Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:10 PM UTC

PDB ID	:	8PDE / pdb_00008pde
Title	:	Crystal Structure of the MADS-box/MEF2 Domain of MEF2D bound to ds-DNA and HDAC4 deacetylase binding motif
Authors	:	Chinellato, M.; Carli, A.; Perin, S.; Mazzocato, Y.; Biondi, B.; Di Giorgio, E.; Brancolini, C.; Angelini, A.; Cendron, L.
Deposited on	:	2023-06-12
Resolution	:	2.40 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 ①) were used in the production of this report:

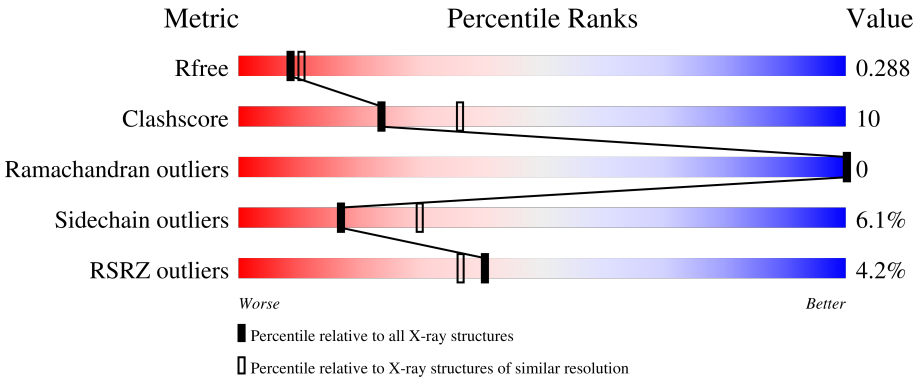
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	95	81% 15%
1	B	95	% 76% 18%
1	D	95	5% 66% 31%
1	E	95	2% 72% 23%
2	C	17	47% 24% 29% 24% 24%

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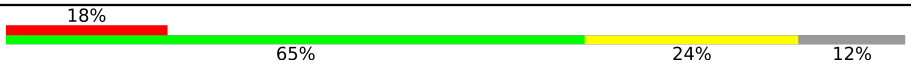
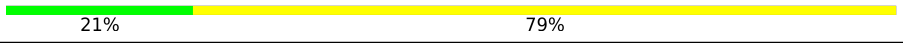
Mol	Chain	Length	Quality of chain
2	X	17	
3	F	14	
3	K	14	
4	G	14	
4	L	14	

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 4476 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 MEF2D protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	91	Total	C	N	O	S	0	0	0
			756	477	136	139	4			
1	B	92	Total	C	N	O	S	0	0	0
			767	486	137	140	4			
1	D	92	Total	C	N	O	S	0	0	0
			767	486	137	140	4			
1	E	91	Total	C	N	O	S	0	0	0
			756	477	136	139	4			

- Molecule 2 is a protein called HDAC4 (histone deacetylase 4) binding motif peptide:GSGE VKMKLQEFVLNKK.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	13	Total	C	N	O	S	0	0	0
			106	69	17	19	1			
2	X	15	Total	C	N	O	S	0	0	0
			116	74	19	22	1			

- Molecule 3 is a DNA chain called DNA (5'-D(P*AP*AP*CP*TP*AP*TP*TP*TP*AP*TP *AP*AP*GP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	F	14	Total	C	N	O	P	0	0	0
			288	139	53	82	14			
3	K	14	Total	C	N	O	P	0	0	0
			288	139	53	82	14			

- Molecule 4 is a DNA chain called DNA (5'-D(P*TP*CP*TP*TP*AP*TP*AP*AP*AP*TP *AP*GP*TP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	G	14	Total 286	C 139	N 47	O 86	P 14	0	0	0
4	L	14	Total 286	C 139	N 47	O 86	P 14	0	0	0

- Molecule 5 is water.

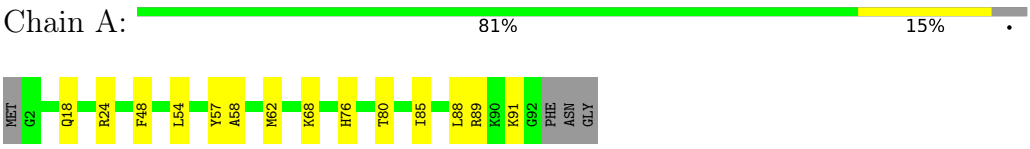
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	13	Total 13	O 13	0	0
5	B	13	Total 13	O 13	0	0
5	C	1	Total 1	O 1	0	0
5	D	7	Total 7	O 7	0	0
5	E	5	Total 5	O 5	0	0
5	F	4	Total 4	O 4	0	0
5	G	6	Total 6	O 6	0	0
5	K	4	Total 4	O 4	0	0
5	L	7	Total 7	O 7	0	0

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.

