.42	2.14	6	1
1:A:659:CYS:SG	1:A:665:MET:HE1	0.42	2.55	11	2
1:A:662:ARG:HA	1:A:710:TYR:HB3	0.42	1.91	12	2
1:A:693:ASP:HA	1:A:709:TYR:CD1	0.42	2.50	16	1
1:A:705:SER:HB3	1:A:709:TYR:OH	0.42	2.15	12	2
1:A:697:LEU:HD23	1:A:698:GLU:HG2	0.41	1.91	5	1
1:A:694:ILE:HG23	1:A:717:PHE:CE1	0.41	2.50	16	1
1:A:664:LEU:O	1:A:684:CYS:HA	0.41	2.15	2	1
1:A:726:ILE:HB	1:A:743:GLN:HG3	0.41	1.92	19	1
1:A:632:PRO:HB3	1:A:645:THR:HG21	0.41	1.93	3	1
1:A:739:THR:HB	1:A:740:GLN:HG3	0.41	1.93	20	1
1:A:697:LEU:HD13	1:A:700:GLY:HA3	0.41	1.91	4	1
1:A:726:ILE:HD12	1:A:743:GLN:HE21	0.41	1.74	16	1
1:A:642:LYS:HB3	1:A:658:TYR:CE2	0.41	2.51	17	1
1:A:725:MET:HA	1:A:743:GLN:O	0.41	2.15	2	1
1:A:667:GLY:HA3	1:A:682:PRO:HA	0.41	1.93	18	1
1:A:643:GLU:HG3	1:A:656:GLU:H	0.41	1.76	6	1
1:A:636:LEU:HD22	1:A:657:TYR:HB3	0.40	1.94	19	1
1:A:725:MET:CE	1:A:742:PRO:HG3	0.40	2.45	15	1
1:A:704:LEU:HD11	1:A:715:VAL:HA	0.40	1.91	14	1
1:A:665:MET:SD	1:A:682:PRO:HB2	0.40	2.56	20	1
1:A:636:LEU:HD12	1:A:637:LEU:H	0.40	1.75	5	1
1:A:647:GLU:H	1:A:649:TYR:HE1	0.40	1.59	12	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	115/127 (91%)	96±2 (83±2%)	17±3 (15±3%)	3±1 (2±1%)	13	52
All	All	2300/2540 (91%)	1913 (83%)	337 (15%)	50 (2%)	13	52

All 11 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	740	GLN	12
1	A	629	SER	8
1	A	669	ASN	8
1	A	739	THR	7
1	A	634	PRO	5
1	A	647	GLU	3
1	A	637	LEU	2
1	A	668	PRO	2
1	A	674	VAL	1
1	A	675	ASP	1
1	A	676	GLY	1

6.3.2 Protein sidechains [i](#)

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	104/111 (94%)	100±1 (96±1%)	4±1 (4±1%)	41	84
All	All	2080/2220 (94%)	1992 (96%)	88 (4%)	41	84

All 20 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	703	GLN	20
1	A	740	GLN	19
1	A	660	ASN	11
1	A	694	ILE	5
1	A	638	ASN	4
1	A	677	GLU	4
1	A	635	GLU	3
1	A	654	VAL	3
1	A	714	SER	3
1	A	711	TYR	2
1	A	644	LYS	2
1	A	664	LEU	2
1	A	681	LEU	2
1	A	640	ASN	2
1	A	730	SER	1
1	A	718	ASN	1
1	A	669	ASN	1
1	A	637	LEU	1
1	A	636	LEU	1
1	A	725	MET	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 carbohydrates 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 93% for the well-defined parts and 92% for the entire structure.

7.1 Chemical shift list 1

File name: 4b2s_cs.cif

Chemical shift list name: *assigned_chem_shift_list*

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	1519
Number of shifts mapped to atoms	1514
Number of unparsed shifts	5
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	2

The following errors were found when reading this chemical shift list.

- Chemical shift has been reported more than once. All 5 occurrences are reported below.

Shift ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
559	A	669	ASN	CA	53.866	0.049	1
561	A	669	ASN	CB	35.836	0.0	1
564	A	669	ASN	H	8.052	0.002	1
566	A	669	ASN	HA	5.492	0.002	1
572	A	669	ASN	N	114.815	0.017	1

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	124	0.05 ± 0.20	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	114	-0.18 ± 0.07	None needed (< 0.5 ppm)
$^{13}\text{C}'$	122	0.48 ± 0.18	None needed (< 0.5 ppm)
^{15}N	114	0.27 ± 0.42	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments [i](#)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 93%, i.e. 1280 atoms were assigned a chemical shift out of a possible 1382. 0 out of 16 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	552/560 (99%)	220/222 (99%)	227/232 (98%)	105/106 (99%)
Sidechain	610/679 (90%)	377/403 (94%)	226/256 (88%)	7/20 (35%)
Aromatic	118/143 (83%)	59/73 (81%)	56/59 (95%)	3/11 (27%)
Overall	1280/1382 (93%)	656/698 (94%)	509/547 (93%)	115/137 (84%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 92%, i.e. 1367 atoms were assigned a chemical shift out of a possible 1490. 0 out of 17 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	598/615 (97%)	238/244 (98%)	246/254 (97%)	114/117 (97%)
Sidechain	651/732 (89%)	402/433 (93%)	241/278 (87%)	8/21 (38%)
Aromatic	118/143 (83%)	59/73 (81%)	56/59 (95%)	3/11 (27%)
Overall	1367/1490 (92%)	699/750 (93%)	543/591 (92%)	125/149 (84%)

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	718	ASN	HB3	0.97	4.41 – 1.11	-5.4
1	A	638	ASN	HB3	1.02	4.41 – 1.11	-5.3

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:

