



Full wwPDB NMR Structure Validation Report ⓘ

Mar 8, 2026 – 06:00 PM UTC

PDB ID : 6BHO / pdb_00006bho
BMRB ID : 26577
Title : Green Light-Absorbing State of NpR6012g4, a Red/Green Cyanobacteriochrome
Authors : Lim, S.; Yu, Q.; Rockwell, N.C.; Martin, S.S.; Lagarias, J.C.; Ames, J.B.
Deposited on : 2017-10-31

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

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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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

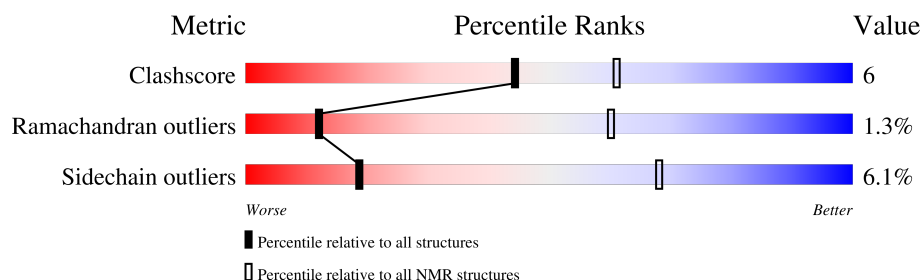
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 40%.

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	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

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	180	

2 Ensemble composition and analysis

This entry contains 10 models. Model 9 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:600-A:648, A:653-A:720, A:724-A:747 (141)	0.82	9

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 1 single-model cluster was found.

Cluster number	Models
1	1, 2, 8, 9, 10
2	5, 6
3	3, 4
Single-model clusters	7

3 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 2552 atoms, of which 1248 are hydrogens and 0 are deuteriums.

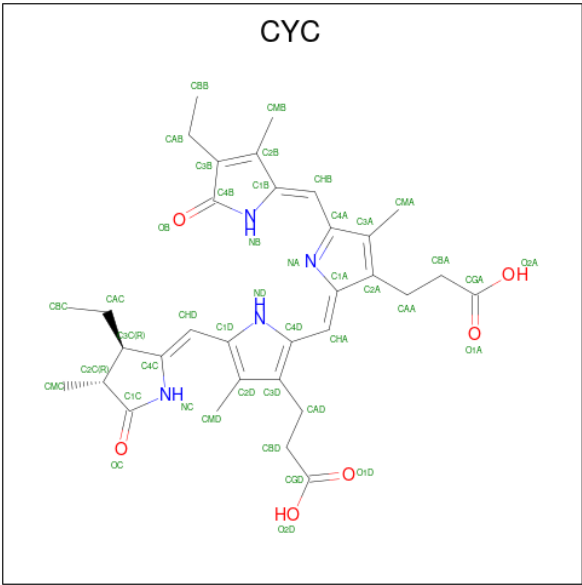
- Molecule 1 is a protein called Methyl-accepting chemotaxis sensory transducer with phytochrome sensor.

Mol	Chain	Residues	Atoms						Trace
1	A	156	Total	C	H	N	O	S	0
			2471	803	1210	214	242	2	

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	583	MET	-	initiating methionine	UNP B2IU14
A	584	GLY	-	expression tag	UNP B2IU14
A	761	PRO	-	expression tag	UNP B2IU14
A	762	GLY	-	expression tag	UNP B2IU14

- Molecule 2 is PHYCOCYANOBILIN (CCD ID: CYC) (formula: C₃₃H₄₀N₄O₆).



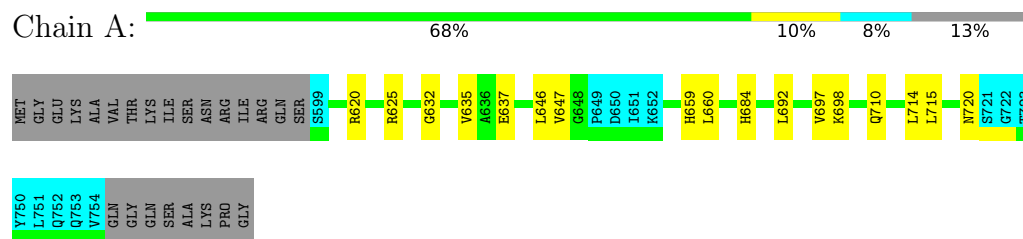
Mol	Chain	Residues	Atoms					
2	A	1	Total	C	H	N	O	
			81	33	38	4	6	

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: Methyl-accepting chemotaxis sensory transducer with phytochrome sensor