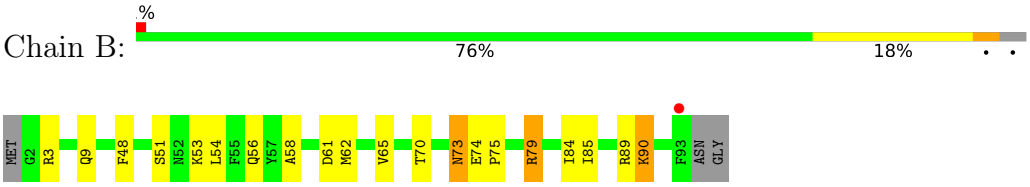
• Molecule 1: MEF2D protein

Chain A:



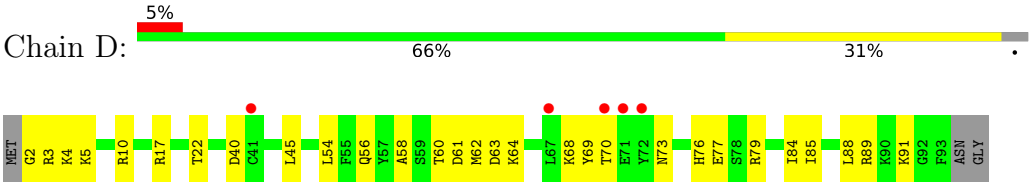
• Molecule 1: MEF2D protein

Chain B:



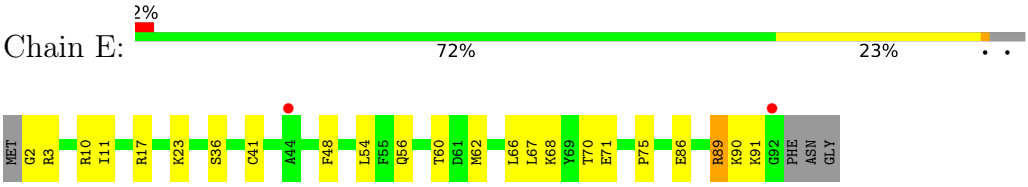
• Molecule 1: MEF2D protein

Chain D:



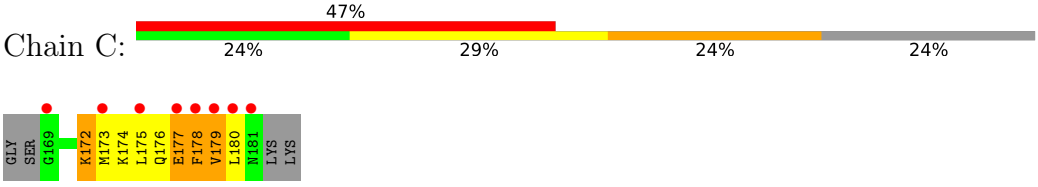
• Molecule 1: MEF2D protein

Chain E:



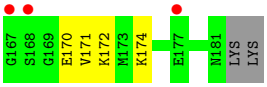
• Molecule 2: HDAC4 (histone deacetylase 4) binding motif peptide:GSGEVKMKLQEFVLNKK

Chain C:



• Molecule 2: HDAC4 (histone deacetylase 4) binding motif peptide:GSGEVKMKLQEFVLNK K

Chain X:

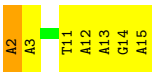


• Molecule 3: DNA (5'-D(P*AP*AP*CP*TP*AP*TP*TP*TP*AP*TP*AP*AP*GP*A)-3')

Chain F:

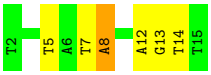
• Molecule 3: DNA (5'-D(P*AP*AP*CP*TP*AP*TP*TP*TP*AP*TP*AP*AP*GP*A)-3')

Chain K:



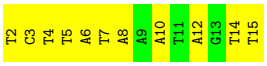
• Molecule 4: DNA (5'-D(P*TP*CP*TP*TP*AP*TP*AP*AP*AP*TP*AP*GP*TP*T)-3')

Chain G:



• Molecule 4: DNA (5'-D(P*TP*CP*TP*TP*AP*TP*AP*AP*AP*TP*AP*GP*TP*T)-3')

