Full wwPDB X-ray Structure Validation Report

May 21, 2020 – 08:42 am BST

PDB ID	:	1DBH
Title	:	DBL AND PLECKSTRIN HOMOLOGY DOMAINS FROM HSOS1
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Deposited on	:	1998-12-17
Resolution	:	2.30 Å(reported)

This is a Full wwPDB X-ray 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/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

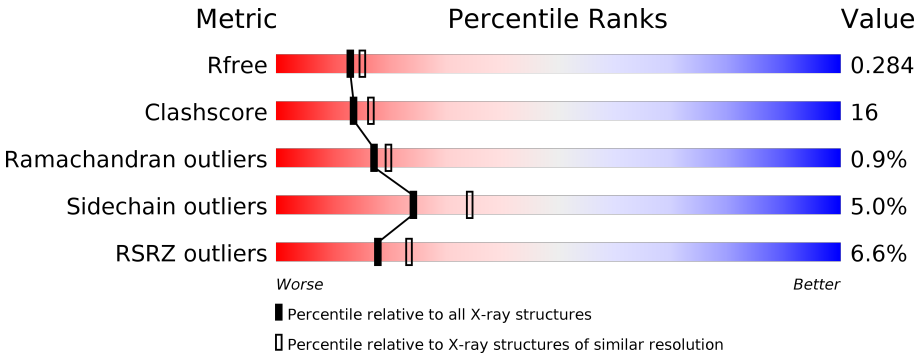
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.

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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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 <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	354	6% 68% 25%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 2817 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called PROTEIN (HUMAN SOS 1).

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	340	Total	C	N	O	S	Se	186	0	0
			2748	1747	466	519	8	8			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	209	MSE	MET	MODIFIED RESIDUE	UNP Q07889
A	269	MSE	MET	MODIFIED RESIDUE	UNP Q07889
A	387	MSE	MET	MODIFIED RESIDUE	UNP Q07889
A	412	MSE	MET	MODIFIED RESIDUE	UNP Q07889
A	422	MSE	MET	MODIFIED RESIDUE	UNP Q07889
A	446	MSE	MET	MODIFIED RESIDUE	UNP Q07889
A	468	MSE	MET	MODIFIED RESIDUE	UNP Q07889
A	496	MSE	MET	MODIFIED RESIDUE	UNP Q07889
A	538	MSE	MET	MODIFIED RESIDUE	UNP Q07889

- Molecule 2 is water.

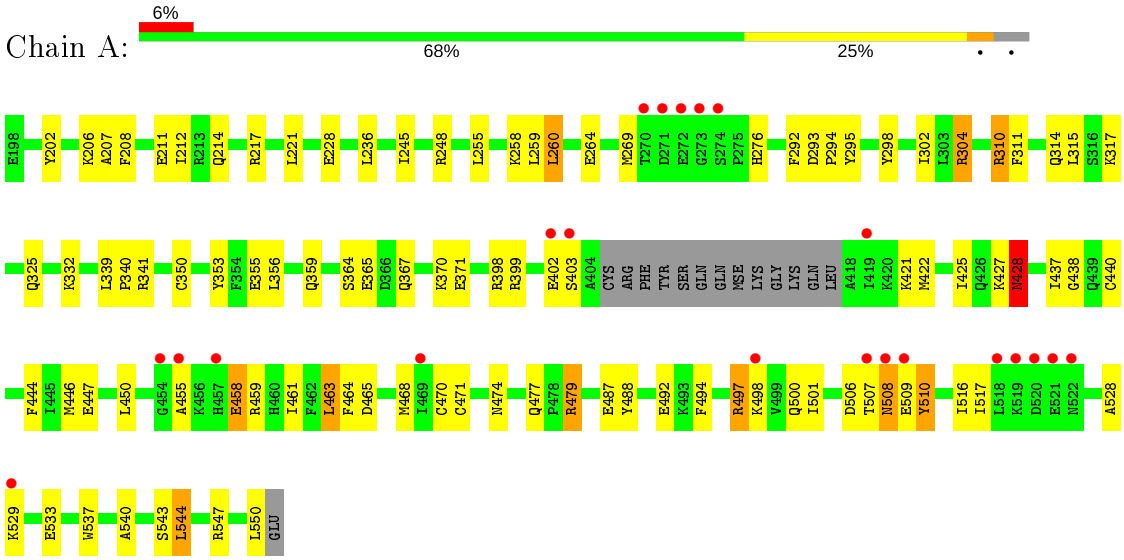
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	69	Total	O	0	0
			69	69		

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-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. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: PROTEIN (HUMAN SOS 1)

