



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 19, 2016 – 07:54 PM GMT

PDB ID : 4XA1
Title : Crystal Structure of the coiled-coil surrounding Skip 1 of MYH7
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Deposited on : 2014-12-12
Resolution : 3.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20026982

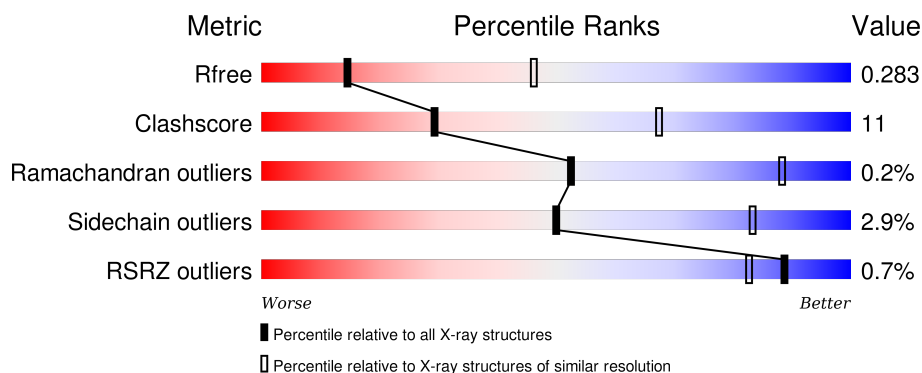
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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}	91344	1124 (3.24-3.16)
Clashscore	102246	1024 (3.22-3.18)
Ramachandran outliers	100387	1004 (3.22-3.18)
Sidechain outliers	100360	1003 (3.22-3.18)
RSRZ outliers	91569	1129 (3.24-3.16)

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. 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	159	 74% 21% . .
1	B	159	 72% 23% . .
1	C	159	 66% 14% . 18%
1	D	159	 55% 18% . . 23%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4626 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 Gp7-MYH7(1173-1238)-EB1 chimera protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	153	Total	C	N	O	S	0	0	0
			1252	776	217	256	3			
1	B	155	Total	C	N	O	S	0	0	0
			1269	785	219	262	3			
1	C	130	Total	C	N	O	S	0	0	0
			1066	659	188	216	3			
1	D	122	Total	C	N	O	S	0	0	0
			1004	623	175	203	3			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP P13848
A	-1	ALA	-	expression tag	UNP P13848
A	0	SER	-	expression tag	UNP P13848
B	-2	GLY	-	expression tag	UNP P13848
B	-1	ALA	-	expression tag	UNP P13848
B	0	SER	-	expression tag	UNP P13848
C	-2	GLY	-	expression tag	UNP P13848
C	-1	ALA	-	expression tag	UNP P13848
C	0	SER	-	expression tag	UNP P13848
D	-2	GLY	-	expression tag	UNP P13848
D	-1	ALA	-	expression tag	UNP P13848
D	0	SER	-	expression tag	UNP P13848

- Molecule 2 is water.

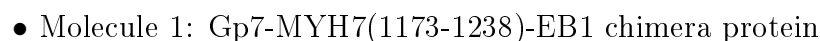
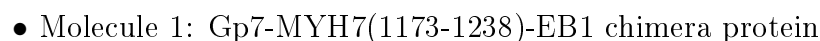
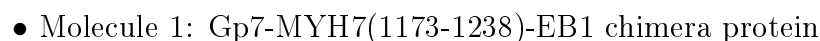
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	9	Total	O	0	0
			9	9		
2	B	12	Total	O	0	0
			12	12		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	5	Total	O	0	0
			5	5		
2	D	9	Total	O	0	0
			9	9		

- Molecule 1: Gp7-MYH7(1173-1238)-EB1 chimera protein



K1216	
E1220	
V1231	
M1234	
M1236	
E1236	
Q1237	
I1238	
E211	
K212	
E213	
R214	
D215	
N223	
I224	
E225	
D236	
P237	
V238	
Y247	
ALA	
THR	
ASP	
GLU	

