



Full wwPDB NMR Structure Validation Report ⓘ

Jun 14, 2020 – 02:12 pm BST

PDB ID : 2N0S
Title : HADDOCK model of ferredoxin and [FeFe] hydrogenase complex
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Deposited on : 2015-03-13

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:

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
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

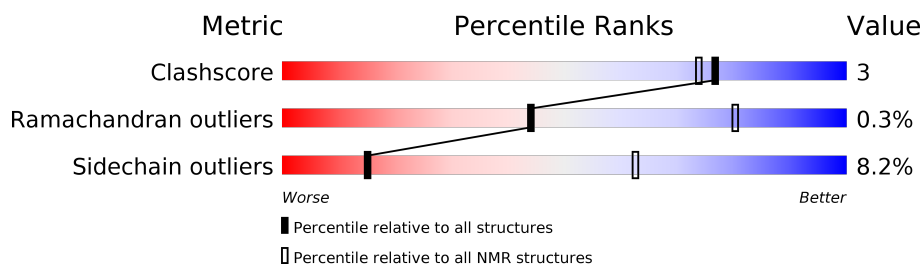
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

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



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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

Mol	Chain	Length	Quality of chain
1	A	442	
2	B	94	

2 Ensemble composition and analysis ⓘ

This entry contains 4 models. Model 3 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 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:25-A:115, A:121-A:200, A:204-A:311, A:323-A:376, A:382-A:390, A:396-A:449 (396)	0.24	3

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

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

The models can be grouped into 2 clusters. No single-model clusters were found.

Cluster number	Models
1	1, 2
2	3, 4

3 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7538 atoms, of which 3755 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Fe-hydrogenase.

Mol	Chain	Residues	Atoms						Trace
1	A	407	Total	C	H	N	O	S	0
			6187	1941	3106	534	583	23	

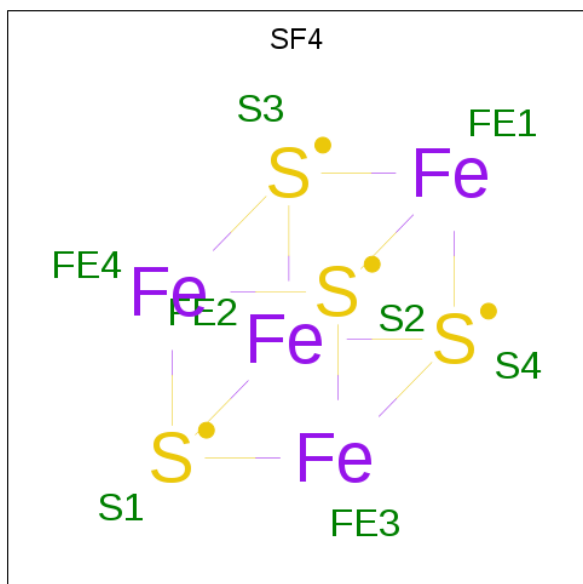
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	16	GLY	-	EXPRESSION TAG	UNP Q9FYU1
A	17	ALA	-	EXPRESSION TAG	UNP Q9FYU1

- Molecule 2 is a protein called Ferredoxin, chloroplastic.

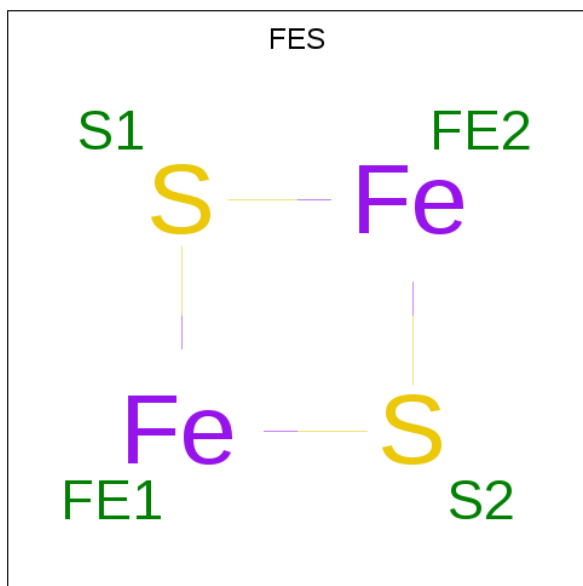
Mol	Chain	Residues	Atoms						Trace
2	B	94	Total	C	H	N	O	S	0
			1339	424	649	109	150	7	

- Molecule 3 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms		
3	A	1	Total	Fe	S
			8	4	4

- Molecule 4 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe_2S_2).



