

Integrative Structure Validation Report ?

July 22, 2024 - 04:10 PM PDT

The following software was used in the production of this report:

Python-IHM Version 1.3
MolProbity Version 4.5.2
Integrative Modeling Validation Version 1.2

PDB ID	9A0J
PDB-Dev ID	PDBDEV_00000055
Structure Title	Deep learning enables the atomic structure determination of the Fanconi Anemia core complex from cryoEM
Structure Authors	Farrell DP; Anishchenko I; Shakeel S; Lauko A; Passmore LA; Baker D; DiMaio F

This is a PDB-Dev IM Structure Validation Report for a publicly released PDB-Dev entry.

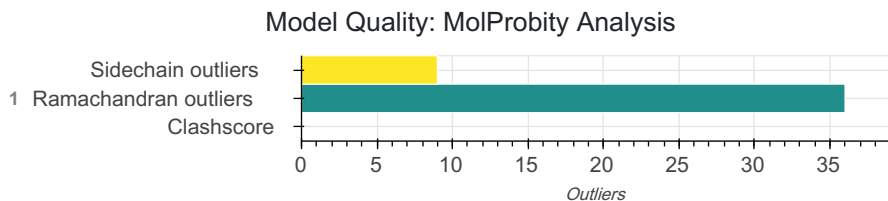
We welcome your comments at pdb-dev@mail.wwpdb.org

A user guide is available at https://pdb-dev.wwpdb.org/validation_help.html with specific help available everywhere you see the ? symbol.

List of references used to build this report is available [here](#).

Overall quality ?

This validation report contains model quality assessments for all structures, data quality assessment for SAS datasets and fit to model assessments for SAS datasets. Data quality and fit to model assessments for other datasets and model uncertainty are under development. Number of plots is limited to 256.



Ensemble information ?

This entry consists of 0 distinct ensemble(s).

Summary

This entry consists of 1 unique models, with 11 subunits in each model. A total of 93 datasets or restraints were used to build this entry. Each model is represented by 76 rigid bodies and 4 flexible or non-rigid units.

Entry composition

There is 1 unique type of models in this entry. This model is titled Top Model/Best scoring model.

Model ID	Subunit number	Subunit ID	Subunit name	Chain ID	Chain ID [auth]	Total residues
1	1	1	fancB	B	B	867
1	2	1	fancB	b	b	867
1	3	2	fancC	C	C	595
1	4	3	fancE	E	E	520
1	5	4	fancF	F	F	350
1	6	5	fancG	G	G	648
1	7	5	fancG	g	g	648
1	8	6	fancL	L	L	373
1	9	6	fancL	l	l	373
1	10	7	faap100	P	P	888
1	11	7	faap100	p	p	888

Datasets used for modeling

There are 93 unique datasets used to build the models in this entry.

ID	Dataset type	Database name	Data access code
1	De Novo model	File	10.5281/zenodo.3979898
2	De Novo model	File	10.5281/zenodo.3979898
3	De Novo model	File	10.5281/zenodo.3979898
4	De Novo model	File	10.5281/zenodo.3979898
5	De Novo model	File	10.5281/zenodo.3979898
6	De Novo model	File	10.5281/zenodo.3979898
7	De Novo model	File	10.5281/zenodo.3979898

ID	Dataset type	Database name	Data access code
8	De Novo model	File	10.5281/zenodo.3979898
9	De Novo model	File	10.5281/zenodo.3979898
10	De Novo model	File	10.5281/zenodo.3979898
11	De Novo model	File	10.5281/zenodo.3979898
12	De Novo model	File	10.5281/zenodo.3979898
13	De Novo model	File	10.5281/zenodo.3979898
14	De Novo model	File	10.5281/zenodo.3979898
15	De Novo model	File	10.5281/zenodo.3979898
16	De Novo model	File	10.5281/zenodo.3979898
17	De Novo model	File	10.5281/zenodo.3979898
18	De Novo model	File	10.5281/zenodo.3979898
19	De Novo model	File	10.5281/zenodo.3979898
20	De Novo model	File	10.5281/zenodo.3979898
21	De Novo model	File	10.5281/zenodo.3979898
22	De Novo model	File	10.5281/zenodo.3979898
23	De Novo model	File	10.5281/zenodo.3979898
24	De Novo model	File	10.5281/zenodo.3979898
25	De Novo model	File	10.5281/zenodo.3979898
26	De Novo model	File	10.5281/zenodo.3979898
27	De Novo model	File	10.5281/zenodo.3979898
28	De Novo model	File	10.5281/zenodo.3979898
29	De Novo model	File	10.5281/zenodo.3979898
30	De Novo model	File	10.5281/zenodo.3979898
31	De Novo model	File	10.5281/zenodo.3979898
32	De Novo model	File	10.5281/zenodo.3979898
33	De Novo model	File	10.5281/zenodo.3979898
34	De Novo model	File	10.5281/zenodo.3979898
35	De Novo model	File	10.5281/zenodo.3979898

ID	Dataset type	Database name	Data access code
36	3DEM volume	EMDB	EMDB-10291
37	3DEM volume	EMDB	EMDB-10292
38	3DEM volume	EMDB	EMDB-10293
39	Crosslinking-MS data	PRIDE	PXD014282
40	Comparative model	File	10.5281/zenodo.3979898
41	Comparative model	File	10.5281/zenodo.3979898
42	Comparative model	File	10.5281/zenodo.3979898
43	Comparative model	File	10.5281/zenodo.3979898
44	Comparative model	File	10.5281/zenodo.3979898
45	Comparative model	File	10.5281/zenodo.3979898
46	Comparative model	File	10.5281/zenodo.3979898
47	Comparative model	File	10.5281/zenodo.3979898
48	Comparative model	File	10.5281/zenodo.3979898
49	Comparative model	File	10.5281/zenodo.3979898
50	Comparative model	File	10.5281/zenodo.3979898
51	Experimental model	PDB	4ccg
52	Experimental model	PDB	4zdt
53	Experimental model	PDB	5o6c
54	Experimental model	PDB	2d8s
55	Experimental model	PDB	1vyx
56	Experimental model	PDB	3k1l
57	Experimental model	PDB	2iqc
58	Experimental model	PDB	1r5m
59	Experimental model	PDB	5m23
60	Experimental model	PDB	6chg
61	Experimental model	PDB	6f9n
62	Experimental model	PDB	2pbi

ID	Dataset type	Database name	Data access code
63	Experimental model	PDB	5m89
64	Experimental model	PDB	4ggc
65	Experimental model	PDB	6eoj
66	Experimental model	PDB	5kdo
67	Experimental model	PDB	5oql
68	Experimental model	PDB	5opt
69	Experimental model	PDB	3odt
70	Experimental model	PDB	5a31
71	Experimental model	PDB	5xyi
72	Experimental model	PDB	2ilr
73	Experimental model	PDB	5orq
74	Experimental model	PDB	1fch
75	Experimental model	PDB	3hym
76	Experimental model	PDB	3fp2
77	Experimental model	PDB	2gw1
78	Experimental model	PDB	6c9m
79	Experimental model	PDB	6eou
80	Experimental model	PDB	3ieg
81	Experimental model	PDB	4rg9
82	Experimental model	PDB	2xpi
83	Experimental model	PDB	3cvp
84	Experimental model	PDB	5i9f
85	Experimental model	PDB	5aio
86	Experimental model	PDB	5dse
87	Experimental model	PDB	4g1t
88	Experimental model	PDB	4zlh
89	Experimental model	PDB	2y4t

ID	Dataset type	Database name	Data access code
90	Experimental model	PDB	3u4t
91	Experimental model	PDB	4pir
92	Experimental model	PDB	4buj
93	3DEM volume	File	10.5281/zenodo.3979898

Representation

This entry has only one representation and includes 76 rigid bodies and 4 flexible units

Chain ID	Rigid bodies	Non-rigid segments
B	378-434, 1-370, 441-780, 231-365, 441-660, 651-770, 1-235, 466-626	435-440
b	378-434, 1-370, 441-780, 231-365, 441-660, 651-770, 1-235, 466-626	435-440
C	331-570, 176-335, 1-335, 1-175	-
E	266-520, 1-150, 261-520	151-170
F	140-341	342-350
G	44-645, 1-320, 181-320, 201-435, 204-315, 1-175, 321-648	-
g	44-645, 1-320, 181-320, 201-435, 204-315, 1-175, 321-648	-
L	191-300, 301-373, 104-373, 101-300, 2-91, 101-205, 1-100	-
l	191-300, 301-373, 104-373, 101-300, 2-91, 101-205, 1-100	-
P	28-442, 1-300, 711-820, 1-200, 186-480, 301-480, 510-609, 491-615, 714-803, 804-888, 453-507, 491-820	-
p	28-442, 1-300, 711-820, 1-200, 186-480, 301-480, 510-609, 491-615, 714-803, 804-888, 453-507, 491-820	-

Methodology and software

This entry is a result of 1 distinct protocol(s).

Step number	Protocol ID	Method name	Method type	Method description	Number of computed models	Multi state modeling	Multi scale modeling
1	1	Monte Carlo	Production sampling	None	None	False	False

Step number	Protocol ID	Method name	Method type	Method description	Number of computed models	Multi state modeling	Multi scale modeling
2	1	Rosetta Hybridize	Rosetta Hybridize	None	None	False	False

There are 3 software packages reported in this entry.

ID	Software name	Software version	Software classification	Software location
1	Rosetta	Rosetta version unknown:ff8ee24ee5f65423d5064cba818ede41d012fa87 2020-08-10 10:39:53 -0700 from git@github.com:RosettaCommons/main.git	RosettaCM/hybridize and unpublished 'complex assembly'	https://www.rosettacommons.org/
2	trRosetta	1.0.0	trRosetta	https://github.com/gjoni/trRosetta
3	HHpred	website	protein homology detection	https://toolkit.tuebingen.mpg.de/hhpred

Data quality

3DEM volume

Validation for this section is under development.

Crosslinking-MS

Validation for this section is under development.

Model quality

For models with atomic structures, molprobtity analysis is performed. For models with coarse-grained or multi-scale structures, excluded volume analysis is performed.