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	104.40Å 70.44Å 73.83Å 90.00° 96.29° 90.00°	Depositor
Resolution (Å)	30.00 – 2.30 19.91 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.1 (30.00-2.30) 98.4 (19.91-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.04	Depositor
$< I/\sigma(I) >$ [1]	2.32 (at 2.09Å)	Xtriage
Refinement program	CNS CNS-03	Depositor
R, R_{free}	0.229 , 0.269 0.243 , 0.284	Depositor DCC
R_{free} test set	3069 reflections (10.02%)	wwPDB-VP
Wilson B-factor (Å^2)	32.1	Xtriage
Anisotropy	0.379	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 62.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	2817	wwPDB-VP
Average B, all atoms (Å^2)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.81% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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 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	0.60	4/2792 (0.1%)	0.70	5/3740 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	427	LYS	C-N	-6.06	1.20	1.34
1	A	428	ASN	N-CA	-5.21	1.35	1.46
1	A	427	LYS	CA-C	-5.16	1.39	1.52
1	A	269	MSE	CG-SE	-5.08	1.78	1.95

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	304	ARG	NE-CZ-NH2	6.52	123.56	120.30
1	A	310	ARG	NE-CZ-NH2	6.51	123.55	120.30
1	A	547	ARG	NE-CZ-NH2	6.42	123.51	120.30
1	A	398	ARG	NE-CZ-NH2	6.31	123.45	120.30
1	A	497	ARG	NE-CZ-NH2	5.58	123.09	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 the 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 within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2748	0	2728	80	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	69	0	0	3	0
All	All	2817	0	2728	80	0

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 16.

All (80) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:422:MSE:HE3	1:A:437:ILE:HG22	1.50	0.93
1:A:428:ASN:ND2	1:A:487:GLU:H	1.68	0.91
1:A:428:ASN:HD21	1:A:487:GLU:H	1.18	0.86
1:A:446:MSE:HE2	1:A:540:ALA:HB3	1.63	0.80
1:A:314:GLN:NE2	1:A:317:LYS:HZ3	1.81	0.77
1:A:446:MSE:HE1	1:A:537:TRP:HA	1.68	0.76
1:A:422:MSE:CE	1:A:437:ILE:HG22	2.20	0.71
1:A:207:ALA:O	1:A:211:GLU:HG3	1.91	0.70
1:A:355:GLU:HG3	1:A:359:GLN:HE21	1.58	0.68
1:A:276:HIS:HE1	1:A:365:GLU:H	1.42	0.67
1:A:341:ARG:HG3	1:A:403:SER:OG	1.95	0.66
1:A:507:THR:C	1:A:509:GLU:H	1.99	0.66
1:A:444:PHE:HZ	1:A:447:GLU:HB2	1.62	0.64
1:A:314:GLN:NE2	1:A:317:LYS:NZ	2.44	0.64
1:A:459:ARG:HG2	1:A:459:ARG:HH11	1.63	0.64
1:A:446:MSE:HE2	1:A:540:ALA:CB	2.27	0.63
1:A:364:SER:HB3	1:A:370:LYS:HG2	1.83	0.61
1:A:260:LEU:HD22	1:A:264:GLU:HG3	1.83	0.61
1:A:450:LEU:HD12	1:A:461:ILE:HD12	1.83	0.61
1:A:202:TYR:O	1:A:206:LYS:HG3	2.00	0.61
1:A:446:MSE:HE3	1:A:463:LEU:HD12	1.83	0.61
1:A:367:GLN:O	1:A:371:GLU:HG2	2.01	0.60
1:A:364:SER:HB3	1:A:370:LYS:CG	2.32	0.60
1:A:221:LEU:HD21	1:A:550:LEU:HD23	1.83	0.59
1:A:260:LEU:O	1:A:264:GLU:HG3	2.03	0.58
1:A:498:LYS:HB3	1:A:517:ILE:O	2.04	0.57
1:A:276:HIS:CE1	1:A:365:GLU:H	2.22	0.55
1:A:479:ARG:HH11	1:A:479:ARG:HG2	1.72	0.55
1:A:314:GLN:HE22	1:A:317:LYS:NZ	2.04	0.54
1:A:507:THR:O	1:A:509:GLU:N	2.40	0.53
1:A:245:ILE:HD11	1:A:314:GLN:HG2	1.91	0.53
1:A:311:PHE:O	1:A:315:LEU:HD13	2.10	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:325:GLN:HA	2:A:35:HOH:O	2.09	0.52
1:A:474:ASN:HB2	1:A:479:ARG:HH21	1.76	0.51
1:A:468:MSE:HE1	1:A:516:ILE:HD12	1.94	0.49
1:A:399:ARG:O	1:A:402:GLU:HB3	2.12	0.49
1:A:314:GLN:HE22	1:A:317:LYS:HZ3	1.56	0.48
1:A:474:ASN:CB	1:A:479:ARG:HH21	2.27	0.48
1:A:500:GLN:C	1:A:501:ILE:HD12	2.35	0.47
1:A:260:LEU:HD22	1:A:264:GLU:CG	2.44	0.47
1:A:341:ARG:NH1	2:A:51:HOH:O	2.46	0.47
1:A:458:GLU:HG3	1:A:458:GLU:O	2.14	0.47
1:A:468:MSE:HE1	1:A:516:ILE:CD1	2.44	0.47
1:A:446:MSE:CE	1:A:463:LEU:HD12	2.42	0.47
1:A:217:ARG:HG3	1:A:217:ARG:HH11	1.80	0.47
1:A:507:THR:C	1:A:509:GLU:N	2.67	0.47
1:A:421:LYS:O	1:A:425:ILE:HG13	2.15	0.47
1:A:510:TYR:CD1	1:A:510:TYR:O	2.69	0.46
1:A:455:ALA:HB3	2:A:23:HOH:O	2.15	0.46
1:A:528:ALA:HB1	1:A:533:GLU:HB3	1.97	0.46
1:A:228:GLU:HA	1:A:228:GLU:OE1	2.15	0.46
1:A:543:SER:HA	1:A:550:LEU:HD12	1.96	0.46
1:A:468:MSE:HE2	1:A:494:PHE:HD2	1.81	0.45
1:A:506:ASP:C	1:A:508:ASN:N	2.68	0.45
1:A:298:TYR:CE2	1:A:302:ILE:HG13	2.52	0.45
1:A:314:GLN:HE21	1:A:317:LYS:HZ3	1.59	0.44
1:A:470:CYS:HB2	1:A:492:GLU:HB2	1.98	0.44
1:A:428:ASN:ND2	1:A:487:GLU:N	2.51	0.44
1:A:364:SER:HB3	1:A:370:LYS:HG3	1.99	0.44
1:A:422:MSE:HG2	1:A:464:PHE:HE2	1.83	0.44
1:A:292:PHE:HE2	1:A:353:TYR:CE2	2.36	0.44
1:A:471:CYS:HB3	1:A:488:TYR:HB3	1.99	0.43
1:A:248:ARG:HA	1:A:248:ARG:NE	2.33	0.43
1:A:339:LEU:N	1:A:340:PRO:HD2	2.34	0.42
1:A:422:MSE:HG2	1:A:464:PHE:CE2	2.54	0.42
1:A:325:GLN:HG3	1:A:332:LYS:HD2	2.02	0.42
1:A:293:ASP:N	1:A:294:PRO:CD	2.82	0.42
1:A:422:MSE:HE1	1:A:438:GLY:HA2	2.02	0.42
1:A:208:PHE:CE1	1:A:353:TYR:HE1	2.37	0.42
1:A:459:ARG:HG2	1:A:459:ARG:NH1	2.32	0.42
1:A:295:TYR:CD1	1:A:350:CYS:HB2	2.55	0.41
1:A:236:LEU:O	1:A:317:LYS:NZ	2.51	0.41
1:A:459:ARG:NE	1:A:492:GLU:OE1	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:355:GLU:HG3	1:A:359:GLN:NE2	2.31	0.41
1:A:371:GLU:OE1	1:A:371:GLU:HA	2.21	0.41
1:A:506:ASP:C	1:A:508:ASN:H	2.25	0.40
1:A:212:ILE:CG2	1:A:260:LEU:HG	2.51	0.40
1:A:479:ARG:NH1	1:A:479:ARG:HG2	2.36	0.40
1:A:465:ASP:HA	1:A:544:LEU:HD21	2.02	0.40
1:A:477:GLN:O	1:A:479:ARG:HD2	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 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 X-ray entries followed by that with respect to entries of similar resolution.