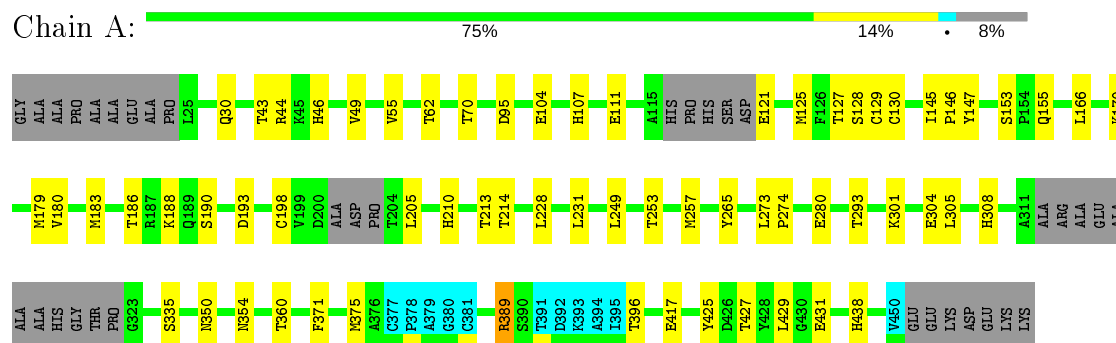
Mol	Chain	Residues	Atoms		
			Total	Fe	S
4	B	1	4	2	2

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: Fe-hydrogenase



- Molecule 2: Ferredoxin, chloroplastic

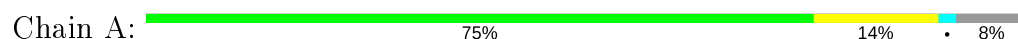


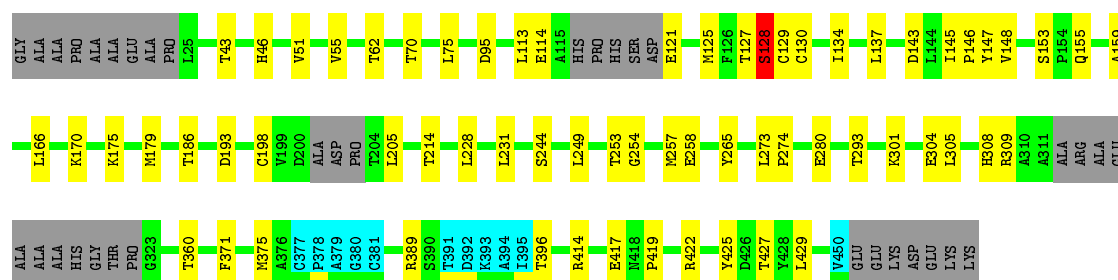
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

