



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 12, 2024 – 07:03 PM EDT

PDB ID : 3CSG
Title : Crystal Structure of Monobody YS1(MBP-74)/Maltose Binding Protein Fusion Complex
Authors : Gilbreth, R.N.; Koide, S.
Deposited on : 2008-04-09
Resolution : 1.80 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 ⓘ 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	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
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)	:	2.36.2

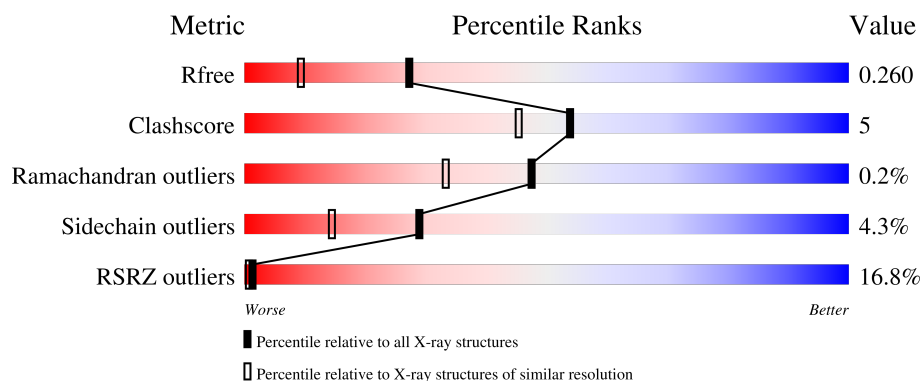
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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 of 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 $\leq 5\%$. 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	461	<div> <div>17%</div> <div>86%</div> <div>11% ..</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3838 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 Maltose-binding protein Monobody YS1 Fusion.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	458	Total	C	N	O	S	0	0	0
			3554	2290	568	690	6			

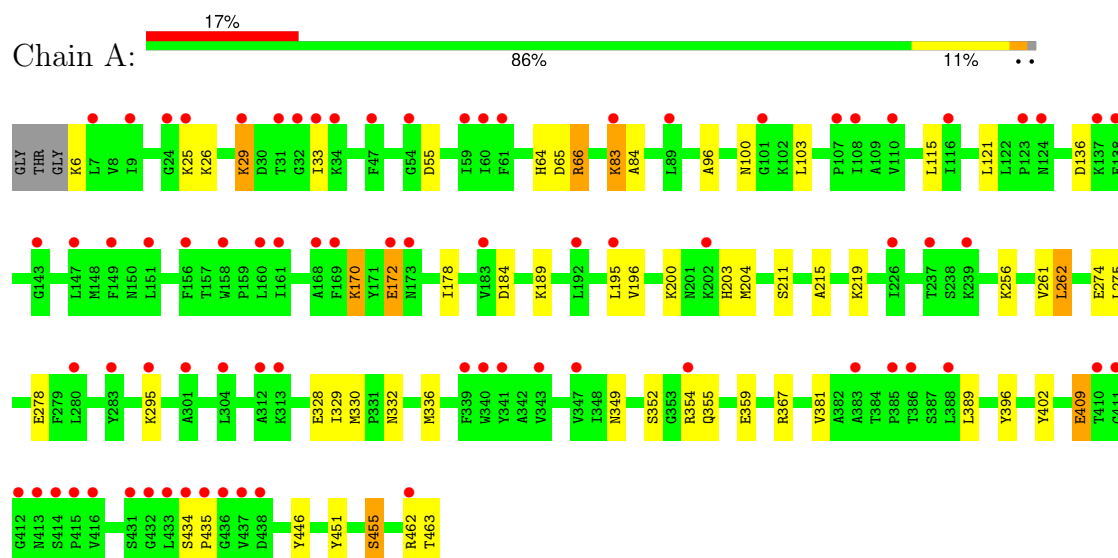
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	284	Total	O	0	0
			284	284		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Maltose-binding protein Monobody YS1 Fusion