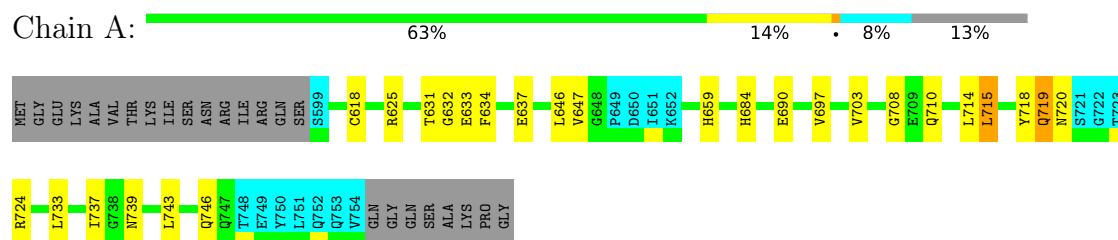


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

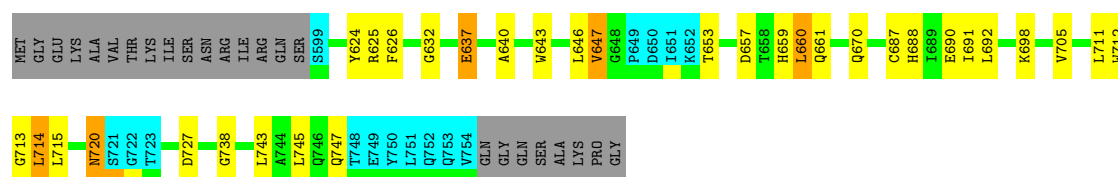
- Molecule 1: Methyl-accepting chemotaxis sensory transducer with phytochrome sensor



4.2.2 Score per residue for model 2

- Molecule 1: Methyl-accepting chemotaxis sensory transducer with phytochrome sensor

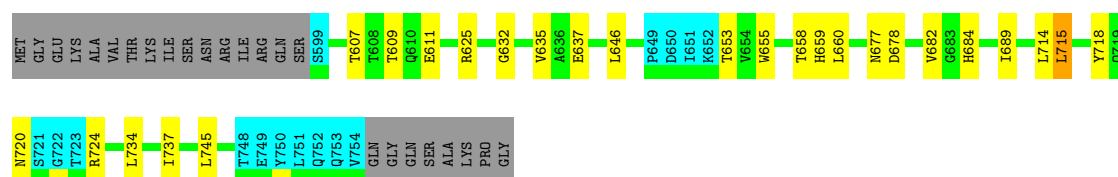




4.2.3 Score per residue for model 3

- Molecule 1: Methyl-accepting chemotaxis sensory transducer with phytochrome sensor

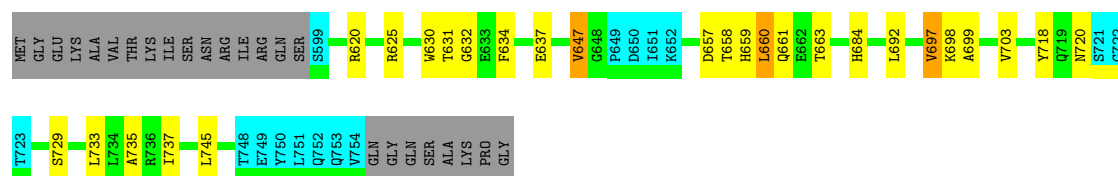
Chain A: 64% 14% 8% 13%



4.2.4 Score per residue for model 4

- Molecule 1: Methyl-accepting chemotaxis sensory transducer with phytochrome sensor

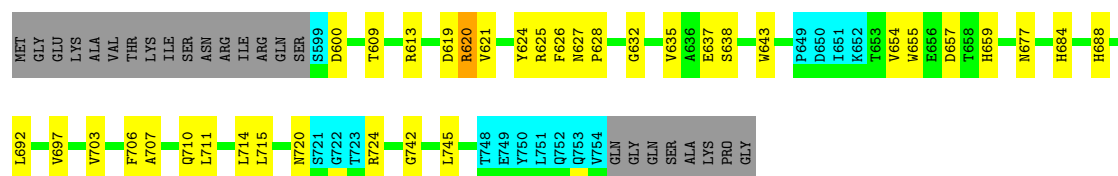
Chain A: 63% 13% 8% 13%



4.2.5 Score per residue for model 5

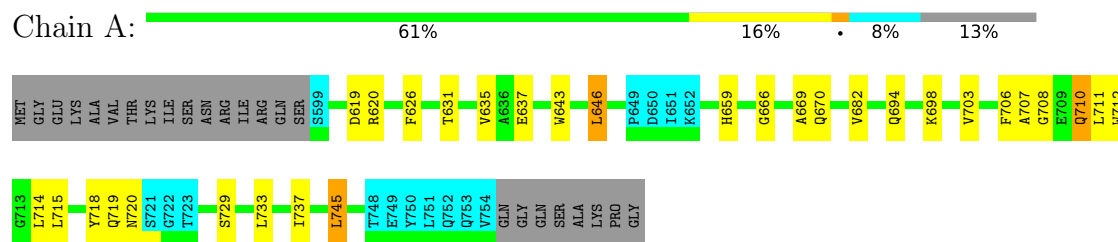
- Molecule 1: Methyl-accepting chemotaxis sensory transducer with phytochrome sensor