Chain L:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	57.02Å 76.33Å 56.24Å 90.00° 92.57° 90.00°	Depositor
Resolution (Å)	45.65 – 2.40 45.65 – 2.40	Depositor EDS
% Data completeness (in resolution range)	94.7 (45.65-2.40) 99.9 (45.65-2.40)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.46 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.8.0405	Depositor
R, R_{free}	0.217 , 0.279 0.222 , 0.288	Depositor DCC
R_{free} test set	1021 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	43.9	Xtriage
Anisotropy	0.069	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 52.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.000 for -l,k,h 0.067 for -h,-k,l 0.000 for l,-k,h	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	4476	wwPDB-VP
Average B, all atoms (Å^2)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 19.22% 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	0.55	0/766	1.09	0/1023
1	B	0.53	0/778	1.09	0/1039
1	D	0.51	0/778	1.10	0/1039
1	E	0.55	0/766	1.11	0/1023
2	C	0.65	0/106	1.18	1/139 (0.7%)
2	X	0.62	0/116	0.97	0/152
3	F	0.55	0/323	1.09	4/496 (0.8%)
3	K	0.55	0/323	1.08	1/496 (0.2%)
4	G	0.54	0/319	1.15	2/490 (0.4%)
4	L	0.54	0/319	1.13	0/490
All	All	0.54	0/4594	1.10	8/6387 (0.1%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	K	2	DA	P-O3'-C3'	-5.86	111.42	120.20
4	G	5	DT	P-O3'-C3'	-5.82	111.48	120.20
3	F	5	DT	P-O3'-C3'	-5.74	111.59	120.20
3	F	3	DA	P-O3'-C3'	-5.65	111.72	120.20
3	F	6	DA	P-O3'-C3'	-5.61	111.79	120.20
3	F	4	DC	P-O3'-C3'	-5.19	112.41	120.20
2	C	179	VAL	N-CA-C	-5.05	106.20	113.07
4	G	8	DA	P-O3'-C3'	-5.00	112.69	120.20

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	756	0	779	11	0
1	B	767	0	788	19	0
1	D	767	0	788	19	0
1	E	756	0	779	20	0
2	C	106	0	112	14	0
2	X	116	0	120	2	0
3	F	288	0	160	8	0
3	K	288	0	160	9	0
4	G	286	0	162	6	0
4	L	286	0	162	9	0
5	A	13	0	0	1	0
5	B	13	0	0	0	0
5	C	1	0	0	0	0
5	D	7	0	0	0	0
5	E	5	0	0	0	0
5	F	4	0	0	0	0
5	G	6	0	0	0	0
5	K	4	0	0	0	0
5	L	7	0	0	0	0
All	All	4476	0	4010	83	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 10.