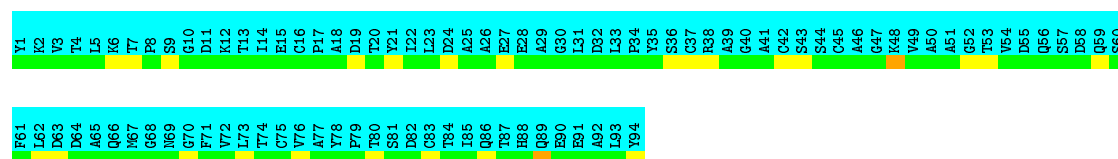
- Molecule 1: Fe-hydrogenase





- Molecule 2: Ferredoxin, chloroplastic

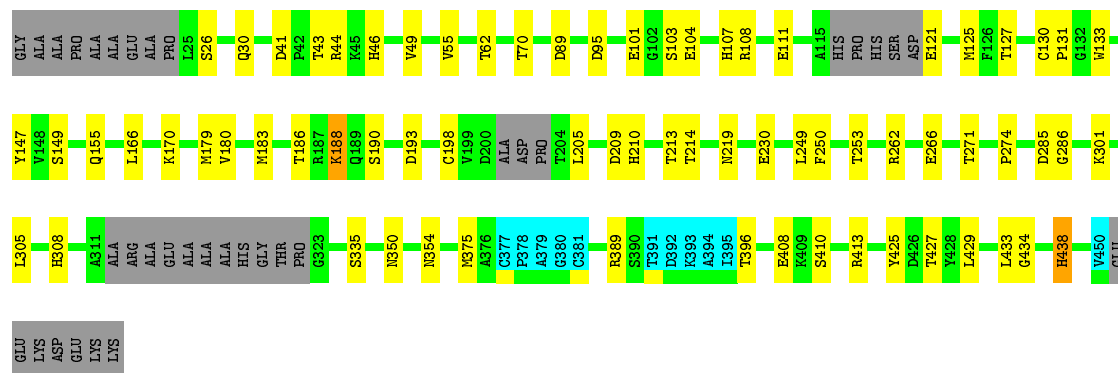
Chain B:  100%



4.2.2 Score per residue for model 2

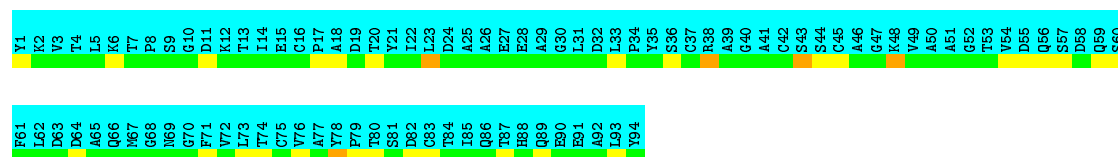
- Molecule 1: Fe-hydrogenase

Chain A:  74% 16% 8%



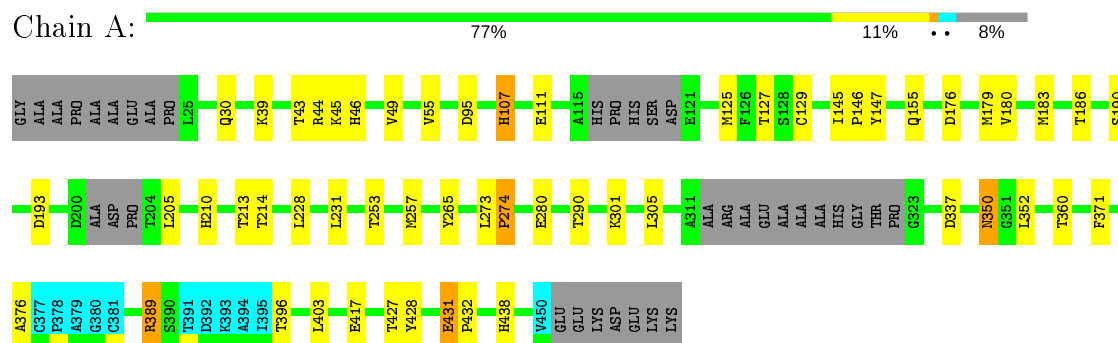
- Molecule 2: Ferredoxin, chloroplastic

Chain B:  100%

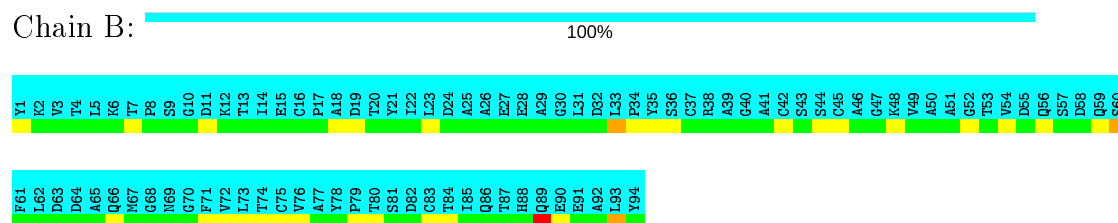


4.2.3 Score per residue for model 3 (medoid)

- Molecule 1: Fe-hydrogenase

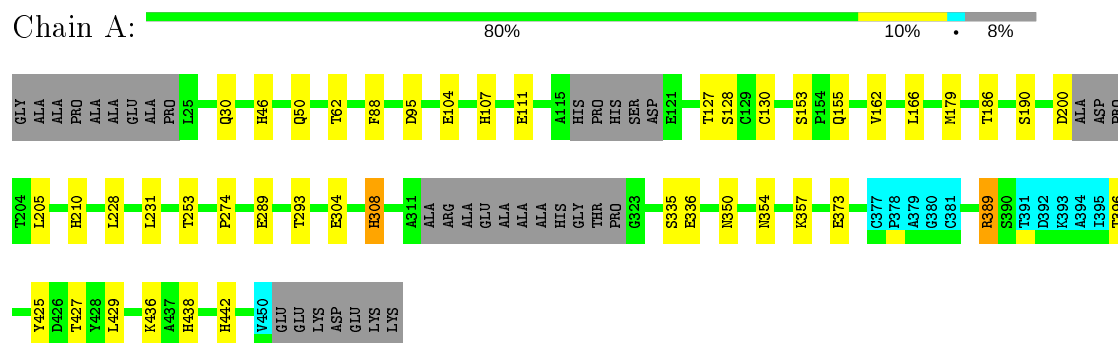


- Molecule 2: Ferredoxin, chloroplastic

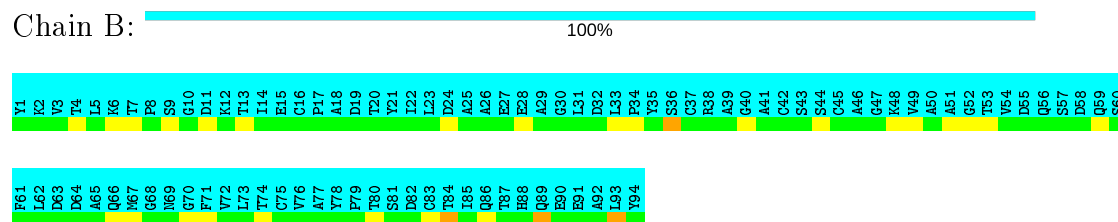


4.2.4 Score per residue for model 4

- Molecule 1: Fe-hydrogenase



- Molecule 2: Ferredoxin, chloroplastic



5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing*.

Of the 200 calculated structures, 4 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
HADDOCK, CNS	refinement	CNS
SPARKY	structure solution	
TOPSPIN	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)	input_cs.cif
Number of chemical shift lists	1
Total number of shifts	180
Number of shifts mapped to atoms	180
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	0%

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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SF4, FES

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	0.27±0.00	0±0/3066 (0.0± 0.0%)	0.42±0.05	1±2/4142 (0.0± 0.1%)
All	All	0.27	0/12264 (0.0%)	0.42	5/16568 (0.0%)

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	129	CYS	O-C-N	12.08	142.03	122.70	1	1
1	A	129	CYS	C-N-CA	-9.48	97.99	121.70	1	1
1	A	129	CYS	CA-C-N	-9.09	97.20	117.20	1	1
1	A	128	SER	N-CA-C	7.08	130.10	111.00	1	1
1	A	128	SER	CB-CA-C	-5.25	100.13	110.10	1	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	3009	3032	3011	18±5
2	B	0	0	0	0±0
3	A	8	0	0	0±0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes
4	B	4	0	0	0±0
All	All	12084	12128	12045	72