Chain A: 58% 19% 8% 13%



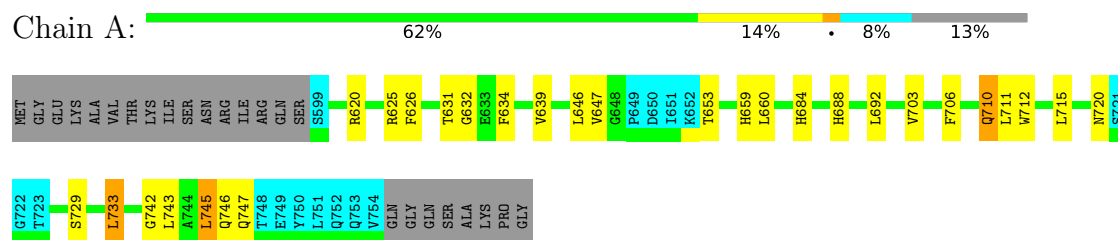
4.2.6 Score per residue for model 6

- Molecule 1: Methyl-accepting chemotaxis sensory transducer with phytochrome sensor



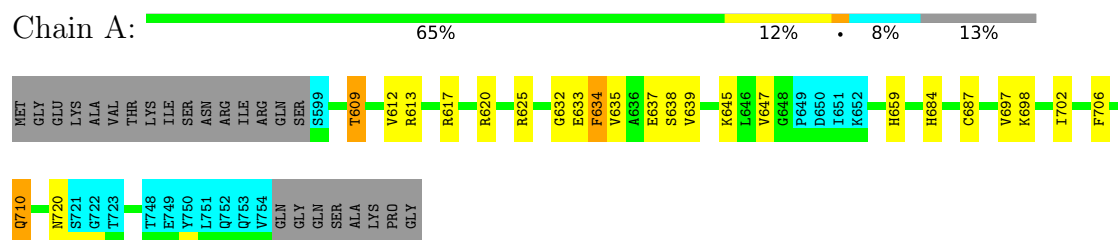
4.2.7 Score per residue for model 7

- Molecule 1: Methyl-accepting chemotaxis sensory transducer with phytochrome sensor



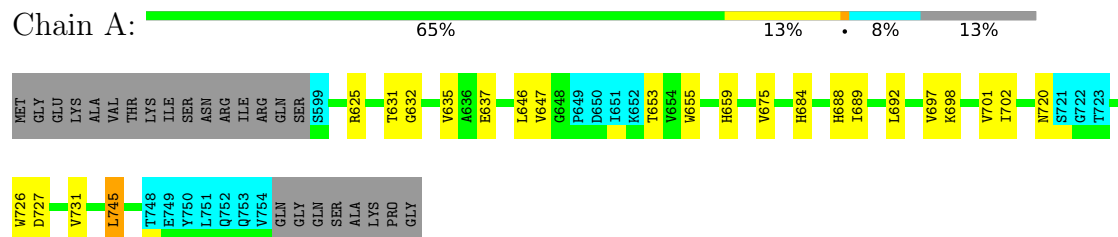
4.2.8 Score per residue for model 8

- Molecule 1: Methyl-accepting chemotaxis sensory transducer with phytochrome sensor



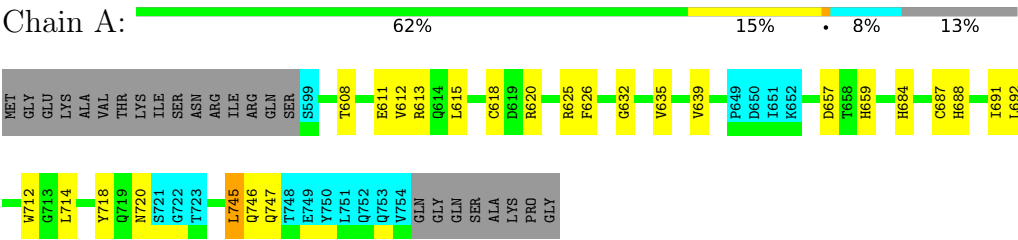
4.2.9 Score per residue for model 9 (medoid)

- Molecule 1: Methyl-accepting chemotaxis sensory transducer with phytochrome sensor



4.2.10 Score per residue for model 10

- Molecule 1: Methyl-accepting chemotaxis sensory transducer with phytochrome sensor



5 Refinement protocol and experimental data overview

The models were refined using the following method: *DGSA-distance geometry simulated annealing*.