All (83) 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:C:178:PHE:HB2	1:D:70:THR:HG22	1.30	1.08
3:F:2:DA:H1'	3:F:3:DA:H5'	1.66	0.77
2:C:176:GLN:O	2:C:180:LEU:HG	1.97	0.65
2:C:176:GLN:HG2	1:E:70:THR:HG21	1.78	0.64
2:C:172:LYS:O	2:C:176:GLN:HG3	2.01	0.61
1:A:48:PHE:CZ	1:A:54:LEU:HD13	2.36	0.60
1:D:40:ASP:HB2	1:E:10:ARG:HD3	1.82	0.60
4:L:2:DT:H1'	4:L:3:DC:H5'	1.83	0.59
1:D:54:LEU:HD23	1:E:75:PRO:HA	1.84	0.59
1:B:73:ASN:HD22	1:B:74:GLU:HG3	1.68	0.59
1:E:36:SER:HA	1:E:41:CYS:SG	2.43	0.58
2:C:172:LYS:HG3	1:E:70:THR:HG22	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:85:ILE:O	1:D:89:ARG:HG3	2.04	0.57
1:D:4:LYS:HE2	1:D:5:LYS:O	2.07	0.55
3:F:3:DA:H62	4:G:14:DT:H3	1.52	0.55
1:E:23:LYS:NZ	3:F:12:DA:N7	2.53	0.55
1:B:3:ARG:HG2	3:K:12:DA:C2	2.42	0.55
1:E:86:GLU:O	1:E:90:LYS:HG2	2.06	0.54
2:X:171:VAL:HA	2:X:174:LYS:HD2	1.90	0.54
3:K:2:DA:H61	4:L:15:DT:H3	1.54	0.54
2:C:173:MET:O	2:C:177:GLU:HB2	2.07	0.54
1:B:3:ARG:HG2	3:K:12:DA:N3	2.22	0.54
1:D:3:ARG:HG2	4:G:12:DA:N3	2.23	0.54
1:B:61:ASP:O	1:B:65:VAL:HG23	2.07	0.53
1:D:3:ARG:HD3	3:F:6:DA:N3	2.24	0.53
1:E:67:LEU:O	1:E:68:LYS:C	2.52	0.53
1:E:3:ARG:HG2	3:F:12:DA:N3	2.25	0.52
1:B:70:THR:HA	2:X:172:LYS:HG2	1.93	0.51
3:K:13:DA:H1'	3:K:14:DG:H5'	1.93	0.50
1:B:85:ILE:O	1:B:89:ARG:HG3	2.11	0.50
3:K:2:DA:H1'	3:K:3:DA:H5'	1.93	0.50
4:L:5:DT:H2"	4:L:6:DA:C8	2.46	0.49
1:A:88:LEU:HA	1:A:91:LYS:HE2	1.95	0.49
1:B:9:GLN:HE22	1:D:73:ASN:HB3	1.78	0.49
1:B:58:ALA:HB2	1:B:62:MET:HE2	1.95	0.48
1:D:56:GLN:HB2	1:D:62:MET:HE3	1.94	0.48
1:A:85:ILE:O	1:A:89:ARG:HG3	2.14	0.48
2:C:178:PHE:CB	1:D:70:THR:HG22	2.23	0.48
3:F:5:DT:H2"	3:F:6:DA:C8	2.49	0.48
2:C:172:LYS:HD3	1:E:70:THR:HA	1.95	0.47
1:D:58:ALA:HB2	1:D:62:MET:HE2	1.95	0.47
1:A:54:LEU:HD23	1:B:75:PRO:HA	1.95	0.47
2:C:175:LEU:O	2:C:179:VAL:HG13	2.14	0.47
1:D:4:LYS:HG2	4:G:13:DG:H5"	1.97	0.47
3:F:9:DT:H1'	3:F:10:DA:H5'	1.96	0.47
4:G:7:DT:H2"	4:G:8:DA:C8	2.50	0.47
1:A:24:ARG:NH2	4:L:12:DA:OP1	2.39	0.46
1:A:80:THR:HA	1:B:58:ALA:O	2.16	0.46
1:D:69:TYR:HE1	1:E:56:GLN:OE1	1.99	0.46
1:D:3:ARG:HG2	4:G:12:DA:C2	2.51	0.46
1:E:48:PHE:CZ	1:E:54:LEU:HD13	2.52	0.45
1:A:76:HIS:HB3	1:B:54:LEU:O	2.16	0.45
3:K:3:DA:H62	4:L:14:DT:H3	1.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:178:PHE:HB2	1:D:70:THR:CG2	2.22	0.45
1:D:76:HIS:HD2	1:D:77:GLU:O	1.99	0.45
1:D:84:ILE:O	1:D:88:LEU:HG	2.16	0.45
1:D:2:GLY:O	3:F:7:DT:H1'	2.17	0.45
3:K:11:DT:H2"	3:K:12:DA:N7	2.32	0.44
1:B:48:PHE:HA	1:B:53:LYS:O	2.17	0.44
2:C:173:MET:HE3	2:C:173:MET:HB3	1.86	0.44
1:B:48:PHE:CE1	1:B:54:LEU:HD13	2.53	0.44
2:C:173:MET:HE3	2:C:174:LYS:HG3	2.00	0.44
1:E:11:ILE:O	1:E:17:ARG:HD3	2.18	0.43
1:B:89:ARG:HG2	1:E:67:LEU:HD13	1.99	0.43
1:E:86:GLU:HA	1:E:89:ARG:HH21	1.84	0.43
1:E:2:GLY:O	4:G:7:DT:H1'	2.18	0.43
1:A:62:MET:HE2	1:A:62:MET:HB2	1.87	0.43
1:B:56:GLN:HB2	1:B:62:MET:HE3	2.01	0.43
3:K:2:DA:N1	4:L:15:DT:O2	2.52	0.43
2:C:172:LYS:CD	1:E:70:THR:HA	2.49	0.42
1:B:89:ARG:HH21	1:E:71:GLU:HG3	1.84	0.42
1:D:68:LYS:HG2	1:E:48:PHE:CZ	2.54	0.42
1:A:58:ALA:HB2	1:A:62:MET:HE2	2.01	0.42
3:K:14:DG:H1'	3:K:15:DA:H5'	2.00	0.42
1:E:62:MET:HE3	1:E:66:LEU:HD11	2.01	0.42
1:B:90:LYS:HB2	1:B:90:LYS:HE2	1.58	0.42
4:L:3:DC:H1'	4:L:4:DT:H5'	2.02	0.42
1:A:57:TYR:CD1	1:A:57:TYR:C	2.98	0.42
1:A:68:LYS:HD2	1:B:48:PHE:CE2	2.55	0.41
2:C:173:MET:CE	2:C:174:LYS:HG3	2.51	0.41
4:L:7:DT:H2"	4:L:8:DA:C8	2.55	0.41
5:A:111:HOH:O	4:L:10:DA:H5"	2.19	0.41
1:B:79:ARG:NH2	1:B:84:ILE:HD13	2.35	0.41

