

Integrative Structure Validation Report

September 11, 2024 - 12:52 AM 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	9A7A
PDB-Dev ID	PDBDEV_00000339
Structure Title	Integrative model of GLPD-YJLD by crosslinking MS and deep learning
Structure Authors	Kolja Stahl; Oliver Brock; Juri Rappsilber

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

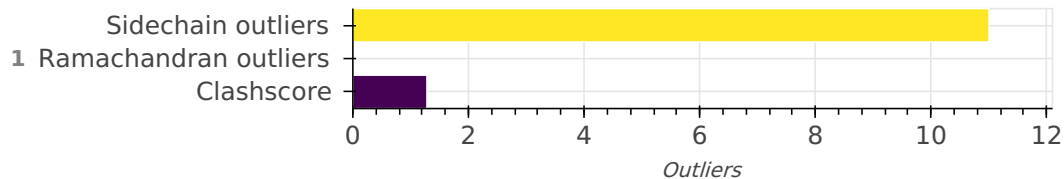
A user guide is available at https://pdb-dev.wwpdb.org/validation_help.html with specific help available everywhere you see the  symbol.

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.

Model Quality: MolProbity Analysis



Ensemble information ?

This entry consists of 0 distinct ensemble(s).

Summary ?

This entry consists of 1 unique models, with 2 subunits in each model. A total of 1 datasets or restraints were used to build this entry. Each model is represented by 0 rigid bodies and 2 flexible or non-rigid units.

Entry composition ?

There is 1 unique type of models in this entry. This model is titled None/None.

Model ID	Subunit number	Subunit ID	Subunit name	Chain ID	Chain ID [auth]	Total residues
1	1	1	GLPD_BACSU	A	A	555
1	2	2	YJLD_BACSU	B	B	392

Datasets used for modeling ?

There is 1 unique dataset used to build the models in this entry.

ID	Dataset type	Database name	Data access code
1	Crosslinking-MS data	PRIDE	PXD035508

Representation ?

This entry has only one representation and includes 0 rigid bodies and 2 flexible units.

Chain ID	Rigid bodies	Non-rigid segments

Chain ID	Rigid bodies	Non-rigid segments
A	-	1-555
B	-	1-392

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	AlphaLink2	AlphaLink2	None	1	False	False

There is 1 software package reported in this entry.

ID	Software name	Software version	Software classification	Software location
1	AlphaLink2	1.0	model building	https://github.com/Rappsilber-Laboratory/AlphaLink2

Data quality ?

Crosslinking-MS

Validation for this section is under development.

Model quality ?

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

Standard geometry: bond outliers ?

There are 7442 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
CD--HD3	1.09	0.97	159

Bond type	Observed distance (Å)	Ideal distance (Å)	Number of outliers
CB--HB2	1.09	0.97	673
CD1--HD13	1.09	0.97	133
CB--HB	1.09	0.97	189
CB--HB3	1.09	0.97	673
CA--HA	1.09	0.97	862
CB--HB1	1.09	0.97	75
CG1--HG13	1.09	0.97	128
CG--HG2	1.09	0.97	274
NZ--HZ2	1.01	0.89	83
CG2--HG21	1.09	0.97	189
CG--HG3	1.09	0.97	274
CD1--HD12	1.09	0.97	133
CA--HA3	1.09	0.97	85
CG2--HG23	1.09	0.97	189
OH--HH	0.96	0.84	33
CE--HE3	1.09	0.97	107
NZ--HZ3	1.01	0.89	83
CD2--HD23	1.09	0.97	86
CD--HD2	1.09	0.97	159
CG2--HG22	1.09	0.97	189
OG--HG	0.96	0.84	52
CD2--HD22	1.09	0.97	86
CD1--HD11	1.09	0.97	133

Bond type	Observed distance (Å)	Ideal distance (Å)	Number of outliers
CE--HE2	1.09	0.97	107
CA--HA2	1.09	0.97	85
CD2--HD21	1.09	0.97	86
CG--HG	1.09	0.97	86
CG1--HG12	1.09	0.97	128
NZ--HZ1	1.01	0.89	83
OG1--HG1	0.96	0.84	61
CE--HE1	1.09	0.97	24
CG1--HG11	1.09	0.97	81
N--H2	1.01	0.89	2
N--H3	1.01	0.89	2
N--H1	1.01	0.89	2
SG--HG	1.34	1.20	1
N--H	1.01	0.86	911
ND2--HD22	1.01	0.86	32
NH2--HH22	1.01	0.86	42
CE1--HE1	1.08	0.93	91
NH1--HH11	1.01	0.86	42
CD1--HD1	1.08	0.93	76
CD2--HD2	1.08	0.93	91
CZ--HZ	1.08	0.93	35
NE2--HE22	1.01	0.86	19
NE2--HE21	1.01	0.86	19
ND1--HD1	1.01	0.86	16

Bond type	Observed distance (Å)	Ideal distance (Å)	Number of outliers
CE2--HE2	1.08	0.93	68
NH1--HH12	1.01	0.86	42
NE1--HE1	1.01	0.86	8
NH2--HH21	1.01	0.86	42
ND2--HD21	1.01	0.86	32
CE3--HE3	1.08	0.93	8
NE2--HE2	1.01	0.86	7
CH2--HH2	1.08	0.93	8
CZ3--HZ3	1.08	0.93	8
NE--HE	1.01	0.86	42
CZ2--HZ2	1.08	0.93	8

Standard geometry: angle outliers?

There are 22 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
NE-CZ-NH2	119.20	124.88	1
OE1-CD-NE2	122.60	117.00	1
CA-CB-CG	112.60	117.74	1
OE1-CD-NE2	122.60	117.47	1
NH1-CZ-NH2	119.30	112.91	1
OE1-CD-NE2	122.60	117.75	1
OE1-CD-NE2	122.60	117.77	1
CB-CG-CD2	131.20	125.19	1
OE1-CD-NE2	122.60	118.04	1
CB-CG-CD2	131.20	125.48	1

Angle type	Observed angle (°)	Ideal angle (°)	Number of outliers
OE1-CD-NE2	122.60	118.22	2
OE1-CD-NE2	122.60	118.27	1
CB-CG-CD2	131.20	125.63	1
OD1-CG-ND2	122.60	118.44	1
CA-CB-CG	113.60	121.51	1
CB-CG-CD2	131.20	125.80	1
CB-CG-CD2	131.20	125.81	1
NE-CZ-NH2	119.20	122.91	1
OE1-CD-NE2	122.60	118.53	1
CB-CG-CD2	131.20	125.99	1
HZ1-NZ-HZ3	96.70	109.00	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
1	1.28	19

All 19 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Model ID	Atom-1	Atom-2	Clash overlap (Å)
1	B:357:ILE:HD11	B:364:LEU:HD12	0.562
1	A:280:ARG:HH22	A:296:THR:HA	0.534
1	A:56:PHE:CE2	A:491:MET:HE3	0.520
1	A:94:TYR:CZ	A:421:SER:HB2	0.505
1	A:193:ASN:H	A:491:MET:HE1	0.489
1	A:192:VAL:HA	A:491:MET:HE1	0.487

Model ID	Atom-1	Atom-2	Clash overlap (Å)
1	A:236:VAL:HG13	A:371:THR:HG23	0.469
1	A:492:THR:HG23	A:497:ASP:HB2	0.468
1	B:315:TRP:C	B:315:TRP:CD1	0.460
1	A:6:PHE:CE2	A:491:MET:HE2	0.424
1	A:11:ARG:HH22	A:214:ASP:CG	0.422
1	A:236:VAL:HG13	A:371:THR:CG2	0.415
1	A:401:LYS:CE	A:403:PHE:CE1	0.414
1	A:80:VAL:HG13	A:131:LEU:HD11	0.410
1	A:105:TRP:HB3	A:165:TYR:CZ	0.409
1	A:345:LEU:HB3	A:356:ILE:CG2	0.409
1	A:127:VAL:CG2	B:378:VAL:HG11	0.407
1	A:401:LYS:HE2	A:403:PHE:CE1	0.401
1	A:56:PHE:HE2	A:491:MET:HE3	0.401

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	Analysed	Favored	Allowed	Outliers
1	943	919	24	0

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	Analysed	Favored	Allowed	Outliers
1	787	763	13	11

Detailed list of outliers are tabulated below.

Model ID	Chain	Residue ID	Residue type
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Model ID	Chain	Residue ID	Residue type
1	A	12	ASP
1	A	75	LEU
1	A	257	ILE
1	A	382	LYS
1	A	480	LEU
1	A	491	MET
1	A	506	LEU
1	A	522	ASP
1	B	176	ILE
1	B	193	LEU
1	B	315	TRP

Fit of model to data used for modeling ?

Crosslinking-MS

Validation for this section is under development.

Fit of model to data used for validation ?

Validation for this section is under development.

Acknowledgements

Development of integrative model validation metrics, implementation of a model validation pipeline, and creation of a validation report for integrative structures, are funded by NSF ABI awards (DBI-1756248, DBI-2112966, DBI-2112967, DBI-2112968, and DBI-1756250). The [PDB-Dev team](#) and members of [Sali lab](#) contributed model validation metrics and software packages.

Implementation of validation methods for SAS data and SAS-based models are funded by [RCSB PDB](#)

(grant number DBI-1832184). Dr. Stephen Burley, Dr. John Westbrook, and Dr. Jasmine Young from [RCSB PDB](#), Dr. Jill Trehella, Dr. Dina Schneidman, and members of the [SASBDB](#) repository are acknowledged for their advice and support in implementing SAS validation methods.

Members of the [wwPDB Integrative/Hybrid Methods Task Force](#) provided recommendations and community support for the project.