Of the 200 calculated structures, 10 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
X-PLOR NIH	refinement	2.44
NMRPipe	structure solution	8.9
Sparky	structure solution	3.12

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	921
Number of shifts mapped to atoms	875
Number of unparsed shifts	0
Number of shifts with mapping errors	46
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	40%

6 Model quality

6.1 Standard geometry

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

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	1145	1097	1097	14±4
2	A	43	38	37	3±2
All	All	11880	11350	11340	148

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 6.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:659:HIS:HB2	2:A:800:CYC:C1A	0.79	2.07	5	7
1:A:657:ASP:HB2	2:A:800:CYC:C1C	0.68	2.18	10	2
1:A:706:PHE:HA	1:A:710:GLN:O	0.64	1.93	8	4
1:A:625:ARG:O	1:A:632:GLY:HA2	0.63	1.94	7	9
1:A:659:HIS:HB2	2:A:800:CYC:CHA	0.60	2.26	3	5
1:A:620:ARG:NH1	1:A:646:LEU:HD21	0.60	2.11	6	1
1:A:619:ASP:OD1	1:A:719:GLN:HA	0.59	1.96	6	1
1:A:627:ASN:OD1	1:A:628:PRO:HD2	0.58	1.98	5	1
1:A:675:VAL:HG13	1:A:701:VAL:HB	0.58	1.74	9	1
2:A:800:CYC:HMD1	2:A:800:CYC:HBD1	0.57	1.76	1	1
1:A:637:GLU:HB2	1:A:647:VAL:CG2	0.57	2.30	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:620:ARG:HG2	1:A:639:VAL:HG23	0.56	1.78	7	3
1:A:708:GLY:HA2	1:A:746:GLN:NE2	0.56	2.16	10	2
2:A:800:CYC:HMA2	2:A:800:CYC:HMB2	0.56	1.78	10	2
1:A:703:VAL:CG1	1:A:735:ALA:HA	0.56	2.31	4	1
1:A:626:PHE:CZ	1:A:714:LEU:HD22	0.55	2.37	10	3
1:A:688:HIS:O	1:A:692:LEU:HG	0.54	2.02	7	5
2:A:800:CYC:HMB3	2:A:800:CYC:HBB3	0.54	1.78	4	1
1:A:703:VAL:HG13	1:A:735:ALA:HA	0.53	1.81	4	1
1:A:626:PHE:CE1	1:A:711:LEU:HG	0.52	2.40	5	4
1:A:675:VAL:HG11	1:A:726:TRP:CD1	0.51	2.40	9	1
2:A:800:CYC:HHAA	2:A:800:CYC:CGA	0.51	2.35	9	2
1:A:678:ASP:O	1:A:682:VAL:HG23	0.51	2.05	3	1
1:A:712:TRP:CE2	1:A:745:LEU:HD11	0.51	2.40	6	2
1:A:630:TRP:O	1:A:661:GLN:HG2	0.50	2.07	4	1
1:A:727:ASP:O	1:A:731:VAL:HG23	0.50	2.07	9	1
1:A:677:ASN:HB2	1:A:724:ARG:O	0.49	2.08	3	1
1:A:729:SER:O	1:A:733:LEU:HB2	0.49	2.08	7	2
1:A:608:THR:O	1:A:612:VAL:HG23	0.49	2.08	10	1
1:A:657:ASP:HA	2:A:800:CYC:OC	0.48	2.08	5	1
1:A:607:THR:O	1:A:611:GLU:HG2	0.48	2.09	3	1
1:A:733:LEU:O	1:A:737:ILE:HG12	0.47	2.09	1	3
1:A:666:GLY:O	1:A:670:GLN:HG3	0.47	2.09	6	1
1:A:625:ARG:HG3	1:A:712:TRP:CH2	0.47	2.45	2	1
2:A:800:CYC:HMA3	2:A:800:CYC:HMB2	0.47	1.85	5	1
1:A:640:ALA:HB3	1:A:643:TRP:CD1	0.47	2.45	2	1
1:A:677:ASN:HB3	1:A:724:ARG:O	0.47	2.10	5	1
1:A:620:ARG:NH1	1:A:643:TRP:HB3	0.46	2.25	5	1
1:A:729:SER:O	1:A:733:LEU:HG	0.46	2.10	6	1
1:A:645:LYS:N	1:A:645:LYS:HD2	0.46	2.25	8	1
1:A:620:ARG:HD2	1:A:637:GLU:CD	0.46	2.36	6	1
1:A:743:LEU:O	1:A:747:GLN:HG2	0.46	2.11	2	1
1:A:634:PHE:HB2	1:A:647:VAL:HG22	0.46	1.88	8	1
1:A:692:LEU:HB3	1:A:697:VAL:O	0.45	2.11	10	3
