



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:08 PM UTC

PDB ID : 4GEH / pdb_00004geh
Title : Crystal structure of MST4 dimerization domain complex with PDCD10
Authors : Zhang, M.; Shi, Z.B.; Zhou, Z.C.
Deposited on : 2012-08-02
Resolution : 1.95 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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

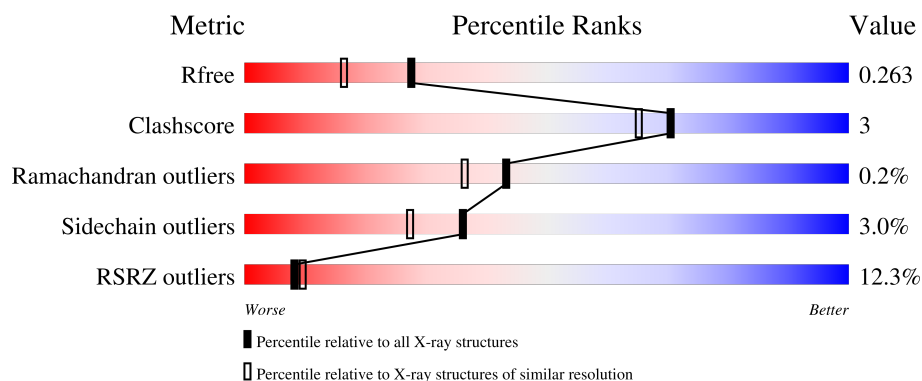
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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}	180053	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	207	
1	C	207	
2	B	91	
2	D	91	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4399 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 Programmed cell death protein 10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	198	Total	C	N	O	S	0	2	0
			1617	1036	268	307	6			
1	C	198	Total	C	N	O	S	0	0	0
			1595	1023	268	298	6			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	6	GLY	-	expression tag	UNP Q9BUL8
A	7	MET	-	expression tag	UNP Q9BUL8
A	8	ALA	-	expression tag	UNP Q9BUL8
C	6	GLY	-	expression tag	UNP Q9BUL8
C	7	MET	-	expression tag	UNP Q9BUL8
C	8	ALA	-	expression tag	UNP Q9BUL8

- Molecule 2 is a protein called Serine/threonine-protein kinase MST4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	65	Total	C	N	O	S	0	0	0
			491	306	81	99	5			
2	D	69	Total	C	N	O	S	0	0	0
			522	325	87	105	5			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	323	MET	-	expression tag	UNP Q9P289
B	324	GLY	-	expression tag	UNP Q9P289
D	323	MET	-	expression tag	UNP Q9P289
D	324	GLY	-	expression tag	UNP Q9P289

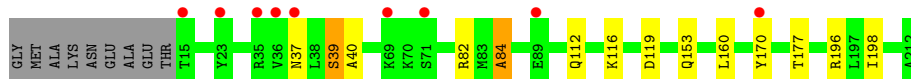
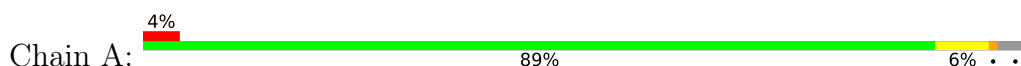
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	88	Total 88	O 88	0	0
3	B	6	Total 6	O 6	0	0
3	C	47	Total 47	O 47	0	0
3	D	33	Total 33	O 33	0	0

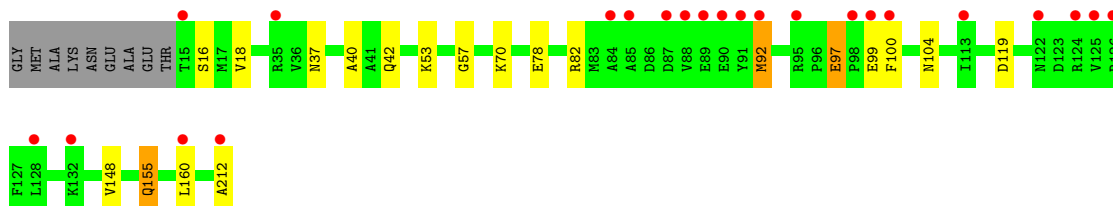
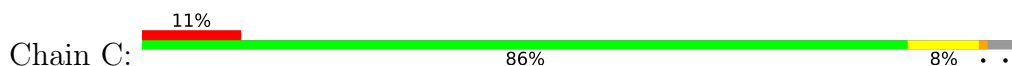
3 Residue-property plots [i](#)

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.

