wwPDB X-ray Structure Validation Summary Report (i)

Apr 28, 2024 – 04:57 pm BST

PDB ID	:	2IZ5
Title	:	FUNCTION AND STRUCTURE OF THE MOLYBDENUM COFACTOR CARRIER PROTEIN MCP FROM CHLAMYDOMONAS REINHARDTII
Authors	:	Fischer, K.; Llamas, A.; Tejada-Jimenez, M.; Schrader, N.; Kuper, J.; Mendel, R.R.; Fernandez, E.; Schwarz, G.
Deposited on	:	2006-07-25
Resolution	:	2.29 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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

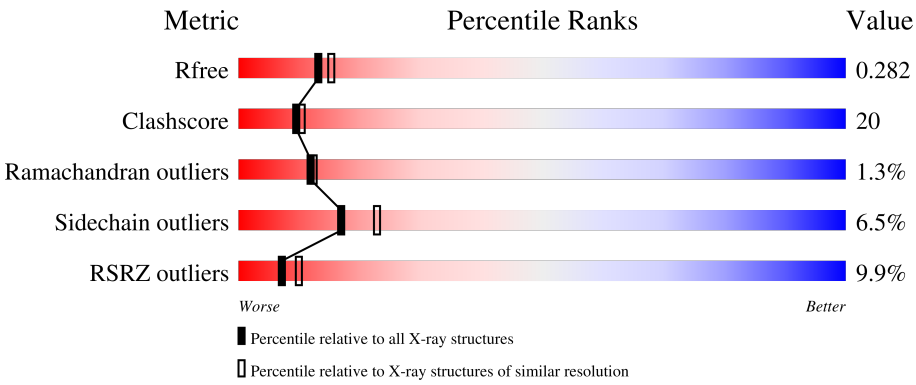
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.29 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 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 <=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	176	5%, 63%, 23%, • •, 9%
1	B	176	10%, 65%, 23%, • •, 9%
1	C	176	10%, 64%, 22%, • •, 10%
1	D	176	11%, 67%, 19%, • •, 9%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 4618 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 MOCO CARRIER PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	160	1114	705	195	209	5	0	0	0
			Total	C	N	O	S			
1	B	161	1127	713	196	213	5	0	0	0
			Total	C	N	O	S			
1	C	158	1104	698	193	208	5	0	0	0
			Total	C	N	O	S			
1	D	160	1110	702	192	211	5	0	0	0

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	HIS	-	expression tag	UNP Q8RV61
A	-6	HIS	-	expression tag	UNP Q8RV61
A	-5	HIS	-	expression tag	UNP Q8RV61
A	-4	HIS	-	expression tag	UNP Q8RV61
A	-3	HIS	-	expression tag	UNP Q8RV61
A	-2	HIS	-	expression tag	UNP Q8RV61
A	-1	GLY	-	expression tag	UNP Q8RV61
A	0	CYS	-	expression tag	UNP Q8RV61
A	166	LYS	-	expression tag	UNP Q8RV61
A	167	LEU	-	expression tag	UNP Q8RV61
A	168	ASN	-	expression tag	UNP Q8RV61
B	-7	HIS	-	expression tag	UNP Q8RV61
B	-6	HIS	-	expression tag	UNP Q8RV61
B	-5	HIS	-	expression tag	UNP Q8RV61
B	-4	HIS	-	expression tag	UNP Q8RV61
B	-3	HIS	-	expression tag	UNP Q8RV61
B	-2	HIS	-	expression tag	UNP Q8RV61
B	-1	GLY	-	expression tag	UNP Q8RV61
B	0	CYS	-	expression tag	UNP Q8RV61
B	166	LYS	-	expression tag	UNP Q8RV61
B	167	LEU	-	expression tag	UNP Q8RV61

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Chain	Residue	Modelled	Actual	Comment	Reference
B	168	ASN	-	expression tag	UNP Q8RV61
C	-7	HIS	-	expression tag	UNP Q8RV61
C	-6	HIS	-	expression tag	UNP Q8RV61
C	-5	HIS	-	expression tag	UNP Q8RV61
C	-4	HIS	-	expression tag	UNP Q8RV61
C	-3	HIS	-	expression tag	UNP Q8RV61
C	-2	HIS	-	expression tag	UNP Q8RV61
C	-1	GLY	-	expression tag	UNP Q8RV61
C	0	CYS	-	expression tag	UNP Q8RV61
C	166	LYS	-	expression tag	UNP Q8RV61
C	167	LEU	-	expression tag	UNP Q8RV61
C	168	ASN	-	expression tag	UNP Q8RV61
D	-7	HIS	-	expression tag	UNP Q8RV61
D	-6	HIS	-	expression tag	UNP Q8RV61
D	-5	HIS	-	expression tag	UNP Q8RV61
D	-4	HIS	-	expression tag	UNP Q8RV61
D	-3	HIS	-	expression tag	UNP Q8RV61
D	-2	HIS	-	expression tag	UNP Q8RV61
D	-1	GLY	-	expression tag	UNP Q8RV61
D	0	CYS	-	expression tag	UNP Q8RV61
D	166	LYS	-	expression tag	UNP Q8RV61
D	167	LEU	-	expression tag	UNP Q8RV61
D	168	ASN	-	expression tag	UNP Q8RV61

- Molecule 2 is water.