2:A:800:CYC:HMA3	2:A:800:CYC:CMB	0.45	2.41	5	1
1:A:675:VAL:HG22	1:A:701:VAL:HG23	0.45	1.87	9	1
1:A:613:ARG:HD3	1:A:613:ARG:C	0.45	2.37	5	1
1:A:707:ALA:O	1:A:712:TRP:HB2	0.45	2.11	6	1
1:A:621:VAL:HB	1:A:638:SER:OG	0.45	2.10	5	1
1:A:675:VAL:CG1	1:A:726:TRP:CD1	0.45	3.00	9	1
1:A:654:VAL:HG23	1:A:655:TRP:CD1	0.45	2.46	5	1
1:A:613:ARG:HG3	1:A:618:CYS:O	0.45	2.11	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:703:VAL:CG2	1:A:715:LEU:HB3	0.44	2.43	5	3
1:A:634:PHE:CB	1:A:647:VAL:HG12	0.44	2.42	7	1
1:A:609:THR:HB	1:A:638:SER:CB	0.44	2.42	8	1
1:A:613:ARG:O	1:A:617:ARG:HA	0.44	2.13	8	1
1:A:710:GLN:OE1	1:A:710:GLN:HA	0.44	2.13	1	1
1:A:637:GLU:OE2	1:A:646:LEU:HB2	0.44	2.12	3	1
1:A:657:ASP:O	2:A:800:CYC:CHB	0.44	2.65	4	1
1:A:618:CYS:HA	1:A:719:GLN:HB2	0.44	1.88	1	1
1:A:699:ALA:O	1:A:718:TYR:HB3	0.44	2.13	4	1
1:A:697:VAL:HG22	1:A:718:TYR:CE1	0.44	2.48	1	1
1:A:745:LEU:C	1:A:745:LEU:HD13	0.44	2.37	5	1
1:A:660:LEU:HD22	1:A:660:LEU:N	0.44	2.27	7	1
1:A:611:GLU:O	1:A:615:LEU:HG	0.44	2.13	10	1
1:A:637:GLU:OE2	1:A:647:VAL:HG22	0.43	2.12	4	1
2:A:800:CYC:HMA2	2:A:800:CYC:CMB	0.43	2.43	10	1
1:A:609:THR:HB	1:A:638:SER:OG	0.43	2.13	8	2
1:A:714:LEU:HD23	1:A:714:LEU:N	0.43	2.28	2	3
1:A:712:TRP:CD1	1:A:745:LEU:HD11	0.43	2.49	7	1
1:A:619:ASP:HB2	1:A:620:ARG:NE	0.43	2.29	5	1
1:A:637:GLU:HB3	1:A:647:VAL:HG23	0.43	1.90	1	1
1:A:637:GLU:CG	1:A:647:VAL:HG22	0.43	2.43	2	1
1:A:714:LEU:HD13	1:A:715:LEU:N	0.43	2.28	3	2
1:A:734:LEU:O	1:A:737:ILE:HG13	0.42	2.13	3	1
1:A:658:THR:HB	1:A:660:LEU:HD12	0.42	1.90	4	1
1:A:620:ARG:HB2	1:A:718:TYR:CE1	0.42	2.49	10	1
2:A:800:CYC:HBA2	2:A:800:CYC:HMA1	0.42	1.91	5	1
1:A:660:LEU:H	1:A:660:LEU:HD22	0.42	1.74	2	1
1:A:660:LEU:HA	1:A:663:THR:HG22	0.42	1.92	4	1
1:A:634:PHE:HB3	1:A:647:VAL:HG12	0.42	1.92	7	1
1:A:703:VAL:HG23	1:A:715:LEU:HB3	0.42	1.92	7	1
1:A:620:ARG:HB2	1:A:718:TYR:CD1	0.42	2.50	4	1
1:A:687:CYS:O	1:A:691:ILE:HG13	0.41	2.15	10	2
1:A:660:LEU:HD22	1:A:660:LEU:H	0.41	1.76	7	1
1:A:742:GLY:O	1:A:746:GLN:HG3	0.41	2.15	7	1
1:A:619:ASP:HB2	1:A:643:TRP:CD1	0.41	2.51	6	1
1:A:687:CYS:HB2	2:A:800:CYC:HBC1	0.41	1.48	10	1
1:A:705:VAL:HB	1:A:713:GLY:O	0.41	2.16	2	1
1:A:624:TYR:O	1:A:713:GLY:HA3	0.41	2.15	2	1
1:A:634:PHE:CB	1:A:647:VAL:HG22	0.41	2.45	8	1
1:A:687:CYS:SG	2:A:800:CYC:HHD	0.41	2.56	8	1
1:A:739:ASN:O	1:A:743:LEU:HG	0.41	2.16	1	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:624:TYR:HB2	1:A:714:LEU:CD2	0.41	2.46	5	1
1:A:707:ALA:HB2	1:A:742:GLY:HA2	0.41	1.92	5	1
1:A:743:LEU:O	1:A:747:GLN:HG3	0.41	2.15	7	1
1:A:705:VAL:HG13	1:A:738:GLY:O	0.41	2.16	2	1
1:A:688:HIS:CE1	1:A:692:LEU:HD11	0.40	2.51	10	1
1:A:620:ARG:NH2	1:A:646:LEU:HB2	0.40	2.31	7	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	141/180 (78%)	131±2 (93±2%)	8±2 (5±2%)	2±1 (1±1%)	12	60
All	All	1410/1800 (78%)	1314 (93%)	77 (5%)	19 (1%)	12	60