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 3.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:205:LEU:CB	1:A:205:LEU:C	0.81	2.49	1	3
1:A:205:LEU:C	1:A:205:LEU:CB	0.78	2.52	3	1
1:A:55:VAL:HG13	1:A:214:THR:HG23	0.71	1.62	3	3
1:A:137:LEU:HD22	1:A:148:VAL:HG21	0.70	1.63	1	1
1:A:130:CYS:SG	1:A:375:MET:HA	0.67	2.29	2	2
1:A:425:TYR:HA	1:A:429:LEU:HB2	0.66	1.67	1	3
1:A:41:ASP:HB3	1:A:44:ARG:HB2	0.64	1.69	2	1
1:A:352:LEU:HG	1:A:376:ALA:HA	0.62	1.70	3	1
1:A:131:PRO:HG3	1:A:188:LYS:HE3	0.61	1.71	2	1
1:A:39:LYS:HA	1:A:44:ARG:HG2	0.61	1.72	3	1
1:A:354:ASN:HA	1:A:357:LYS:HE2	0.61	1.71	4	1
1:A:107:HIS:O	1:A:111:GLU:HG2	0.61	1.95	3	3
1:A:114:GLU:HA	1:A:309:ARG:NH1	0.60	2.12	1	1
1:A:128:SER:O	1:A:134:ILE:HD11	0.55	2.02	1	1
1:A:301:LYS:O	1:A:305:LEU:HG	0.55	2.02	1	3
1:A:45:LYS:HD3	1:A:176:ASP:HA	0.54	1.79	3	1
1:A:249:LEU:HD11	1:A:419:PRO:HD3	0.53	1.80	1	1
1:A:166:LEU:HD11	1:A:170:LYS:HE3	0.52	1.81	2	2
1:A:414:ARG:HB2	1:A:417:GLU:OE1	0.51	2.06	1	1
1:A:257:MET:HG3	1:A:371:PHE:HE2	0.50	1.65	3	2
1:A:438:HIS:HA	1:A:442:HIS:HB2	0.49	1.85	4	1
1:A:376:ALA:HB3	3:A:501:SF4:S1	0.48	2.48	3	1
1:A:51:VAL:HG11	1:A:75:LEU:HD21	0.48	1.85	1	1
1:A:249:LEU:HB2	1:A:413:ARG:HD3	0.47	1.85	2	1
1:A:417:GLU:HA	1:A:422:ARG:NH2	0.47	2.24	1	1
1:A:113:LEU:O	1:A:309:ARG:HD2	0.47	2.10	1	1
1:A:134:ILE:HA	1:A:137:LEU:CD2	0.47	2.39	1	1
1:A:30:GLN:HB3	1:A:210:HIS:CE1	0.45	2.47	2	3
1:A:183:MET:O	1:A:213:THR:HA	0.45	2.12	2	2
1:A:49:VAL:HA	1:A:180:VAL:O	0.44	2.13	2	2
1:A:50:GLN:HA	1:A:88:PHE:O	0.44	2.12	4	1
1:A:286:GLY:HA3	1:A:354:ASN:ND2	0.44	2.28	2	1
1:A:108:ARG:HG2	1:A:121:GLU:HB2	0.44	1.89	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:250:PHE:CE1	1:A:408:GLU:HG2	0.44	2.47	2	1
1:A:228:LEU:HD23	1:A:231:LEU:HD12	0.44	1.89	1	2
1:A:273:LEU:HD12	1:A:274:PRO:HD2	0.44	1.89	3	1
1:A:125:MET:HA	1:A:147:TYR:O	0.44	2.12	2	3
1:A:304:GLU:O	1:A:308:HIS:HB2	0.42	2.14	4	1
1:A:145:ILE:HB	1:A:146:PRO:HD3	0.42	1.91	1	2
1:A:162:VAL:O	1:A:166:LEU:HB3	0.42	2.15	4	1
1:A:431:GLU:HG2	1:A:432:PRO:HD2	0.42	1.90	3	1
1:A:159:ALA:HA	1:A:179:MET:SD	0.42	2.54	1	1
1:A:108:ARG:NH2	1:A:149:SER:HA	0.41	2.30	2	1
1:A:265:TYR:CD2	1:A:273:LEU:HB2	0.41	2.50	3	2
1:A:101:GLU:HA	1:A:101:GLU:OE1	0.41	2.16	2	1
1:A:262:ARG:O	1:A:266:GLU:HG3	0.41	2.16	2	1
1:A:434:GLY:O	1:A:438:HIS:HB2	0.41	2.16	2	1
1:A:103:SER:HB2	1:A:433:LEU:HD13	0.40	1.92	2	1
1:A:254:GLY:HA3	1:A:258:GLU:OE1	0.40	2.16	1	1
1:A:228:LEU:HA	1:A:231:LEU:HD12	0.40	1.94	3	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	388/442 (88%)	375±2 (97±1%)	12±2 (3±1%)	1±0 (0±0%)	44	80
2	B	0	-	-	-	-	-
All	All	1552/2144 (72%)	1499 (97%)	48 (3%)	5 (0%)	44	80