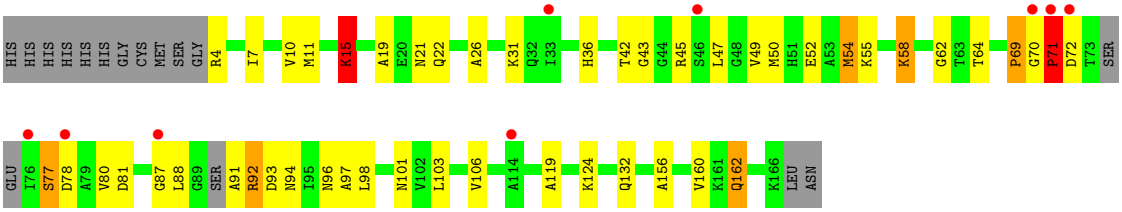
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	34	34	34	0	0
			Total	O		
2	B	50	50	50	0	0
			Total	O		
2	C	41	41	41	0	0
			Total	O		
2	D	38	38	38	0	0

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.

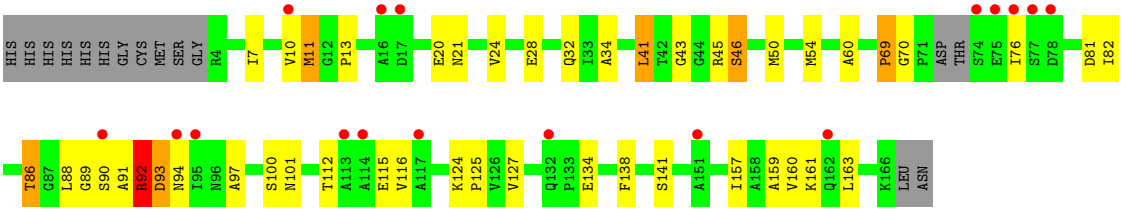
• Molecule 1: MOCO CARRIER PROTEIN

Chain A:



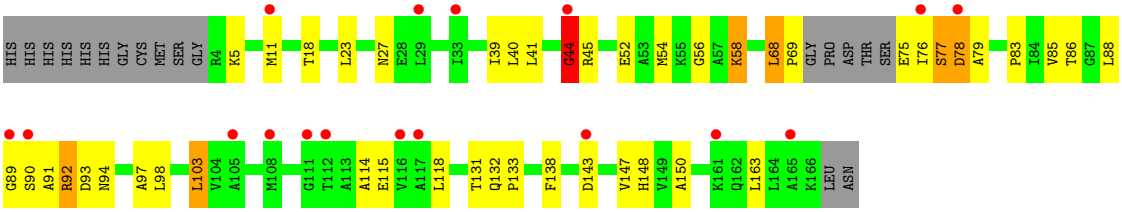
• Molecule 1: MOCO CARRIER PROTEIN

Chain B:



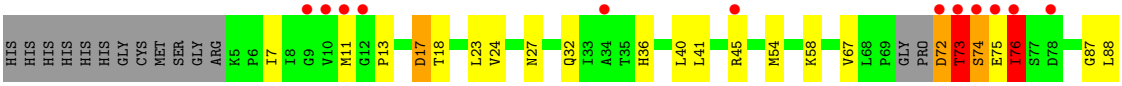
• Molecule 1: MOCO CARRIER PROTEIN

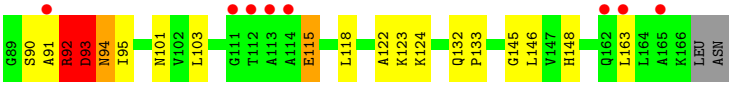
Chain C:



• Molecule 1: MOCO CARRIER PROTEIN

Chain D:




G89
S90
A91
R92
D93
N94
I95
N101
V102
L103
G111
T112
A113
A114
E115
L118
A122
K123
K124
Q132
P133
G145
L146
V147
H148
Q162
L163
L164
A165
K166
LEU
ASN