Standard geometry: bond outliers

There are 39748 bond outliers in this entry. A summary is provided below, and a detailed list of outliers can be found here.

Bond type	Observed distance (Å)	Ideal distance (Å)	Number of outliers
CB--1HB	1.05	0.97	45
CG--HG	1.05	0.97	17
CD1--1HD1	1.05	0.97	11
CG--1HG	1.05	0.97	14
CB--HB	1.05	0.97	15
CB--2HB	1.05	0.97	51
CD1--2HD1	1.05	0.97	15
CB--3HB	1.05	0.97	7

Bond type	Observed distance (Å)	Ideal distance (Å)	Number of outliers
CG2--3HG2	1.05	0.97	8
CD1--3HD1	1.05	0.97	16
CD2--2HD2	1.05	0.97	11
CD2--3HD2	1.05	0.97	10
CD2--1HD2	1.05	0.97	7
CG1--3HG1	1.05	0.97	7
CG1--1HG1	1.05	0.97	5
CG2--2HG2	1.05	0.97	12
CD--1HD	1.05	0.97	6
CD--2HD	1.05	0.97	3
CG1--2HG1	1.05	0.97	10
CG--2HG	1.05	0.97	4
CE--1HE	1.05	0.97	2
CD1--HD1	1.01	0.93	1
CA--2HA	1.05	0.97	1
CE--2HE	1.05	0.97	1
CG2--1HG2	1.05	0.97	3
CA--HA	1.05	0.97	1
CB--1HB	1.06	0.97	169
CG1--2HG1	1.06	0.97	35
CD2--2HD2	1.06	0.97	25
CB--3HB	1.06	0.97	29
CD1--3HD1	1.06	0.97	60
CD2--1HD2	1.06	0.97	32
CG2--1HG2	1.06	0.97	33
CD1--1HD1	1.06	0.97	51
CB--2HB	1.06	0.97	176
CD1--2HD1	1.06	0.97	46

Bond type	Observed distance (Å)	Ideal distance (Å)	Number of outliers
CG1--1HG1	1.06	0.97	29
CG2--3HG2	1.06	0.97	37
CG--2HG	1.06	0.97	31
CG--1HG	1.06	0.97	41
CD2--3HD2	1.06	0.97	48
CB--HB	1.06	0.97	48
CA--1HA	1.06	0.97	3
CG2--2HG2	1.06	0.97	44
CG--HG	1.06	0.97	50
CG1--3HG1	1.06	0.97	15
CA--2HA	1.06	0.97	3
CD--2HD	1.06	0.97	21
CA--HA	1.06	0.97	34
CD--1HD	1.06	0.97	22
CE--2HE	1.06	0.97	7
CE3--HE3	1.02	0.93	1
CE--3HE	1.06	0.97	3
CD2--HD2	1.02	0.93	1
CE--1HE	1.06	0.97	6
CB--1HB	1.07	0.97	327
CB--2HB	1.07	0.97	330
CZ--HZ	1.03	0.93	1
CD1--3HD1	1.07	0.97	147
CA--HA	1.07	0.97	183
CG2--3HG2	1.07	0.97	93
CG2--1HG2	1.07	0.97	76
CD2--2HD2	1.07	0.97	87
CD--1HD	1.07	0.97	33

Bond type	Observed distance (Å)	Ideal distance (Å)	Number of outliers
CE--3HE	1.07	0.97	7
CB--3HB	1.07	0.97	44
CD2--1HD2	1.07	0.97	75
CD2--3HD2	1.07	0.97	124
CG1--3HG1	1.07	0.97	36
CG--HG	1.07	0.97	97
CD1--2HD1	1.07	0.97	155
CG1--1HG1	1.07	0.97	76
CB--HB	1.07	0.97	77
CG1--2HG1	1.07	0.97	69
CG2--2HG2	1.07	0.97	93
CD--2HD	1.07	0.97	50
CG--1HG	1.07	0.97	83
CD1--1HD1	1.07	0.97	97
CA--2HA	1.07	0.97	15
CE--2HE	1.07	0.97	19
CG--2HG	1.07	0.97	84
CE--1HE	1.07	0.97	16
CA--1HA	1.07	0.97	7
CE1--HE1	1.03	0.93	1
CD2--HD2	1.03	0.93	1
CD1--1HD1	1.08	0.97	278
CD--1HD	1.08	0.97	113
CG--2HG	1.08	0.97	278
CD1--3HD1	1.08	0.97	318
CB--1HB	1.08	0.97	773
CG2--1HG2	1.08	0.97	251
CG2--3HG2	1.08	0.97	235