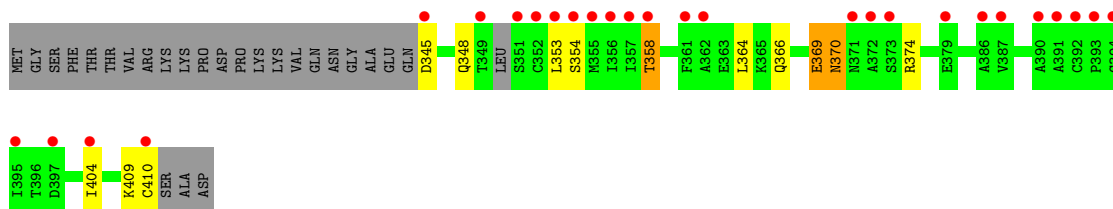
- Molecule 1: Programmed cell death protein 10



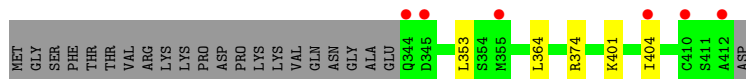
- Molecule 1: Programmed cell death protein 10



- Molecule 2: Serine/threonine-protein kinase MST4



- Molecule 2: Serine/threonine-protein kinase MST4



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	75.24Å 84.02Å 109.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.97 – 1.95 45.97 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.9 (45.97-1.95) 99.9 (45.97-1.95)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.60 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.220 , 0.253 0.226 , 0.263	Depositor DCC
R_{free} test set	2618 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	28.1	Xtriage
Anisotropy	0.203	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 27.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4399	wwPDB-VP
Average B, all atoms (Å ²)	35.0	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 22.36 % 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 5.7889e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	0.73	0/1648	0.81	1/2219 (0.0%)
1	C	0.67	0/1620	0.84	1/2184 (0.0%)
2	B	0.66	0/493	0.94	1/661 (0.2%)
2	D	0.69	0/525	0.86	0/705
All	All	0.69	0/4286	0.84	3/5769 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	155	GLN	N-CA-C	8.22	121.05	111.02
2	B	369	GLU	N-CA-C	5.30	117.05	111.28
1	A	84	ALA	N-CA-C	5.05	117.52	111.71

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	1617	0	1649	10	0
1	C	1595	0	1617	13	0
2	B	491	0	490	6	0
2	D	522	0	535	3	0
3	A	88	0	0	0	0
3	B	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	47	0	0	0	0
3	D	33	0	0	0	0
All	All	4399	0	4291	29	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 3.

All (29) 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)
2:B:364:LEU:O	2:B:374:ARG:NH2	2.20	0.75
2:D:364:LEU:O	2:D:374:ARG:NH2	2.20	0.74
1:C:37:ASN:HD22	1:C:40:ALA:H	1.43	0.67
1:C:97:GLU:HG2	1:C:100:PHE:CD2	2.31	0.65
1:A:37:ASN:HD22	1:A:40:ALA:H	1.45	0.64
1:C:99:GLU:HB3	1:C:148:VAL:HG22	1.80	0.62
1:C:70:LYS:HG3	2:D:404:ILE:HD11	1.81	0.62
2:B:354:SER:HA	2:B:358:THR:OG1	2.05	0.57
1:A:153:GLN:HG3	1:A:153:GLN:O	2.09	0.53
1:A:112[A]:GLN:HE21	1:A:116:LYS:HE2	1.74	0.53
1:C:97:GLU:HG2	1:C:100:PHE:HD2	1.74	0.52
1:C:82:ARG:NH2	1:C:119:ASP:OD1	2.40	0.51
1:C:18:VAL:HG22	1:C:57:GLY:HA2	1.93	0.51
2:B:409:LYS:O	2:B:410:CYS:HB2	2.11	0.50
1:A:39:SER:OG	1:C:42:GLN:NE2	2.49	0.46
2:B:366:GLN:HA	2:B:369:GLU:HG3	1.99	0.45
1:A:160:LEU:C	1:A:160:LEU:HD13	2.42	0.44
1:A:84:ALA:CB	1:A:198:ILE:HD13	2.48	0.44
2:B:370:ASN:O	2:B:370:ASN:CG	2.62	0.43
1:C:37:ASN:ND2	1:C:40:ALA:H	2.13	0.43
1:C:92:MET:SD	1:C:104:ASN:HB3	2.59	0.42
1:A:37:ASN:ND2	1:A:40:ALA:H	2.15	0.42
1:A:84:ALA:HB2	1:A:198:ILE:HD13	2.01	0.41
1:C:70:LYS:CG	2:D:404:ILE:HD11	2.47	0.41
1:A:82:ARG:NH2	1:A:119:ASP:OD1	2.45	0.41
2:B:409:LYS:O	2:B:410:CYS:CB	2.68	0.41
1:A:170:TYR:CE1	1:A:196:ARG:HD3	2.56	0.40
1:C:155:GLN:HE22	1:C:212:ALA:HB3	1.86	0.40
1:C:78:GLU:O	1:C:82:ARG:HG3	2.22	0.40

There are no symmetry-related clashes.