4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	68.58Å 68.58Å 108.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.80 19.73 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.5 (20.00-1.80) 99.6 (19.73-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.81 (at 1.80Å)	Xtriage
Refinement program	REFMAC 5.2, CNS 5.2	Depositor
R, R_{free}	0.187 , 0.235 0.224 , 0.260	Depositor DCC
R_{free} test set	4615 reflections (10.02%)	wwPDB-VP
Wilson B-factor (Å ²)	33.3	Xtriage
Anisotropy	0.152	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 50.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.049 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3838	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.13% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.99	4/3646 (0.1%)	0.90	4/4966 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	402	TYR	CG-CD2	5.33	1.46	1.39
1	A	446	TYR	CE1-CZ	-5.32	1.31	1.38
1	A	451	TYR	CD2-CE2	5.29	1.47	1.39
1	A	359	GLU	CG-CD	5.06	1.59	1.51

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	172	GLU	C-N-CA	-5.68	107.49	121.70
1	A	262	LEU	CB-CG-CD1	5.49	120.34	111.00
1	A	336	MET	CG-SD-CE	5.45	108.92	100.20
1	A	455	SER	CB-CA-C	5.13	119.84	110.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	3554	0	3490	37	0
2	A	284	0	0	9	0
All	All	3838	0	3490	37	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 5.

All (37) 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:6:LYS:HB2	1:A:33:ILE:HG23	1.46	0.98
1:A:66:ARG:HD2	2:A:1143:HOH:O	1.72	0.90
1:A:96:ALA:HB2	1:A:329:ILE:HD12	1.54	0.89
1:A:64:HIS:HD2	1:A:261:VAL:H	1.26	0.84
1:A:64:HIS:CD2	1:A:261:VAL:H	2.08	0.70
1:A:136:ASP:OD2	1:A:203:HIS:HD2	1.83	0.62
1:A:381:VAL:HG22	1:A:389:LEU:HB3	1.82	0.60
1:A:328:GLU:HB2	2:A:1203:HOH:O	2.02	0.59
1:A:100:ASN:ND2	2:A:1151:HOH:O	2.34	0.58
1:A:64:HIS:HE1	1:A:330:MET:O	1.89	0.56
1:A:256:LYS:HE2	1:A:328:GLU:HG2	1.88	0.55
1:A:204:MET:CE	2:A:1020:HOH:O	2.54	0.54
1:A:178:ILE:HD11	1:A:396:TYR:CE1	2.42	0.54
1:A:349:ASN:HD22	1:A:355:GLN:NE2	2.05	0.53
1:A:274:GLU:O	1:A:278:GLU:HG2	2.08	0.53
1:A:215:ALA:HB1	1:A:219:LYS:HE2	1.93	0.51
1:A:55:ASP:HB3	2:A:1241:HOH:O	2.11	0.49
1:A:170:LYS:HA	1:A:170:LYS:HD3	1.71	0.49
1:A:204:MET:HE2	2:A:1020:HOH:O	2.12	0.48
1:A:196:VAL:HG12	1:A:200:LYS:HD2	1.96	0.48
1:A:381:VAL:HG21	1:A:389:LEU:HD22	1.96	0.48
1:A:6:LYS:HG3	1:A:33:ILE:HD12	1.95	0.48
1:A:349:ASN:HD22	1:A:355:GLN:HE21	1.62	0.47
1:A:409:GLU:H	1:A:409:GLU:CD	2.19	0.46
1:A:435:PRO:HA	1:A:463:THR:HG22	1.98	0.46
1:A:26:LYS:O	1:A:29:LYS:HB3	2.17	0.45
1:A:178:ILE:HD11	1:A:396:TYR:CZ	2.52	0.44
1:A:352:SER:OG	1:A:354:ARG:HG3	2.18	0.43
1:A:367:ARG:NH1	2:A:1183:HOH:O	2.51	0.43
1:A:65:ASP:OD2	1:A:66:ARG:N	2.52	0.43
1:A:83:LYS:HE3	1:A:84:ALA:HB2	2.00	0.42
1:A:100:ASN:HA	2:A:1151:HOH:O	2.19	0.42
1:A:184:ASP:O	1:A:189:LYS:HE2	2.19	0.42
1:A:434:SER:HA	1:A:435:PRO:HD2	1.84	0.42
1:A:275:LEU:HD23	1:A:275:LEU:HA	1.80	0.42
1:A:29:LYS:HE3	2:A:1277:HOH:O	2.19	0.41
1:A:6:LYS:CB	1:A:33:ILE:HG23	2.34	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	456/461 (99%)	441 (97%)	14 (3%)	1 (0%)	47 33