Bond type	Observed distance (Å)	Ideal distance (Å)	Number of outliers
CE--3HE	1.08	0.97	28
CD2--1HD2	1.08	0.97	175
CB--2HB	1.08	0.97	724
CA--HA	1.08	0.97	1202
CG--HG	1.08	0.97	180
CG--1HG	1.08	0.97	205
CA--1HA	1.08	0.97	34
CD1--2HD1	1.08	0.97	318
CD2--3HD2	1.08	0.97	313
CD2--2HD2	1.08	0.97	163
CD--2HD	1.08	0.97	103
CB--HB	1.08	0.97	166
CE--2HE	1.08	0.97	43
CG1--1HG1	1.08	0.97	141
CB--3HB	1.08	0.97	143
CG1--2HG1	1.08	0.97	175
CA--2HA	1.08	0.97	46
CG1--3HG1	1.08	0.97	93
CG2--2HG2	1.08	0.97	194
CE--1HE	1.08	0.97	57
NZ--3HZ	1.00	0.89	29
CE1--HE1	1.04	0.93	2
NZ--2HZ	1.00	0.89	30
NZ--1HZ	1.00	0.89	25
OG1--HG1	0.95	0.84	1
CD1--HD1	1.04	0.93	4
CE3--HE3	1.04	0.93	1
CD2--HD2	1.04	0.93	1

Bond type	Observed distance (Å)	Ideal distance (Å)	Number of outliers
OG--HG	0.95	0.84	7
OH--HH	0.95	0.84	6
CZ--HZ	1.04	0.93	1
CE2--HE2	1.04	0.93	2
CZ3--HZ3	1.04	0.93	2
CH2--HH2	1.04	0.93	1
CA--HA	1.09	0.97	3225
CB--2HB	1.09	0.97	2458
CD2--3HD2	1.09	0.97	249
CB--1HB	1.09	0.97	2399
CG1--1HG1	1.09	0.97	270
CG1--3HG1	1.09	0.97	165
CG2--3HG2	1.09	0.97	350
NZ--3HZ	1.01	0.89	165
CG2--1HG2	1.09	0.97	369
CG1--2HG1	1.09	0.97	231
CG2--2HG2	1.09	0.97	382
CD1--1HD1	1.09	0.97	505
CA--1HA	1.09	0.97	251
CD2--1HD2	1.09	0.97	450
CD1--3HD1	1.09	0.97	405
NZ--1HZ	1.01	0.89	174
CG--2HG	1.09	0.97	861
CD2--2HD2	1.09	0.97	437
CD--1HD	1.09	0.97	456
CE--1HE	1.09	0.97	253
CD--2HD	1.09	0.97	431
CD1--2HD1	1.09	0.97	416

Bond type	Observed distance (Å)	Ideal distance (Å)	Number of outliers
CB--3HB	1.09	0.97	181
OG--HG	0.96	0.84	252
CG--1HG	1.09	0.97	905
CB--HB	1.09	0.97	391
CA--2HA	1.09	0.97	232
CG--HG	1.09	0.97	346
CE--2HE	1.09	0.97	260
CE--3HE	1.09	0.97	52
NZ--2HZ	1.01	0.89	161
CD2--HD2	1.05	0.93	9
CD1--HD1	1.05	0.93	10
OH--HH	0.96	0.84	59
OG1--HG1	0.96	0.84	55
CZ3--HZ3	1.05	0.93	2
N--2H	1.01	0.89	8
CH2--HH2	1.05	0.93	2
CE3--HE3	1.05	0.93	4
CE1--HE1	1.05	0.93	3
NE2--2HE2	0.98	0.86	1
CE2--HE2	1.05	0.93	5
N--1H	1.01	0.89	8
ND2--1HD2	0.98	0.86	1
CZ--HZ	1.05	0.93	2
N--3H	1.01	0.89	6
CG--HG	1.10	0.97	34
CD1--2HD1	1.10	0.97	9
CB--1HB	1.10	0.97	259
CD--2HD	1.10	0.97	107

Bond type	Observed distance (Å)	Ideal distance (Å)	Number of outliers
CD--1HD	1.10	0.97	90
OG1--HG1	0.97	0.84	77
CA--HA	1.10	0.97	189
CG1--3HG1	1.10	0.97	6
CG2--2HG2	1.10	0.97	4
CD1--1HD1	1.10	0.97	13
CD2--2HD2	1.10	0.97	15
CB--2HB	1.10	0.97	213
CZ2--HZ2	1.06	0.93	7
CD2--HD2	1.06	0.93	17
CD1--3HD1	1.10	0.97	5
OG--HG	0.97	0.84	62
CB--HB	1.10	0.97	21
CG--1HG	1.10	0.97	172
CG--2HG	1.10	0.97	183
NZ--3HZ	1.02	0.89	20
NZ--2HZ	1.02	0.89	22
CG2--3HG2	1.10	0.97	10
CD2--1HD2	1.10	0.97	10
CG1--2HG1	1.10	0.97	4
NZ--1HZ	1.02	0.89	19
N--3H	1.02	0.89	2
CE--2HE	1.10	0.97	3
CE2--HE2	1.06	0.93	9
OH--HH	0.97	0.84	9
CG2--1HG2	1.10	0.97	2
CD2--3HD2	1.10	0.97	2