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	89/95 (94%)	86 (97%)	3 (3%)	0	100	100
1	B	90/95 (95%)	88 (98%)	2 (2%)	0	100	100
1	D	90/95 (95%)	84 (93%)	6 (7%)	0	100	100
1	E	89/95 (94%)	85 (96%)	4 (4%)	0	100	100
2	C	11/17 (65%)	11 (100%)	0	0	100	100
2	X	13/17 (76%)	12 (92%)	1 (8%)	0	100	100
All	All	382/414 (92%)	366 (96%)	16 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	84/87 (97%)	83 (99%)	1 (1%)	63	81
1	B	85/87 (98%)	81 (95%)	4 (5%)	23	41
1	D	85/87 (98%)	75 (88%)	10 (12%)	5	7
1	E	84/87 (97%)	81 (96%)	3 (4%)	31	52
2	C	12/15 (80%)	9 (75%)	3 (25%)	0	1
2	X	13/15 (87%)	12 (92%)	1 (8%)	12	20
All	All	363/378 (96%)	341 (94%)	22 (6%)	17	30

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	GLN
1	B	51	SER
1	B	73	ASN
1	B	79	ARG

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Mol	Chain	Res	Type
1	B	90	LYS
2	C	172	LYS
2	C	177	GLU
2	C	178	PHE
1	D	10	ARG
1	D	17	ARG
1	D	22	THR
1	D	45	LEU
1	D	60	THR
1	D	61	ASP
1	D	63	ASP
1	D	64	LYS
1	D	79	ARG
1	D	91	LYS
1	E	60	THR
1	E	89	ARG
1	E	91	LYS
2	X	170	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	GLN
1	A	73	ASN
1	B	18	GLN
1	B	73	ASN
2	C	176	GLN
1	D	9	GLN
1	D	18	GLN
1	D	56	GLN
1	E	52	ASN

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 oligosaccharides 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, 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	91/95 (95%)	0.25	0 100 100	46, 59, 92, 115	0
1	B	92/95 (96%)	0.41	1 (1%) 78 74	45, 62, 92, 112	0
1	D	92/95 (96%)	0.75	5 (5%) 31 28	44, 68, 113, 137	0
1	E	91/95 (95%)	0.61	2 (2%) 62 58	51, 65, 98, 105	0
2	C	13/17 (76%)	2.45	8 (61%) 0 0	69, 101, 130, 135	0
2	X	15/17 (88%)	1.36	3 (20%) 3 2	65, 79, 112, 115	0
3	F	14/14 (100%)	0.26	0 100 100	49, 62, 84, 116	0
3	K	14/14 (100%)	0.13	0 100 100	51, 61, 106, 116	0
4	G	14/14 (100%)	0.04	0 100 100	49, 61, 83, 104	0
4	L	14/14 (100%)	0.07	0 100 100	52, 64, 99, 125	0
All	All	450/470 (95%)	0.54	19 (4%) 40 36	44, 64, 105, 137	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	70	THR	4.9
2	C	181	ASN	4.8
1	D	72	TYR	4.6
2	C	179	VAL	3.5
1	D	41	CYS	3.4
2	C	180	LEU	3.3
2	C	173	MET	3.0
2	C	178	PHE	2.9
2	C	177	GLU	2.9
2	X	167	GLY	2.8
1	B	93	PHE	2.8
2	C	169	GLY	2.7
1	D	71	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
2	C	175	LEU	2.6
2	X	168	SER	2.6
1	E	44	ALA	2.4
1	D	67	LEU	2.0
1	E	92	GLY	2.0
2	X	177	GLU	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.