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	56.26 Å 59.32 Å 67.72 Å 96.05° 110.01° 92.89°	Depositor
Resolution (Å)	34.86 – 3.20 34.86 – 3.19	Depositor EDS
% Data completeness (in resolution range)	97.6 (34.86-3.20) 92.8 (34.86-3.19)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.77 (at 3.18 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.234 , 0.285 0.234 , 0.283	Depositor DCC
R_{free} test set	659 reflections (5.06%)	DCC
Wilson B-factor (Å ²)	65.8	Xtriage
Anisotropy	0.794	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 30.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 13198 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4626	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.40% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.53	0/1266	0.69	1/1700 (0.1%)
1	B	0.62	0/1283	0.93	14/1723 (0.8%)
1	C	0.67	1/1076 (0.1%)	0.74	1/1442 (0.1%)
1	D	0.70	1/1013 (0.1%)	0.78	3/1354 (0.2%)
All	All	0.63	2/4638 (0.0%)	0.79	19/6219 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	237	PRO	N-CD	5.38	1.55	1.47
1	D	1212	ARG	CG-CD	5.03	1.64	1.51

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1228	LEU	CB-CA-C	-8.79	93.50	110.20
1	B	1226	LEU	CA-CB-CG	8.03	133.77	115.30
1	B	1228	LEU	CA-CB-CG	7.21	131.87	115.30
1	B	39	PHE	CB-CA-C	-6.84	96.71	110.40
1	A	211	GLU	CB-CA-C	-6.76	96.87	110.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	26	THR	Peptide

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	1252	0	1239	20	0
1	B	1269	0	1249	44	0
1	C	1066	0	1056	29	0
1	D	1004	0	1005	40	1
2	A	9	0	0	0	0
2	B	12	0	0	0	0
2	C	5	0	0	0	0
2	D	9	0	0	0	0
All	All	4626	0	4549	103	1

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 11.

The worst 5 of 103 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:C:36:TYR:CE2	1:D:3:LEU:HD12	1.91	1.06
1:C:36:TYR:HE2	1:D:3:LEU:HD12	1.17	1.04
1:D:7:GLU:O	1:D:10:ASP:OD1	1.77	1.03
1:B:1173:LYS:HE2	1:B:1177:ASP:OD2	1.58	1.00
1:C:214:ARG:NH1	1:D:1238:ILE:HG23	1.88	0.88

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:49:SER:OG	1:D:215:ASP:OD2[1_654]	2.15	0.05

5.3 Torsion angles

5.3.1 Protein backbone

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	151/159 (95%)	144 (95%)	7 (5%)	0	100	100
1	B	153/159 (96%)	145 (95%)	8 (5%)	0	100	100
1	C	128/159 (80%)	128 (100%)	0	0	100	100
1	D	118/159 (74%)	109 (92%)	8 (7%)	1 (1%)	24	69
All	All	550/636 (86%)	526 (96%)	23 (4%)	1 (0%)	52	88

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	4	LYS

5.3.2 Protein sidechains

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	139/143 (97%)	134 (96%)	5 (4%)	42	79
1	B	141/143 (99%)	136 (96%)	5 (4%)	43	80
1	C	117/143 (82%)	114 (97%)	3 (3%)	54	85
1	D	112/143 (78%)	110 (98%)	2 (2%)	66	89
All	All	509/572 (89%)	494 (97%)	15 (3%)	50	83

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	39	PHE
1	B	1229	ASP
1	C	1233	SER
1	B	6	GLU
1	C	33	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	8	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

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	153/159 (96%)	-0.13	0	100 100	22, 44, 83, 128	0
1	B	155/159 (97%)	-0.20	0	100 100	21, 48, 77, 84	0
1	C	130/159 (81%)	-0.14	1 (0%)	87 80	22, 42, 89, 110	0
1	D	122/159 (76%)	-0.09	3 (2%)	61 47	21, 40, 93, 109	0
All	All	560/636 (88%)	-0.14	4 (0%)	89 83	21, 44, 84, 128	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	235	ASN	3.7
1	D	7	GLU	3.6
1	D	15	LEU	2.6
1	D	45	ASP	2.1

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 [i](#)

There are no such residues in this entry.