Bond type	Observed distance (Å)	Ideal distance (Å)	Number of outliers
CD1--HD1	1.06	0.93	17
CE1--HE1	1.06	0.93	17
CZ--HZ	1.06	0.93	5
SG--HG	1.33	1.20	22
CA--1HA	1.10	0.97	1
CE3--HE3	1.06	0.93	3
NE--HE	0.99	0.86	1
CZ3--HZ3	1.06	0.93	2
CB--3HB	1.10	0.97	1
ND1--HD1	0.99	0.86	3
NE2--1HE2	0.99	0.86	11
CH2--HH2	1.06	0.93	1
ND2--2HD2	0.99	0.86	4
ND2--1HD2	0.99	0.86	7
N--H	0.99	0.86	2
NE1--HE1	0.99	0.86	1
NE2--2HE2	0.99	0.86	4
OG--HG	0.98	0.84	40
NE2--1HE2	1.00	0.86	214
CG--2HG	1.11	0.97	14
ND2--1HD2	1.00	0.86	105
SG--HG	1.34	1.20	47
CG--1HG	1.11	0.97	23
CD--1HD	1.11	0.97	8
ND2--2HD2	1.00	0.86	100
CE1--HE1	1.07	0.93	25
CD--2HD	1.11	0.97	18
CA--HA	1.11	0.97	4

Bond type	Observed distance (Å)	Ideal distance (Å)	Number of outliers
OG1--HG1	0.98	0.84	53
CD2--HD2	1.07	0.93	32
CD1--HD1	1.07	0.93	51
CZ--HZ	1.07	0.93	17
CB--1HB	1.11	0.97	21
CZ3--HZ3	1.07	0.93	12
NH1--1HH1	1.00	0.86	54
CH2--HH2	1.07	0.93	6
N--H	1.00	0.86	96
CE3--HE3	1.07	0.93	15
CB--2HB	1.11	0.97	10
NE2--2HE2	1.00	0.86	190
NZ--1HZ	1.03	0.89	14
NH1--2HH1	1.00	0.86	11
OH--HH	0.98	0.84	8
NZ--3HZ	1.03	0.89	8
NZ--2HZ	1.03	0.89	13
CZ2--HZ2	1.07	0.93	5
NE1--HE1	1.00	0.86	11
NH2--2HH2	1.00	0.86	35
ND1--HD1	1.00	0.86	28
CE2--HE2	1.07	0.93	26
NH2--1HH2	1.00	0.86	6
NE--HE	1.00	0.86	2
NE2--HE2	1.00	0.86	1
NH2--2HH2	1.01	0.86	184
NE2--1HE2	1.01	0.86	30
NH1--1HH1	1.01	0.86	143

Bond type	Observed distance (Å)	Ideal distance (Å)	Number of outliers
NZ--2HZ	1.04	0.89	11
NH2--1HH2	1.01	0.86	150
N--H	1.01	0.86	1353
CH2--HH2	1.08	0.93	24
CZ--HZ	1.08	0.93	45
OG--HG	0.99	0.84	30
NH1--2HH1	1.01	0.86	178
ND1--HD1	1.01	0.86	13
NE2--2HE2	1.01	0.86	23
NE1--HE1	1.01	0.86	40
CZ3--HZ3	1.08	0.93	20
OG1--HG1	0.99	0.84	16
CD1--HD1	1.08	0.93	95
SG--HG	1.35	1.20	51
ND2--2HD2	1.01	0.86	8
CE3--HE3	1.08	0.93	24
CE1--HE1	1.08	0.93	75
ND2--1HD2	1.01	0.86	5
CE2--HE2	1.08	0.93	67
NE--HE	1.01	0.86	142
CZ2--HZ2	1.08	0.93	14
NZ--1HZ	1.04	0.89	6
CG--2HG	1.12	0.97	1
CD2--HD2	1.08	0.93	77
CG--1HG	1.12	0.97	1
NZ--3HZ	1.04	0.89	14
OH--HH	0.99	0.84	15
NE2--HE2	1.01	0.86	42

Bond type	Observed distance (Å)	Ideal distance (Å)	Number of outliers
N--H	1.02	0.86	2439
NE2--2HE2	1.02	0.86	30
CZ2--HZ2	1.09	0.93	50
CD1--HD1	1.09	0.93	149
CE3--HE3	1.09	0.93	28
CE1--HE1	1.09	0.93	258
CD2--HD2	1.09	0.93	245
NE2--HE2	1.02	0.86	11
SG--HG	1.36	1.20	30
CH2--HH2	1.09	0.93	41
NH1--1HH1	1.02	0.86	21
NH1--2HH1	1.02	0.86	33
NE--HE	1.02	0.86	49
NE2--1HE2	1.02	0.86	16
CE2--HE2	1.09	0.93	147
CZ--HZ	1.09	0.93	81
CZ3--HZ3	1.09	0.93	38
NH2--2HH2	1.02	0.86	14
NH2--1HH2	1.02	0.86	36
NE1--HE1	1.02	0.86	8
OG--HG	1.00	0.84	15
ND2--1HD2	1.02	0.86	8
ND1--HD1	1.02	0.86	11
OH--HH	1.00	0.84	8
OG1--HG1	1.00	0.84	9
ND2--2HD2	1.02	0.86	10
NZ--3HZ	1.05	0.89	5
NZ--1HZ	1.05	0.89	4