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	455	SER

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	374/375 (100%)	358 (96%)	16 (4%)	29 14

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	LYS
1	A	29	LYS
1	A	66	ARG
1	A	83	LYS
1	A	103	LEU
1	A	115	LEU
1	A	121	LEU

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Mol	Chain	Res	Type
1	A	170	LYS
1	A	172	GLU
1	A	195	LEU
1	A	211	SER
1	A	262	LEU
1	A	295	LYS
1	A	332	ASN
1	A	409	GLU
1	A	462	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	ASN
1	A	49	GLN
1	A	64	HIS
1	A	86	GLN
1	A	100	ASN
1	A	201	ASN
1	A	203	HIS
1	A	218	ASN
1	A	332	ASN
1	A	355	GLN
1	A	413	ASN
1	A	460	ASN

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 monosaccharides 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

There are no chain breaks in this entry.

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, 95th 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	458/461 (99%)	0.98	77 (16%) 1 1	20, 37, 47, 56	0

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	437	VAL	4.9
1	A	414	SER	4.7
1	A	415	PRO	4.4
1	A	385	PRO	4.3
1	A	411	GLY	4.1
1	A	462	ARG	4.0
1	A	33	ILE	4.0
1	A	83	LYS	3.9
1	A	413	ASN	3.9
1	A	161	ILE	3.8
1	A	183	VAL	3.8
1	A	25	LYS	3.8
1	A	160	LEU	3.5
1	A	60	ILE	3.5
1	A	339	PHE	3.4
1	A	354	ARG	3.4
1	A	343	VAL	3.4
1	A	123	PRO	3.3
1	A	438	ASP	3.3
1	A	116	ILE	3.2
1	A	301	ALA	3.2
1	A	29	LYS	3.2
1	A	61	PHE	3.2
1	A	59	ILE	3.1
1	A	54	GLY	3.0
1	A	158	TRP	3.0
1	A	412	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	237	THR	3.0
1	A	386	THR	3.0
1	A	435	PRO	3.0
1	A	295	LYS	3.0
1	A	433	LEU	3.0
1	A	169	PHE	2.9
1	A	436	GLY	2.8
1	A	239	LYS	2.8
1	A	34	LYS	2.8
1	A	108	ILE	2.7
1	A	431	SER	2.7
1	A	101	GLY	2.7
1	A	192	LEU	2.7
1	A	195	LEU	2.7
1	A	410	THR	2.7
1	A	89	LEU	2.6
1	A	283	TYR	2.6
1	A	7	LEU	2.6
1	A	341	TYR	2.6
1	A	32	GLY	2.5
1	A	31	THR	2.5
1	A	173	ASN	2.5
1	A	124	ASN	2.5
1	A	432	GLY	2.5
1	A	147	LEU	2.5
1	A	434	SER	2.5
1	A	151	LEU	2.5
1	A	137	LYS	2.4
1	A	313	LYS	2.4
1	A	347	VAL	2.4
1	A	138	GLU	2.4
1	A	172	GLU	2.4
1	A	110	VAL	2.3
1	A	312	ALA	2.3
1	A	9	ILE	2.3
1	A	149	PHE	2.3
1	A	107	PRO	2.3
1	A	24	GLY	2.3
1	A	226	ILE	2.2
1	A	143	GLY	2.2
1	A	202	LYS	2.2
1	A	383	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	280	LEU	2.1
1	A	156	PHE	2.1
1	A	47	PHE	2.1
1	A	416	VAL	2.1
1	A	304	LEU	2.1
1	A	168	ALA	2.0
1	A	388	LEU	2.0
1	A	340	TRP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.