All 6 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	720	ASN	10
1	A	647	VAL	3
1	A	710	GLN	3
1	A	719	GLN	1
1	A	669	ALA	1
1	A	708	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	121/154 (79%)	114±2 (94±2%)	7±2 (6±2%)	19	68
All	All	1210/1540 (79%)	1136 (94%)	74 (6%)	19	68

All 31 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	684	HIS	8
1	A	745	LEU	7
1	A	635	VAL	6
1	A	631	THR	5
1	A	653	THR	4
1	A	697	VAL	4
1	A	634	PHE	3
1	A	715	LEU	3
1	A	637	GLU	3
1	A	660	LEU	3
1	A	633	GLU	2
1	A	690	GLU	2
1	A	609	THR	2
1	A	655	TRP	2
1	A	689	ILE	2
1	A	718	TYR	2
1	A	702	ILE	2
1	A	724	ARG	1
1	A	661	GLN	1
1	A	670	GLN	1
1	A	714	LEU	1
1	A	727	ASP	1
1	A	658	THR	1
1	A	659	HIS	1
1	A	600	ASP	1
1	A	620	ARG	1
1	A	646	LEU	1
1	A	682	VAL	1
1	A	694	GLN	1
1	A	733	LEU	1
1	A	612	VAL	1

6.3.3 RNA ⓘ

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 oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

1 ligand is 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
2	CYC	A	800	1	46,46,46	1.97±0.06	10±1 (20±2%)

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
2	CYC	A	800	1	63,67,67	2.39±0.02	18±1 (27±1%)

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
2	CYC	A	800	1	-	0±0,26,74,74	0±0,4,4,4

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
2	A	800	CYC	C1A-NA	6.94	1.53	1.38	9	10
2	A	800	CYC	C1B-C2B	5.93	1.55	1.45	9	10
2	A	800	CYC	C4A-C3A	5.89	1.33	1.45	5	10
2	A	800	CYC	C4A-NA	3.97	1.45	1.36	5	10
2	A	800	CYC	C2A-C3A	3.75	1.28	1.36	8	10
2	A	800	CYC	C4D-C3D	2.80	1.49	1.42	6	10
2	A	800	CYC	O1A-CGA	2.79	1.31	1.22	10	1
2	A	800	CYC	C4C-NC	2.69	1.32	1.37	3	10
2	A	800	CYC	CHD-C1D	2.56	1.46	1.40	6	10
2	A	800	CYC	C2C-C3C	2.27	1.60	1.54	2	7
2	A	800	CYC	C3C-C4C	2.20	1.55	1.50	6	6
2	A	800	CYC	CHB-C4A	2.17	1.45	1.40	6	1