Bond type	Observed distance (Å)	Ideal distance (Å)	Number of outliers
NZ--2HZ	1.05	0.89	3
N--H	1.03	0.86	986
CE1--HE1	1.10	0.93	11
CD2--HD2	1.10	0.93	9
CD1--HD1	1.10	0.93	12
CE2--HE2	1.10	0.93	7
NH1--1HH1	1.03	0.86	34
NH2--1HH2	1.03	0.86	39
NH2--2HH2	1.03	0.86	18
OG1--HG1	1.01	0.84	3
NE2--1HE2	1.03	0.86	11
NE--HE	1.03	0.86	36
NH1--2HH1	1.03	0.86	28
SG--HG	1.37	1.20	9
CH2--HH2	1.10	0.93	1
ND2--1HD2	1.03	0.86	1
ND2--2HD2	1.03	0.86	6
NZ--2HZ	1.06	0.89	2
ND1--HD1	1.03	0.86	6
NE2--HE2	1.03	0.86	6
NE2--2HE2	1.03	0.86	30
NE1--HE1	1.03	0.86	7
CZ--HZ	1.10	0.93	4
OG--HG	1.01	0.84	7
OH--HH	1.01	0.84	2
NZ--3HZ	1.06	0.89	1
NH2--2HH2	1.04	0.86	11
N--H	1.04	0.86	16

Bond type	Observed distance (Å)	Ideal distance (Å)	Number of outliers
NH2--1HH2	1.04	0.86	29
NE2--1HE2	1.04	0.86	4
NE--HE	1.04	0.86	28
NH1--1HH1	1.04	0.86	9
NE2--2HE2	1.04	0.86	8
SG--HG	1.38	1.20	1
NH1--2HH1	1.04	0.86	10
NE2--HE2	1.04	0.86	4
OG--HG	1.02	0.84	1
NE1--HE1	1.04	0.86	5
OG1--HG1	1.02	0.84	4
ND2--1HD2	1.04	0.86	1
ND1--HD1	1.04	0.86	1
NH1--2HH1	1.05	0.86	2
NH2--1HH2	1.05	0.86	2
NE2--HE2	1.05	0.86	3
NH1--1HH1	1.05	0.86	1
NE--HE	1.05	0.86	4
NE1--HE1	1.05	0.86	3
NE1--HE1	1.06	0.86	1
N--2H	1.86	0.96	1
N--1H	1.88	0.96	1
N--1H	1.89	0.96	1
N--2H	1.89	0.96	1
N--2H	1.92	0.96	1
N--1H	1.93	0.96	1

Standard geometry: angle outliers 

There are 260 angle outliers in this entry. A summary is provided below, and a detailed list of outliers can be found [here](#).

Angle type	Observed angle (°)	Ideal angle (°)	Number of outliers
CA-CB-CG	113.80	101.00	1
C-N-CA	121.70	140.14	1
N-CA-CB	103.00	92.73	1
C-N-CA	121.70	138.30	1
CA-CB-CG	112.60	121.80	1
C-N-CA	121.70	137.98	1
N-CA-CB	103.00	93.71	1
C-N-CA	121.70	136.20	1
C-N-CA	121.70	136.02	1
CA-CB-CG	113.80	121.68	2
C-N-CA	121.70	135.66	1
C-N-CA	121.70	135.28	1
C-N-CA	121.70	135.22	1
N-CA-C	111.00	131.72	1
C-N-CA	121.70	134.75	1
N-CA-C	111.00	130.93	1
C-N-CA	121.70	134.46	1
CA-CB-CG	113.80	120.83	1
CA-CB-CG	113.80	106.82	1
CA-CB-CG	113.80	106.88	1
C-N-CA	121.70	133.58	1
N-CA-C	111.00	129.35	1
CA-CB-CG	113.80	120.34	1
CA-CB-CG	113.80	120.30	1
CA-CB-CG	112.60	119.09	2
O-C-N	123.00	112.71	1
C-N-CA	121.70	133.11	1
N-CA-C	111.00	93.37	1

Angle type	Observed angle (°)	Ideal angle (°)	Number of outliers
C-CA-CB	110.10	98.26	1
N-CA-C	111.00	128.34	1
C-N-CA	121.70	132.83	1
CA-CB-CG	113.80	119.96	1
N-CA-C	112.10	127.34	1
C-N-CA	121.70	132.64	1
C-N-CA	121.70	132.58	1
C-N-CA	121.70	132.44	1
C-N-CA	121.70	132.37	1
C-N-CA	121.70	132.30	1
CA-CB-CG	112.60	118.46	1
N-CA-CB	110.50	120.45	1
C-N-CA	121.70	132.22	1
CA-CB-CG	113.80	119.64	1
CA-CB-CG	113.80	119.62	1
CA-CB-CG	113.80	119.61	1
CA-CB-CG	113.80	108.02	1
CA-CB-CG	113.80	119.56	1
C-N-CA	121.70	131.99	1
CA-CB-CG	112.60	106.88	1
CA-CB-CG	113.80	119.42	1
N-CA-CB	110.50	120.01	1
CA-CB-CG	113.80	119.37	1
C-CA-CB	110.10	120.68	1
C-N-CA	121.70	131.66	1
CA-CB-CG	113.80	108.27	1
CA-CB-CG	112.60	118.10	1
CA-CB-CG	113.90	104.00	1