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	68.31Å 75.88Å 126.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	65.09 – 2.29 33.17 – 2.29	Depositor EDS
% Data completeness (in resolution range)	95.9 (65.09-2.29) 96.1 (33.17-2.29)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.90 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.215 , 0.273 0.225 , 0.282	Depositor DCC
R_{free} test set	1471 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å^2)	52.6	Xtriage
Anisotropy	0.118	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 56.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	4618	wwPDB-VP
Average B, all atoms (Å^2)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 59.50 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.7496e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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 (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	1.08	2/1126 (0.2%)	1.05	6/1526 (0.4%)
1	B	0.82	0/1140	0.85	1/1546 (0.1%)
1	C	0.83	0/1116	0.87	3/1513 (0.2%)
1	D	0.89	2/1122 (0.2%)	0.87	3/1523 (0.2%)
All	All	0.91	4/4504 (0.1%)	0.92	13/6108 (0.2%)

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	B	0	3
1	C	0	3
1	D	1	8
All	All	1	14

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	71	PRO	C-N	18.69	1.77	1.34
1	A	69	PRO	C-N	-12.60	1.10	1.33
1	D	74	SER	C-N	-8.40	1.14	1.34
1	D	115	GLU	CG-CD	6.18	1.61	1.51

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	71	PRO	C-N-CA	-14.77	84.77	121.70
1	A	71	PRO	O-C-N	8.26	135.91	122.70
1	D	76	ILE	O-C-N	-7.90	110.06	122.70
1	A	69	PRO	O-C-N	-7.49	110.47	123.20
1	A	71	PRO	CA-C-N	-7.39	100.94	117.20

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	D	75	GLU	CA

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	69	PRO	Peptide
1	B	70	GLY	Peptide
1	B	92	ARG	Peptide
1	C	44	GLY	Peptide
1	C	76	ILE	Peptide

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	1114	0	1156	51	0
1	B	1127	0	1177	51	0
1	C	1104	0	1152	43	0
1	D	1110	0	1149	49	0
2	A	34	0	0	9	0
2	B	50	0	0	15	0
2	C	41	0	0	9	0
2	D	38	0	0	12	0
All	All	4618	0	4634	178	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 20.

The worst 5 of 178 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:71:PRO:C	1:A:72:ASP:N	1.77	1.38
1:D:11:MET:SD	1:D:103:LEU:HD21	1.82	1.20
1:B:93:ASP:HA	2:B:2027:HOH:O	0.98	1.14
1:A:71:PRO:C	1:A:72:ASP:CA	2.19	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:24:VAL:HA	2:D:2003:HOH:O	1.54	1.06

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	154/176 (88%)	145 (94%)	5 (3%)	4 (3%)	5 4
1	B	157/176 (89%)	153 (98%)	4 (2%)	0	100 100
1	C	154/176 (88%)	143 (93%)	9 (6%)	2 (1%)	12 12
1	D	156/176 (89%)	148 (95%)	6 (4%)	2 (1%)	12 12
All	All	621/704 (88%)	589 (95%)	24 (4%)	8 (1%)	12 12

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	90	SER
1	A	77	SER
1	C	78	ASP
1	D	94	ASN
1	A	15	LYS

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	110/128 (86%)	101 (92%)	9 (8%)	11	14
1	B	113/128 (88%)	105 (93%)	8 (7%)	14	19
1	C	110/128 (86%)	105 (96%)	5 (4%)	27	39
1	D	110/128 (86%)	103 (94%)	7 (6%)	17	23
All	All	443/512 (86%)	414 (94%)	29 (6%)	17	23

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	86	THR
1	D	93	ASP
1	C	41	LEU
1	D	73	THR
1	B	93	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	148	HIS
1	D	101	ASN
1	C	51	HIS
1	B	101	ASN
1	C	148	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 monosaccharides 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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	2
1	D	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	71:PRO	C	72:ASP	N	1.77
1	D	74:SER	C	75:GLU	N	1.14
1	A	69:PRO	C	70:GLY	N	1.10

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

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	160/176 (90%)	0.46	9 (5%)	24	30	43, 52, 68, 82	0
1	B	161/176 (91%)	0.62	17 (10%)	6	8	44, 51, 66, 78	0
1	C	158/176 (89%)	0.67	17 (10%)	5	8	47, 56, 71, 87	0
1	D	160/176 (90%)	0.80	20 (12%)	3	5	47, 57, 75, 83	0
All	All	639/704 (90%)	0.64	63 (9%)	7	10	43, 55, 70, 87	0

The worst 5 of 63 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	76	ILE	7.8
1	D	76	ILE	5.7
1	C	90	SER	5.7
1	B	75	GLU	5.1
1	C	78	ASP	4.7

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.