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

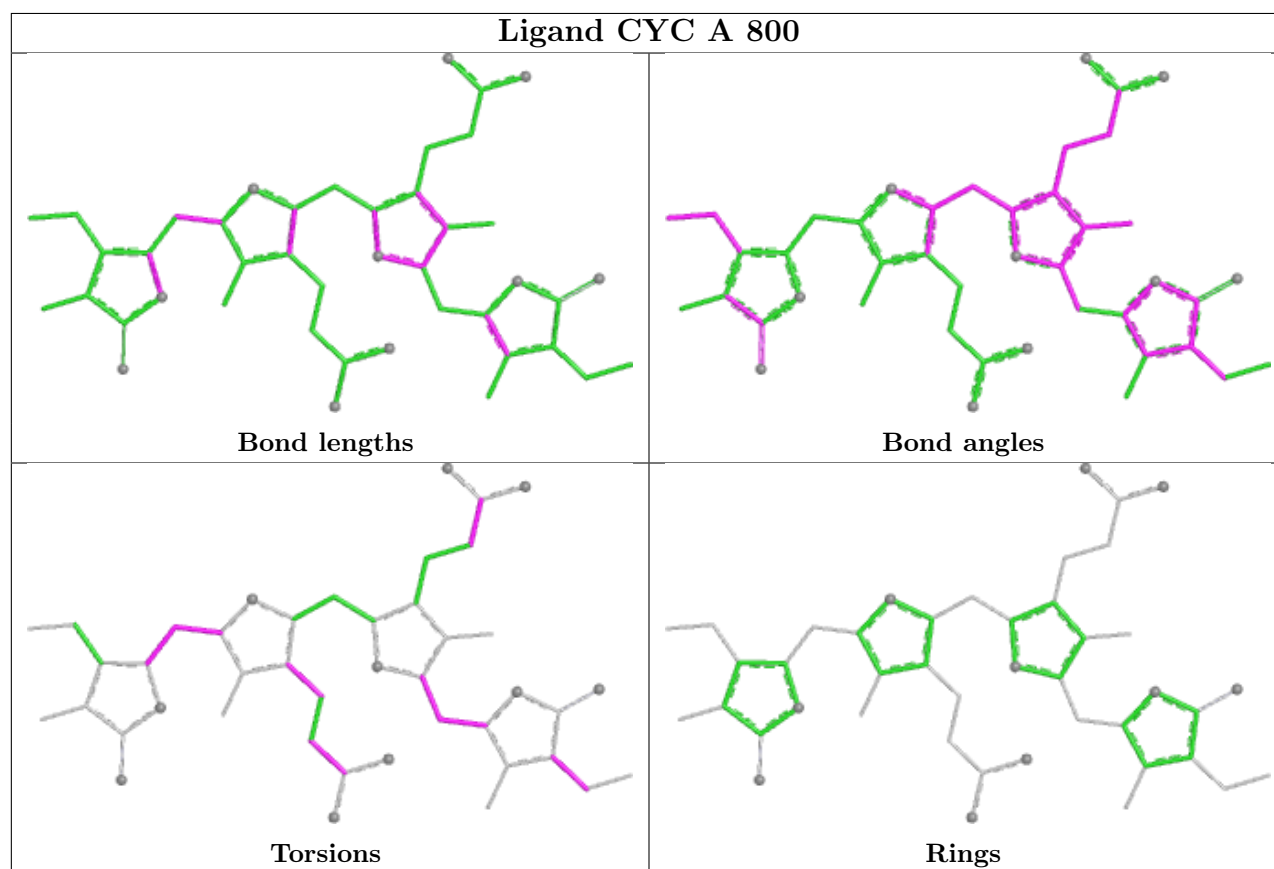
Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	A	800	CYC	C4A-C3A-C2A	9.28	117.01	106.48	2	10
2	A	800	CYC	C2A-C1A-NA	8.19	98.45	110.04	9	10
2	A	800	CYC	C1A-C2A-C3A	5.23	112.39	106.73	8	10
2	A	800	CYC	C1B-NB-C4B	4.57	116.27	110.66	10	10
2	A	800	CYC	C2B-C1B-NB	4.41	100.54	106.97	9	10
2	A	800	CYC	CHB-C4A-C3A	3.80	134.63	124.87	10	10
2	A	800	CYC	C3A-C4A-NA	3.72	102.46	110.58	8	10
2	A	800	CYC	CHA-C4D-ND	3.71	133.68	125.29	5	10
2	A	800	CYC	CHA-C1A-C2A	3.60	133.71	125.40	2	10
2	A	800	CYC	CAB-C3B-C2B	3.11	133.27	127.56	4	10
2	A	800	CYC	CHA-C4D-C3D	3.05	120.66	127.22	7	10
2	A	800	CYC	CAA-CBA-CGA	2.57	106.84	113.67	8	6
2	A	800	CYC	CBC-CAC-C3C	2.57	107.96	113.41	7	10
2	A	800	CYC	CAA-C2A-C3A	2.57	123.06	127.87	9	8
2	A	800	CYC	CMA-C3A-C4A	2.52	121.19	125.10	5	10
2	A	800	CYC	C1C-NC-C4C	2.45	116.48	113.41	3	9
2	A	800	CYC	C3B-C4B-NB	2.41	104.84	106.77	3	9
2	A	800	CYC	CHA-C1A-NA	2.37	129.57	124.60	5	2
2	A	800	CYC	OC-C1C-C2C	2.26	127.97	126.17	2	6
2	A	800	CYC	C1A-NA-C4A	2.07	110.32	106.52	3	3
2	A	800	CYC	C1B-C2B-C3B	2.04	109.96	107.86	3	1
2	A	800	CYC	CHB-C1B-NB	2.02	130.37	126.06	7	1