Angle type	Observed angle (°)	Ideal angle (°)	Number of outliers
CA-CB-CG	113.80	119.26	1
CA-CB-CG	113.80	108.34	1
C-N-CA	121.70	131.49	1
C-CA-CB	111.60	100.73	1
CA-C-N	116.90	124.99	1
C-CA-CB	110.10	120.35	1
C-CA-CB	110.10	99.99	1
CA-C-N	116.90	124.81	1
CA-CB-CG	113.80	119.07	1
N-CA-C	111.00	125.73	1
C-N-CA	121.70	131.14	1
C-N-CA	121.70	131.03	1
CA-CB-CG	112.60	117.78	1
C-N-CA	121.70	131.02	1
CA-CB-CG	113.80	118.98	1
CA-C-O	120.80	112.09	1
C-CA-CB	110.10	119.81	1
C-N-CA	121.70	112.51	1
CA-C-N	116.20	126.38	1
C-N-CA	121.70	130.85	1
C-N-CA	121.70	130.84	1
CA-CB-CG	112.60	117.68	1
N-CA-C	111.00	125.15	1
C-N-CA	121.70	130.77	1
CA-CB-CG	113.80	118.83	1
CA-C-N	116.20	126.24	1
C-N-CA	121.70	130.72	1
CA-C-N	116.20	126.22	1

Angle type	Observed angle (°)	Ideal angle (°)	Number of outliers
N-CA-C	111.00	97.00	1
C-CA-CB	110.10	119.57	1
N-CA-C	113.30	98.86	1
CA-CB-CG	113.80	108.84	1
CA-CB-CG	112.60	117.56	1
C-CA-CB	111.60	101.72	1
C-N-CA	121.70	112.86	1
CA-CB-CG	113.80	108.89	1
CA-CB-CG	113.80	118.71	1
N-CA-C	111.00	124.71	1
C-N-CA	121.70	130.51	1
CA-C-N	116.20	125.98	1
N-CA-C	111.00	97.39	1
N-CA-C	111.00	97.40	1
CA-CB-CG	113.80	118.62	1
C-N-CA	121.70	130.37	1
CA-C-N	116.90	124.12	1
C-N-CA	121.70	130.35	1
N-CA-C	111.00	124.40	2
C-CA-CB	110.10	119.18	1
CA-CB-CG	112.60	117.37	1
CA-CB-CG	113.80	109.04	1
CA-C-N	116.90	124.02	1
CA-CB-CG	113.80	109.07	1
N-CA-C	111.00	124.08	1
C-N-CA	121.70	130.10	1
CA-CB-CG	112.60	117.26	1
CA-CB-CG	113.80	118.45	1

Angle type	Observed angle (°)	Ideal angle (°)	Number of outliers
CA-C-N	116.90	123.88	1
N-CA-C	111.00	123.95	1
CA-C-N	116.90	123.83	1
C-CA-CB	110.10	118.85	1
N-CA-C	111.00	98.12	1
CA-C-N	116.90	123.80	1
C-N-CA	121.70	129.96	2
N-CA-C	112.10	100.63	1
C-CA-CB	110.10	118.82	1
CA-CB-CG	113.80	109.21	1
CA-CB-CG	113.90	122.14	1
C-CA-CB	110.10	101.41	1
CA-CB-CG	113.80	109.23	1
CA-C-N	116.90	123.76	1
C-N-CA	121.70	129.91	1
C-N-CA	121.70	113.50	1
C-N-CA	121.70	129.89	1
CA-C-N	116.20	125.30	1
N-CA-C	111.00	98.26	1
C-N-CA	121.70	129.88	1
CA-CB-CG	113.80	109.27	2
CA-C-N	116.90	123.68	1
CA-CB-CG	113.80	109.29	1
CA-CB-CG	112.60	108.09	1
CA-CB-CG	112.60	117.10	1
C-N-CA	121.70	113.63	1
C-N-CA	121.70	113.67	1

Angle type	Observed angle (°)	Ideal angle (°)	Number of outliers
NE-CZ-NH2	119.20	123.20	1
C-CA-CB	110.10	118.55	1
C-CA-CB	110.10	101.66	1
C-N-CA	121.70	129.68	1
CA-CB-CG	112.60	108.18	2
N-CA-C	112.10	101.07	1
C-N-CA	121.70	113.79	1
N-CA-C	112.10	123.08	1
C-N-CA	121.70	129.60	1
NE-CZ-NH2	119.20	123.14	1
CA-CB-CG	113.80	109.42	1
CA-CB-CG	112.60	116.98	1
C-CA-CB	110.10	118.40	1
N-CA-C	111.00	98.77	1
NE-CZ-NH2	119.20	115.27	1
NE-CZ-NH2	119.20	115.28	1
C-N-CA	121.70	113.86	1
N-CA-CB	110.50	117.90	1
CA-CB-CG	113.80	109.45	1
N-CA-C	112.10	101.29	1
C-N-CA	121.70	129.48	1
C-N-CA	121.70	113.93	1
C-N-CA	121.70	129.46	1
C-N-CA	121.70	129.45	2
N-CA-CB	111.50	104.18	1
CA-CB-CG	112.60	116.90	2
CA-CB-CG	112.60	108.30	1
C-N-CA	121.70	129.43	1