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	198/207 (96%)	198 (100%)	0	0	100	100
1	C	196/207 (95%)	195 (100%)	1 (0%)	0	100	100
2	B	61/91 (67%)	58 (95%)	2 (3%)	1 (2%)	7	2
2	D	67/91 (74%)	65 (97%)	2 (3%)	0	100	100
All	All	522/596 (88%)	516 (99%)	5 (1%)	1 (0%)	43	36

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	348	GLN

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	179/186 (96%)	177 (99%)	2 (1%)	65	64
1	C	173/186 (93%)	168 (97%)	5 (3%)	37	29
2	B	53/78 (68%)	48 (91%)	5 (9%)	8	2
2	D	58/78 (74%)	56 (97%)	2 (3%)	32	23
All	All	463/528 (88%)	449 (97%)	14 (3%)	36	27

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	SER
1	A	177	THR
2	B	345	ASP
2	B	353	LEU
2	B	358	THR
2	B	370	ASN
2	B	404	ILE
1	C	16	SER
1	C	53	LYS
1	C	92	MET
1	C	97	GLU
1	C	160	LEU
2	D	353	LEU
2	D	401	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	37	ASN
1	A	129	GLN
2	B	370	ASN
1	C	37	ASN
1	C	42	GLN
2	D	348	GLN
2	D	408	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 oligosaccharides 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	198/207 (95%)	0.36	9 (4%) 38 44	15, 28, 44, 56	2 (1%)
1	C	198/207 (95%)	0.91	23 (11%) 9 11	20, 34, 59, 84	0
2	B	65/91 (71%)	1.92	27 (41%) 0 0	32, 52, 71, 78	0
2	D	69/91 (75%)	0.54	6 (8%) 16 18	23, 30, 54, 66	0
All	All	530/596 (88%)	0.78	65 (12%) 8 9	15, 32, 60, 84	2 (0%)

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	91	TYR	7.0
1	C	88	VAL	6.6
2	B	391	ALA	5.4
2	B	390	ALA	5.1
1	C	92	MET	5.0
1	C	89	GLU	4.8
1	C	212	ALA	4.8
1	C	85	ALA	4.6
2	B	349	THR	4.5
1	C	90	GLU	4.2
1	C	15	THR	4.1
1	C	125	VAL	4.1
1	C	87	ASP	4.0
2	B	355	MET	3.7
1	A	15	THR	3.5
2	B	394	GLY	3.4
2	B	353	LEU	3.3
2	D	410	CYS	3.3
2	B	351	SER	3.2
2	B	361	PHE	3.2
1	A	35	ARG	3.2

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Mol	Chain	Res	Type	RSRZ
2	D	412	ALA	3.2
1	C	35	ARG	3.2
2	B	387	VAL	3.1
2	B	352	CYS	3.1
1	C	128	LEU	3.1
2	B	397	ASP	3.0
1	A	36	VAL	2.9
2	B	410	CYS	2.9
1	A	71	SER	2.9
2	D	344	GLN	2.8
2	B	386	ALA	2.8
1	A	37	ASN	2.8
1	C	98	PRO	2.7
1	C	99	GLU	2.6
2	B	393	PRO	2.6
1	A	170	TYR	2.6
1	C	100	PHE	2.6
2	D	404	ILE	2.6
2	B	357	ILE	2.5
2	B	362	ALA	2.5
2	B	372	ALA	2.5
1	C	113	ILE	2.5
2	B	395	ILE	2.4
1	C	132	LYS	2.4
2	B	358	THR	2.4
2	B	392	CYS	2.4
1	C	126	ARG	2.4
2	B	354	SER	2.4
1	A	69	LYS	2.4
1	A	89	GLU	2.3
1	C	84	ALA	2.3
2	B	373	SER	2.3
1	C	124	ARG	2.3
1	A	23	TYR	2.2
2	B	356	ILE	2.2
1	C	122	ASN	2.2
1	C	95	ARG	2.2
2	B	379	GLU	2.2
2	B	404	ILE	2.2
2	D	345	ASP	2.1
2	B	371	ASN	2.1
2	D	355	MET	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	160	LEU	2.0
2	B	345	ASP	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 oligosaccharides 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.