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	336/354 (95%)	323 (96%)	10 (3%)	3 (1%)	17 20

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	497	ARG
1	A	508	ASN
1	A	440	CYS

5.3.2 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 X-ray entries followed by that with respect to entries of similar resolution.

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	301/305 (99%)	286 (95%)	15 (5%)	24 34

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	214	GLN
1	A	255	LEU
1	A	258	LYS
1	A	259	LEU
1	A	260	LEU
1	A	304	ARG
1	A	310	ARG
1	A	356	LEU
1	A	428	ASN
1	A	458	GLU
1	A	463	LEU
1	A	479	ARG
1	A	510	TYR
1	A	529	LYS
1	A	544	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	240	ASN
1	A	244	ASN
1	A	276	HIS
1	A	314	GLN
1	A	359	GLN
1	A	375	GLN
1	A	428	ASN
1	A	477	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	427:LYS	C	428:ASN	N	1.20

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	332/354 (93%)	0.20	22 (6%) 18 23	21, 38, 74, 88	47 (14%)

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	273	GLY	5.9
1	A	454	GLY	5.3
1	A	507	THR	4.7
1	A	271	ASP	4.4
1	A	274	SER	4.1
1	A	509	GLU	3.8
1	A	455	ALA	3.8
1	A	520	ASP	3.7
1	A	272	GLU	3.5
1	A	518	LEU	3.4
1	A	508	ASN	3.3
1	A	270	THR	3.3
1	A	457	HIS	2.9
1	A	519	LYS	2.7
1	A	498	LYS	2.6
1	A	522	ASN	2.6
1	A	419	ILE	2.5
1	A	469	ILE	2.5
1	A	403	SER	2.3
1	A	402	GLU	2.3
1	A	521	GLU	2.2
1	A	529	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.