Angle type	Observed angle (°)	Ideal angle (°)	Number of outliers
C-N-CA	121.70	113.98	1
CA-CB-CG	113.80	118.08	1
CA-CB-CG	113.90	121.60	1
N-CA-C	111.00	122.97	1
C-N-CA	121.70	129.39	1
CA-C-N	116.20	124.74	1
CA-CB-CG	113.80	109.53	1
C-N-CA	121.70	129.38	1
CA-CB-CG	113.80	109.54	1
C-N-CA	121.70	114.04	1
C-N-CA	121.70	129.35	1
N-CA-C	111.00	122.90	1
C-N-CA	121.70	114.05	1
C-CA-CB	110.10	102.02	1
CA-CB-CG	112.60	116.84	1
CA-C-N	116.90	123.26	1
C-N-CA	121.70	129.31	1
CA-CB-CG	113.80	118.03	1
CA-CB-CG	113.90	106.31	1
C-N-CA	121.70	129.27	1
C-N-CA	121.70	129.26	1
NE-CZ-NH2	119.20	115.43	1
CA-CB-CG	113.80	117.98	2
C-N-CA	121.70	129.23	1
CA-CB-CG	113.90	106.38	1
CB-CG-CD	112.60	119.70	1
N-CA-CB	110.50	103.41	1
C-N-CA	121.70	114.22	1

Angle type	Observed angle (°)	Ideal angle (°)	Number of outliers
N-CA-C	111.00	99.38	1
C-N-CA	121.70	129.17	1
CA-CB-CG	113.80	117.95	1
CA-C-N	116.20	124.49	1
C-N-CA	121.70	114.26	1
C-CA-CB	110.10	117.95	1
C-N-CA	121.70	114.27	1
C-N-CA	121.70	129.12	1
C-N-CA	121.70	129.11	1
CA-CB-CG	112.60	116.71	1
CA-CB-CG	113.80	117.91	1
C-N-CA	121.70	129.10	1
N-CA-C	111.00	122.51	1
NE-CZ-NH2	119.20	122.90	1
C-N-CA	121.70	129.09	1
C-N-CA	121.70	129.07	1
CA-CB-CG	112.60	116.69	1
N-CA-C	112.10	101.88	1
CA-CB-CG	113.80	109.72	1
C-N-CA	121.70	129.04	1
CA-CB-CG	113.80	109.73	3
CA-C-N	116.90	123.00	1
C-N-CA	121.70	128.97	1
C-N-CA	121.70	114.44	1
C-N-CA	121.70	114.46	1
C-N-CA	121.70	128.92	1
N-CA-C	111.00	122.22	1
CA-C-N	116.90	122.91	1

Angle type	Observed angle (°)	Ideal angle (°)	Number of outliers
CA-CB-CG	113.80	109.80	2
C-N-H	112.29	124.30	1
C-N-H	112.06	124.30	1
C-N-H	111.98	124.30	1
C-N-H	111.93	124.30	1
C-N-H	111.70	124.30	1
C-N-H	111.59	124.30	1
C-N-H	111.56	124.30	1
CA-N-2H	96.36	109.47	1
CA-N-2H	96.10	109.47	1
C-N-H	110.69	124.30	1
C-N-H	110.63	124.30	1
C-N-H	109.60	124.30	1
CA-N-1H	88.89	109.47	1
CA-N-1H	88.64	109.47	1
CA-N-2H	87.61	109.47	1
CD-N-1H	133.47	109.47	1
CD-N-2H	134.82	109.47	1
CD-N-1H	138.86	109.47	1
CD-N-2H	143.60	109.47	1
CD-N-2H	145.89	109.47	1
CD-N-1H	146.52	109.47	1
1H-N-2H	52.87	109.47	1
1H-N-2H	52.69	109.47	1
1H-N-2H	52.38	109.47	1

Too-close contacts

The following all-atom clashscore is based on a MolProbity analysis. All-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The table below contains clashscores for all the models in this entry.

Model ID	Clash score	Number of clashes
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Model ID	Clash score	Number of clashes
1	0.00	0

All 0 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Torsion angles: Protein backbone ?

In the following table, Ramachandran outliers are listed. The Analysed column shows the number of residues for which the backbone conformation was analysed.

Model ID	Analyzed	Favored	Allowed	Outliers
1	5079	4875	168	36

Detailed list of outliers are tabulated below.

Torsion angles: Protein sidechains ?

In the following table, sidechain outliers are listed. The Analysed column shows the number of residues for which the sidechain conformation was analysed.

Model ID	Analyzed	Favored	Allowed	Outliers
1	4426	4367	50	9

Detailed list of outliers are tabulated below.

Model ID	Chain	Residue ID	Residue type
1	B	427	OILE
1	G	33	OARG
1	P	100	OTHR
1	P	240	OCYS
1	b	427	OILE
1	b	441	OLYS
1	b	669	OMET
1	g	213	OTHR
1	p	150	OMET

Fit of model to data used for modeling ?

3DEM volume

Validation for this section is under development.

Crosslinking-MS

Validation for this section is under development.

Fit of model to data used for validation

Validation for this section is under development.

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