All 2 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	274	PRO	4
1	A	428	TYR	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	317/348 (91%)	291±3 (92±1%)	26±3 (8±1%)	15 62
2	B	0	-	-	-
All	All	1268/1692 (75%)	1164 (92%)	104 (8%)	15 62

All 54 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	186	THR	4
1	A	46	HIS	4
1	A	95	ASP	4
1	A	396	THR	4
1	A	127	THR	4
1	A	389	ARG	4
1	A	427	THR	4
1	A	253	THR	4
1	A	155	GLN	4
1	A	193	ASP	3
1	A	62	THR	3
1	A	43	THR	3
1	A	308	HIS	3
1	A	179	MET	3
1	A	190	SER	3
1	A	128	SER	2
1	A	104	GLU	2
1	A	293	THR	2
1	A	198	CYS	2
1	A	280	GLU	2
1	A	153	SER	2
1	A	360	THR	2
1	A	350	ASN	2
1	A	438	HIS	2
1	A	335	SER	2
1	A	70	THR	2
1	A	290	THR	1
1	A	285	ASP	1

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Mol	Chain	Res	Type	Models (Total)
1	A	188	LYS	1
1	A	230	GLU	1
1	A	336	GLU	1
1	A	129	CYS	1
1	A	337	ASP	1
1	A	143	ASP	1
1	A	89	ASP	1
1	A	436	LYS	1
1	A	271	THR	1
1	A	410	SER	1
1	A	26	SER	1
1	A	130	CYS	1
1	A	121	GLU	1
1	A	175	LYS	1
1	A	304	GLU	1
1	A	403	LEU	1
1	A	289	GLU	1
1	A	417	GLU	1
1	A	107	HIS	1
1	A	373	GLU	1
1	A	133	TRP	1
1	A	219	ASN	1
1	A	200	ASP	1
1	A	244	SER	1
1	A	209	ASP	1
1	A	431	GLU	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

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
3	SF4	A	501	1	0,12,12	0.00±0.00	-
4	FES	B	101	2	0,4,4	0.00±0.00	-

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
3	SF4	A	501	1	-	-	-
4	FES	B	101	2	-	-	-

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SF4	A	501	1	-	-	0±0,6,5,5
4	FES	B	101	2	-	-	0±0,1,1,1

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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 0% for the well-defined parts and 3% for the entire structure.

7.1 Chemical shift list 1

File name: input_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

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	180
Number of shifts mapped to atoms	180
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	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
$^{13}\text{C}_\alpha$	0	—	None (insufficient data)
$^{13}\text{C}_\beta$	0	—	None (insufficient data)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	90	-0.69 ± 0.20	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 0%, i.e. 0 atoms were assigned a chemical shift out of a possible 4711. 0 out of 68 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	0/1934 (0%)	0/769 (0%)	0/792 (0%)	0/373 (0%)
Sidechain	0/2470 (0%)	0/1448 (0%)	0/921 (0%)	0/101 (0%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	0/307 (0%)	0/159 (0%)	0/122 (0%)	0/26 (0%)
Overall	0/4711 (0%)	0/2376 (0%)	0/1835 (0%)	0/500 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 3%, i.e. 179 atoms were assigned a chemical shift out of a possible 5832. 0 out of 81 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	179/2449 (7%)	89/974 (9%)	0/1002 (0%)	90/473 (19%)
Sidechain	0/3010 (0%)	0/1761 (0%)	0/1134 (0%)	0/115 (0%)
Aromatic	0/373 (0%)	0/193 (0%)	0/152 (0%)	0/28 (0%)
Overall	179/5832 (3%)	89/2928 (3%)	0/2288 (0%)	90/616 (15%)

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
2	B	50	ALA	N	102.77	141.07 – 105.37	-5.7

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 B:

