Full wwPDB Integrative Structure Validation Report

July 06, 2020 -- 08:04 PM

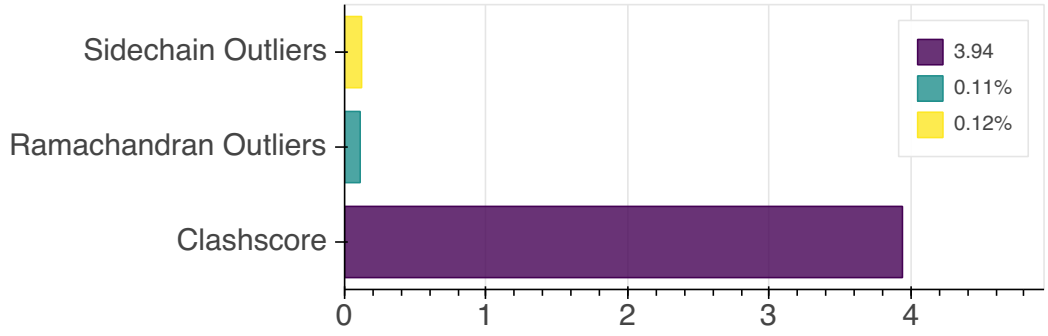
The following software were used in the production of this report:

Molprobity : Version 4.4
Integrative Modeling Validation Package : Version 1.0

PDB ID	PDBDEV_00000007
Molecule Name	Serum Albumin Domain C Structure
Title	Serum Albumin Domain Structures in Human Blood Serum by Mass Spectrometry and Computational Biology
Authors	Belsom A;Schneider M;Fischer L;Brock O;Rappsilber J

Overall quality

Model Quality: Molprobity Analysis



Ensemble information

This entry consists of 0 distinct ensemble.

Summary

This entry consists of 5 unique models, with 1 subunits in each model. A total of 2 datasets or restraints was used to build this entry. Each model is represented by 1 rigid bodies and 0 flexible or non-rigid units.

Entry composition

There are 5 unique types of models in this entry.These models are titled Best scoring model (domain C), 2nd best scoring model (domain C), 3rd best scoring model (domain C), 4th best scoring model (domain C), 5th best scoring model (domain C) respectively.

Model ID	Subunit number	Subunit ID	Subunit name	Chain ID	Total residues
1	1	1	HSA_C	A	192
2	1	1	HSA_C	A	192
3	1	1	HSA_C	A	192
4	1	1	HSA_C	A	192
5	1	1	HSA_C	A	192

Methodology and software

Step number	Protocol ID	Method name	Method type	Number of computed models	Multi state modeling	Multi scale modeling
1	1	Model-based search (MBS) in Rosetta	Conformational search	5000	False	False

Data quality

Model quality

Standard geometry

There are 7680 bond outliers in this entry.

Bond type	Observed distance (Å)	Ideal distance (Å)	Number of outliers
CD2--HD2	1.089	0.93	84
CE2--HE2	1.088	0.93	64
CE1--HE1	1.089	0.93	84
CD1--HD1	1.089	0.93	64
CZ--HZ	1.088	0.93	44
NE--HE	1.01	0.86	34
N--H	1.008	0.86	914
NH2--HH21	1.01	0.86	34
NH1--HH11	1.009	0.86	34
NE2--HE2	1.009	0.86	19
NH1--HH12	1.009	0.86	34
NH2--HH22	1.008	0.86	34
NE2--HE21	1.0	0.86	39
ND2--HD21	0.999	0.86	29
NE2--HE22	0.999	0.86	39
ND2--HD22	0.998	0.86	29
CB--HB2	1.088	0.97	769
CG--HG3	1.087	0.97	339

Bond type	Observed distance (Å)	Ideal distance (Å)	Number of outliers
CA--HA	1.088	0.97	939
CG--HG2	1.088	0.97	339
CD--HD3	1.088	0.97	189
CB--HB3	1.087	0.97	769
CD--HD2	1.088	0.97	189
SG--HG	1.328	1.2	59
CG--HG	1.089	0.97	84
CD2--HD21	1.089	0.97	84
CE--HE2	1.088	0.97	124
NZ--HZ2	1.009	0.89	114
CE--HE3	1.088	0.97	124
CG1--HG11	1.089	0.97	94
OG1--HG1	0.958	0.84	64
CD1--HD12	1.089	0.97	94
CB--HB	1.089	0.97	169
CG2--HG23	1.088	0.97	169
CE--HE1	1.089	0.97	9
CD1--HD11	1.089	0.97	94
CD2--HD22	1.089	0.97	84
CD2--HD23	1.089	0.97	84
CG2--HG22	1.088	0.97	169
NZ--HZ1	1.008	0.89	114
CG2--HG21	1.088	0.97	169

Bond type	Observed distance (Å)	Ideal distance (Å)	Number of outliers
OH--HH	0.959	0.84	19
CG1--HG13	1.088	0.97	104
CB--HB1	1.089	0.97	84
OG--HG	0.959	0.84	44
NZ--HZ3	1.009	0.89	114
CD1--HD13	1.088	0.97	94
CG1--HG12	1.088	0.97	104
CA--HA2	1.089	0.97	19
CA--HA3	1.089	0.97	19
N--H1	1.0	0.89	4
N--H3	1.0	0.89	4
N--H2	1.0	0.89	4

There are 160 angle outliers in this entry.

Angle type	Observed angle (°)	Ideal angle (°)	Number of outliers
CA-CB-HB3	93.414	109.0	29
CB-CG-HG3	94.641	109.0	39
CB-CG-HG2	122.703	109.0	39
H1-N-H3	97.22	109.47	4
H2-N-H3	97.207	109.47	4
H1-N-H2	97.258	109.47	4
CZ-NE-HE	105.887	117.9	34

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
Model 1	3.94	12
Model 2	2.63	8
Model 3	2.63	8
Model 4	2.63	8
Model 5	4.27	13

All 49 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	190	185	5	0
2	190	185	4	1
3	190	189	1	0
4	190	185	5	0
5	190	183	7	0

Detailed list of outliers are tabulated below.

Model ID	Chain and res ID	Residue type
2	A:93	ASN

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	171	169	2	0

Model ID	Analyzed	Favored	Allowed	Outliers
2	171	169	1	1
3	171	171	0	0
4	171	171	0	0
5	171	171	0	0

Detailed list of outliers are tabulated below.

Model ID	Chain and res ID	Residue type
2	A:110	LYS

Fit of model to data used for modeling

Fit of model to data not used for modeling

Uncertainty of data and model