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



6.7 Other polymers [i](#)

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 40% for the well-defined parts and 41% for the entire structure.

7.1 Chemical shift list 1

File name: working_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	921
Number of shifts mapped to atoms	875
Number of unparsed shifts	0
Number of shifts with mapping errors	46
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- No matching atom found in the structure. All 46 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	755	GLN	H	8.368	?	1
1	A	755	GLN	HA	4.309	?	1
1	A	755	GLN	C	176.8	?	1
1	A	755	GLN	CA	56.46	?	1
1	A	755	GLN	CB	29.22	?	1
1	A	755	GLN	N	122.9	?	1
1	A	756	GLY	H	8.362	?	1
1	A	756	GLY	HA2	3.977	?	2
1	A	756	GLY	HA3	3.977	?	2
1	A	756	GLY	C	174.3	?	1
1	A	756	GLY	CA	45.52	?	1
1	A	756	GLY	N	109.6	?	1
1	A	757	GLN	H	8.212	?	1
1	A	757	GLN	HA	4.416	?	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	757	GLN	C	176.2	?	1
1	A	757	GLN	CA	55.95	?	1
1	A	757	GLN	CB	29.52	?	1
1	A	757	GLN	N	119.7	?	1
1	A	758	SER	H	8.358	?	1
1	A	758	SER	HA	4.436	?	1
1	A	758	SER	C	174.1	?	1
1	A	758	SER	CA	58.45	?	1
1	A	758	SER	CB	63.98	?	1
1	A	758	SER	N	116.9	?	1
1	A	759	ALA	H	8.303	?	1
1	A	759	ALA	HA	4.343	?	1
1	A	759	ALA	C	177.3	?	1
1	A	759	ALA	CA	52.38	?	1
1	A	759	ALA	CB	19.33	?	1
1	A	759	ALA	N	125.9	?	1
1	A	760	LYS	H	8.301	?	1
1	A	760	LYS	HA	4.622	?	1
1	A	760	LYS	C	174.6	?	1
1	A	760	LYS	CA	54.18	?	1
1	A	760	LYS	CB	32.65	?	1
1	A	760	LYS	N	122.2	?	1
1	A	761	PRO	HA	4.444	?	1
1	A	761	PRO	C	176.4	?	1
1	A	761	PRO	CA	63.49	?	1
1	A	761	PRO	CB	32.15	?	1
1	A	762	GLY	H	8.009	?	1
1	A	762	GLY	HA2	3.773	?	2
1	A	762	GLY	HA3	3.773	?	2
1	A	762	GLY	C	179.0	?	1
1	A	762	GLY	CA	46.16	?	1
1	A	762	GLY	N	115.5	?	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
$^{13}\text{C}_\alpha$	163	-0.41 ± 0.23	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	138	0.21 ± 0.10	None needed (< 0.5 ppm)
$^{13}\text{C}'$	162	-0.08 ± 0.16	None needed (< 0.5 ppm)

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Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
^{15}N	157	0.51 ± 0.29	None needed (imprecise)

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 40%, i.e. 790 atoms were assigned a chemical shift out of a possible 1964. 0 out of 30 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	672/709 (95%)	256/289 (89%)	279/282 (99%)	137/138 (99%)
Sidechain	118/1062 (11%)	0/689 (0%)	118/331 (36%)	0/42 (0%)
Aromatic	0/193 (0%)	0/96 (0%)	0/88 (0%)	0/9 (0%)
Overall	790/1964 (40%)	256/1074 (24%)	397/701 (57%)	137/189 (72%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 41%, i.e. 875 atoms were assigned a chemical shift out of a possible 2157. 0 out of 32 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	743/783 (95%)	284/319 (89%)	309/312 (99%)	150/152 (99%)
Sidechain	132/1172 (11%)	0/760 (0%)	132/367 (36%)	0/45 (0%)
Aromatic	0/202 (0%)	0/100 (0%)	0/93 (0%)	0/9 (0%)
Overall	875/2157 (41%)	284/1179 (24%)	441/772 (57%)	150/206 (73%)

7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

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. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:

