



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 26, 2025 – 01:57 AM JST

PDB ID : 8ZLX
Title : Crystal Structure of mPPEF2 IQ motif/apo-CaM Complex
Authors : Liu, J.; Ding, Y.Z.; Li, J.C.; Liu, W.
Deposited on : 2024-05-21
Resolution : 2.50 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:

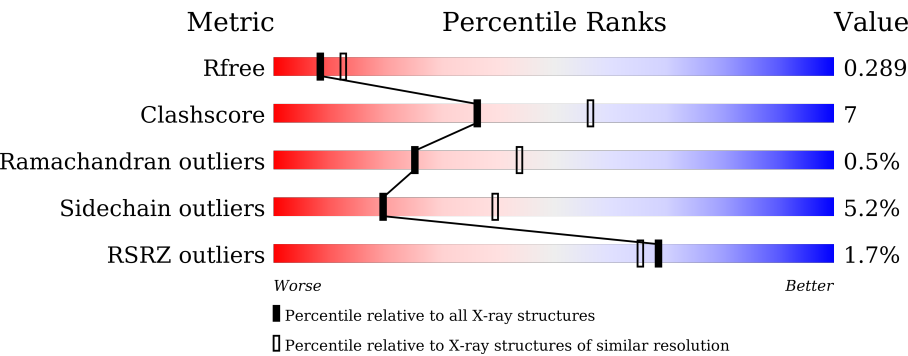
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.21
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.41.2

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 2.50 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}	164625	5504 (2.50-2.50)
Clashscore	180529	6282 (2.50-2.50)
Ramachandran outliers	177936	6191 (2.50-2.50)
Sidechain outliers	177891	6193 (2.50-2.50)
RSRZ outliers	164620	5504 (2.50-2.50)

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	155	 82% 12% . .
1	B	155	 74% 14% . 12%
1	C	155	 65% 22% . 11%
1	D	155	 82% 15% . .
2	a	24	 92% 8%
2	b	24	 88% 12%

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Mol	Chain	Length	Quality of chain
2	c	24	<div><div><div>4%</div><div>88%</div><div>8%</div></div></div>
2	d	24	<div><div><div></div><div>88%</div><div>8%</div></div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5059 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 Calmodulin (CaM).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	137	Total	C	N	O	S	0	0	0
			978	609	154	207	8			
1	D	151	Total	C	N	O	S	0	0	0
			1156	711	186	250	9			
1	C	138	Total	C	N	O	S	0	1	0
			1041	647	163	221	10			
1	A	149	Total	C	N	O	S	0	1	0
			1165	716	186	253	10			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	GLY	-	expression tag	UNP A0A7N4P457
B	2	PRO	-	expression tag	UNP A0A7N4P457
B	3	GLY	-	expression tag	UNP A0A7N4P457
B	4	SER	-	expression tag	UNP A0A7N4P457
B	5	GLU	-	expression tag	UNP A0A7N4P457
B	6	PHE	-	expression tag	UNP A0A7N4P457
D	1	GLY	-	expression tag	UNP A0A7N4P457
D	2	PRO	-	expression tag	UNP A0A7N4P457
D	3	GLY	-	expression tag	UNP A0A7N4P457
D	4	SER	-	expression tag	UNP A0A7N4P457
D	5	GLU	-	expression tag	UNP A0A7N4P457
D	6	PHE	-	expression tag	UNP A0A7N4P457
C	1	GLY	-	expression tag	UNP A0A7N4P457
C	2	PRO	-	expression tag	UNP A0A7N4P457
C	3	GLY	-	expression tag	UNP A0A7N4P457
C	4	SER	-	expression tag	UNP A0A7N4P457
C	5	GLU	-	expression tag	UNP A0A7N4P457
C	6	PHE	-	expression tag	UNP A0A7N4P457
A	1	GLY	-	expression tag	UNP A0A7N4P457
A	2	PRO	-	expression tag	UNP A0A7N4P457
A	3	GLY	-	expression tag	UNP A0A7N4P457

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Chain	Residue	Modelled	Actual	Comment	Reference
A	4	SER	-	expression tag	UNP A0A7N4P457
A	5	GLU	-	expression tag	UNP A0A7N4P457
A	6	PHE	-	expression tag	UNP A0A7N4P457

- Molecule 2 is a protein called Serine/threonine-protein phosphatase with EF-hands 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	d	22	Total	C	N	O	S	0	0	0
			172	113	30	28	1			
2	a	22	Total	C	N	O	S	0	0	0
			178	116	33	28	1			
2	b	21	Total	C	N	O	S	0	0	0
			170	110	32	27	1			
2	c	22	Total	C	N	O	S	0	0	0
			184	119	36	28	1			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
d	1	GLY	-	expression tag	UNP O35385
d	2	PRO	-	expression tag	UNP O35385
d	3	GLY	-	expression tag	UNP O35385
d	4	SER	-	expression tag	UNP O35385
d	5	GLU	-	expression tag	UNP O35385
d	6	PHE	-	expression tag	UNP O35385
a	1	GLY	-	expression tag	UNP O35385
a	2	PRO	-	expression tag	UNP O35385
a	3	GLY	-	expression tag	UNP O35385
a	4	SER	-	expression tag	UNP O35385
a	5	GLU	-	expression tag	UNP O35385
a	6	PHE	-	expression tag	UNP O35385
b	1	GLY	-	expression tag	UNP O35385
b	2	PRO	-	expression tag	UNP O35385
b	3	GLY	-	expression tag	UNP O35385
b	4	SER	-	expression tag	UNP O35385
b	5	GLU	-	expression tag	UNP O35385
b	6	PHE	-	expression tag	UNP O35385
c	1	GLY	-	expression tag	UNP O35385
c	2	PRO	-	expression tag	UNP O35385
c	3	GLY	-	expression tag	UNP O35385
c	4	SER	-	expression tag	UNP O35385
c	5	GLU	-	expression tag	UNP O35385

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Chain	Residue	Modelled	Actual	Comment	Reference
c	6	PHE	-	expression tag	UNP O35385

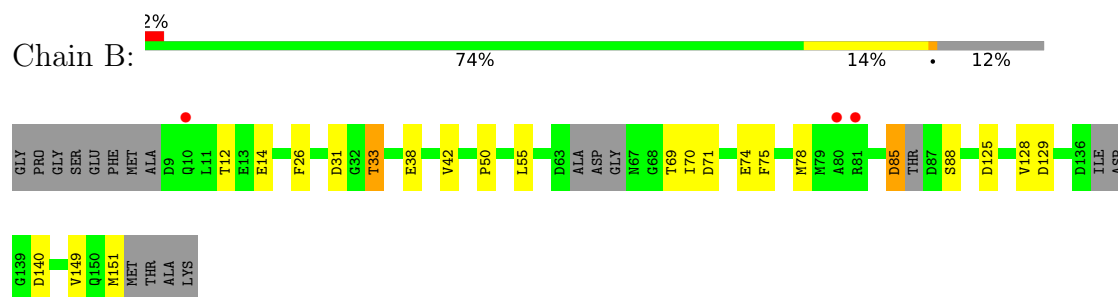
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	4	Total O 4 4	0	0
3	D	3	Total O 3 3	0	0
3	d	1	Total O 1 1	0	0
3	C	1	Total O 1 1	0	0
3	A	6	Total O 6 6	0	0

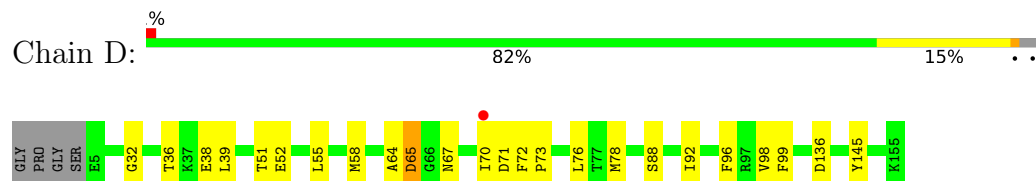
3 Residue-property plots [i](#)

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.

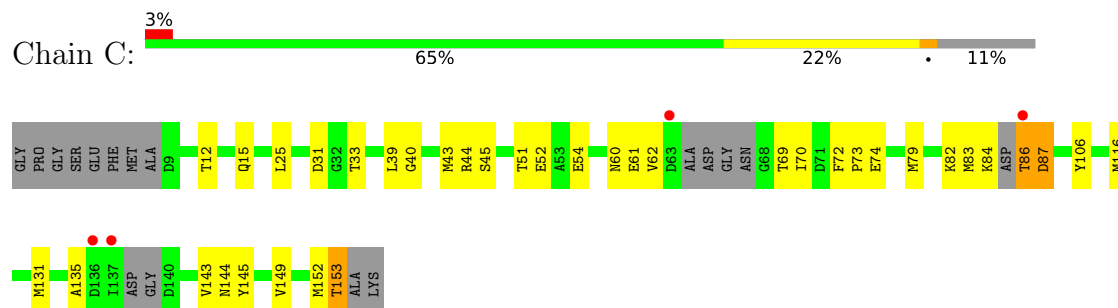
- Molecule 1: Calmodulin (CaM)



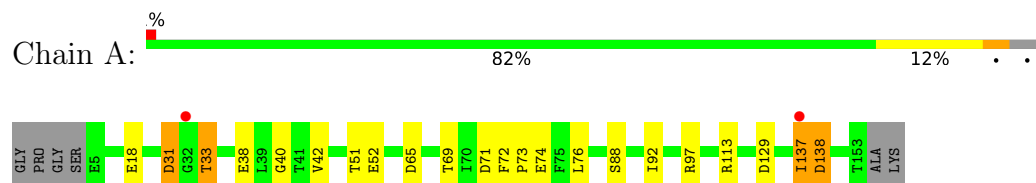
- Molecule 1: Calmodulin (CaM)




- Molecule 1: Calmodulin (CaM)



- Molecule 1: Calmodulin (CaM)



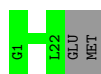
- Molecule 2: Serine/threonine-protein phosphatase with EF-hands 2

Chain d:  88% 8%




- Molecule 2: Serine/threonine-protein phosphatase with EF-hands 2

Chain a:  92% 8%




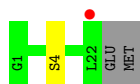
- Molecule 2: Serine/threonine-protein phosphatase with EF-hands 2

Chain b:  88% 12%



- Molecule 2: Serine/threonine-protein phosphatase with EF-hands 2

Chain c:  4% 88% 8%



4 Data and refinement statistics

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α , β , γ	134.45Å 134.45Å 35.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.83 – 2.50 19.83 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.7 (19.83-2.50) 99.7 (19.83-2.50)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.26 (at 2.50Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.208 , 0.291 0.212 , 0.289	Depositor DCC
R_{free} test set	1161 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	48.7	Xtriage
Anisotropy	0.131	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 31.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.036 for h,-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5059	wwPDB-VP
Average B, all atoms (Å ²)	54.0	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 40.06 % 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 2.8953e-04. 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	0.72	0/1181	0.90	0/1589
1	B	0.77	0/986	0.85	0/1331
1	C	0.76	0/1050	0.89	0/1412
1	D	0.74	0/1169	0.90	0/1576
2	a	0.71	0/183	0.96	0/246
2	b	0.64	0/175	0.84	0/235
2	c	0.71	0/189	0.83	0/253
2	d	0.72	0/177	0.82	0/239
All	All	0.74	0/5110	0.88	0/6881

There are no bond length outliers.

There are no bond angle outliers.

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	1165	0	1071	11	0
1	B	978	0	842	14	0
1	C	1041	0	935	21	0
1	D	1156	0	1048	14	0
2	a	178	0	174	0	0
2	b	170	0	163	0	0
2	c	184	0	185	0	0
2	d	172	0	163	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	6	0	0	1	0
3	B	4	0	0	0	0
3	C	1	0	0	0	0
3	D	3	0	0	1	0
3	d	1	0	0	0	0
All	All	5059	0	4581	59	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 7.

All (59) 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:D:51:THR:HG21	3:D:201:HOH:O	1.35	1.23
1:C:51:THR:OG1	1:C:54:GLU:HB2	1.86	0.76
1:D:36:THR:HG22	1:D:70:ILE:HG13	1.68	0.73
1:A:71:ASP:HB3	1:A:73:PRO:HD2	1.71	0.72
1:A:51:THR:HG21	1:A:97:ARG:HG2	1.74	0.70
1:B:38:GLU:O	1:B:42:VAL:HG23	1.93	0.67
1:A:88:SER:O	1:A:92:ILE:HD12	1.96	0.66
1:B:85:ASP:C	1:B:85:ASP:OD1	2.38	0.61
1:C:135:ALA:HB1	1:C:143:VAL:HG13	1.83	0.60
1:B:50:PRO:HB2	1:B:55:LEU:CD2	2.32	0.59
1:C:60:ASN:C	1:C:62:VAL:H	2.07	0.58
1:C:145:TYR:O	1:C:149:VAL:HG23	2.05	0.57
1:C:40:GLY:O	1:C:44:ARG:HG3	2.05	0.56
1:D:58:MET:HB3	1:D:78:MET:CE	2.36	0.55
1:B:26:PHE:CD2	1:B:42:VAL:HG22	2.41	0.55
1:A:33:THR:HG23	1:A:69:THR:HB	1.89	0.55
1:D:58:MET:HB3	1:D:78:MET:HE2	1.89	0.55
1:C:39:LEU:HG	1:C:43:MET:CE	2.37	0.55
1:B:75:PHE:HA	1:B:78:MET:HE3	1.89	0.55
1:C:87:ASP:N	1:C:87:ASP:OD1	2.40	0.54
1:A:113:ARG:NH2	1:A:129:ASP:OD1	2.40	0.54
1:B:70:ILE:HG21	1:B:78:MET:HE1	1.91	0.53
1:C:84:LYS:O	1:C:86:THR:OG1	2.25	0.53
1:D:32:GLY:HA2	1:C:25:LEU:HD23	1.90	0.53
1:C:12:THR:HG23	1:C:15:GLN:OE1	2.09	0.52
1:D:72:PHE:HB3	1:D:73:PRO:HD3	1.92	0.52
1:C:52:GLU:OE2	1:C:153:THR:HG21	2.10	0.51
1:B:50:PRO:CG	1:B:55:LEU:HD21	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:88:SER:O	1:D:92:ILE:HG12	2.10	0.51
1:A:31:ASP:HB3	1:A:33:THR:HB	1.93	0.51
1:D:64:ALA:HA	1:D:67:ASN:HD22	1.75	0.51
1:C:70:ILE:HG23	1:C:74:GLU:HG3	1.96	0.47
1:B:70:ILE:HG21	1:B:78:MET:CE	2.45	0.46
1:C:116:MET:HG3	1:C:131:MET:CE	2.46	0.46
1:C:72:PHE:HB3	1:C:73:PRO:HD3	1.98	0.45
1:B:75:PHE:HA	1:B:78:MET:CE	2.47	0.45
1:B:149:VAL:O	1:B:151:MET:HG3	2.17	0.45
1:D:98:VAL:HG22	1:D:99:PHE:CE2	2.52	0.45
1:A:137:ILE:HD12	1:A:138:ASP:OD1	2.17	0.45
1:C:33:THR:HG23	1:C:69:THR:HB	1.99	0.44
1:D:39:LEU:HG	1:D:55:LEU:HD22	2.00	0.44
1:A:72:PHE:CE2	1:A:76:LEU:HD11	2.52	0.44
1:B:140:ASP:OD1	1:B:140:ASP:N	2.50	0.43
1:C:31:ASP:OD1	1:C:33:THR:HB	2.18	0.43
1:A:40:GLY:N	3:A:201:HOH:O	2.51	0.43
1:D:38:GLU:HA	1:D:38:GLU:OE1	2.19	0.43
1:C:116:MET:HG3	1:C:131:MET:HE1	2.00	0.42
1:B:71:ASP:OD1	1:B:74:GLU:HG2	2.20	0.42
1:C:39:LEU:HD11	1:C:43:MET:HE2	2.02	0.42
1:D:76:LEU:HD23	1:D:76:LEU:HA	1.91	0.42
1:C:79[B]:MET:O	1:C:83:MET:HG2	2.20	0.42
1:C:60:ASN:C	1:C:62:VAL:N	2.73	0.41
1:A:38:GLU:O	1:A:42:VAL:HG23	2.19	0.41
1:A:71:ASP:HB2	1:A:74:GLU:HG3	2.02	0.41
1:B:31:ASP:O	1:B:33:THR:HG23	2.19	0.41
1:C:106:TYR:CE2	1:C:144:ASN:HB2	2.55	0.41
1:D:96:PHE:HB3	1:D:145:TYR:CD1	2.56	0.41
1:D:98:VAL:HG22	1:D:99:PHE:CD2	2.56	0.41
1:B:128:VAL:O	1:B:128:VAL:HG22	2.21	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	148/155 (96%)	138 (93%)	10 (7%)	0	100	100
1	B	129/155 (83%)	123 (95%)	6 (5%)	0	100	100
1	C	131/155 (84%)	126 (96%)	4 (3%)	1 (1%)	16	31
1	D	149/155 (96%)	140 (94%)	7 (5%)	2 (1%)	10	19
2	a	20/24 (83%)	20 (100%)	0	0	100	100
2	b	19/24 (79%)	19 (100%)	0	0	100	100
2	c	20/24 (83%)	20 (100%)	0	0	100	100
2	d	20/24 (83%)	20 (100%)	0	0	100	100
All	All	636/716 (89%)	606 (95%)	27 (4%)	3 (0%)	25	44

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	61	GLU
1	D	65	ASP
1	D	136	ASP

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	124/131 (95%)	117 (94%)	7 (6%)	17	36
1	B	91/131 (70%)	83 (91%)	8 (9%)	8	17
1	C	105/131 (80%)	99 (94%)	6 (6%)	17	35
1	D	119/131 (91%)	116 (98%)	3 (2%)	42	69
2	a	15/18 (83%)	15 (100%)	0	100	100
2	b	14/18 (78%)	14 (100%)	0	100	100
2	c	16/18 (89%)	15 (94%)	1 (6%)	15	30
2	d	14/18 (78%)	13 (93%)	1 (7%)	12	25

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	498/596 (84%)	472 (95%)	26 (5%)	19	39

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	12	THR
1	B	14	GLU
1	B	33	THR
1	B	69	THR
1	B	85	ASP
1	B	88	SER
1	B	125	ASP
1	B	129	ASP
1	D	52	GLU
1	D	65	ASP
1	D	71	ASP
2	d	5	GLU
1	C	45	SER
1	C	82	LYS
1	C	86	THR
1	C	87	ASP
1	C	152	MET
1	C	153	THR
2	c	4	SER
1	A	18	GLU
1	A	31	ASP
1	A	33	THR
1	A	52	GLU
1	A	65	ASP
1	A	137	ILE
1	A	138	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	118	ASN
1	D	60	ASN
1	D	118	ASN
1	A	60	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 [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	149/155 (96%)	-0.37	2 (1%) 74 71	25, 46, 72, 96	1 (0%)
1	B	137/155 (88%)	-0.03	3 (2%) 62 59	35, 60, 102, 122	0
1	C	138/155 (89%)	-0.09	4 (2%) 54 50	27, 57, 87, 113	1 (0%)
1	D	151/155 (97%)	-0.24	1 (0%) 84 81	34, 49, 83, 117	0
2	a	22/24 (91%)	-0.20	0 100 100	34, 40, 59, 68	0
2	b	21/24 (87%)	-0.20	0 100 100	34, 41, 69, 82	0
2	c	22/24 (91%)	-0.38	1 (4%) 39 36	32, 40, 61, 97	0
2	d	22/24 (91%)	-0.40	0 100 100	35, 41, 59, 64	0
All	All	662/716 (92%)	-0.20	11 (1%) 69 65	25, 50, 90, 122	2 (0%)

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	63	ASP	3.2
1	A	32	GLY	2.9
1	B	10	GLN	2.7
1	B	80	ALA	2.6
1	A	137	ILE	2.6
1	C	136	ASP	2.5
1	C	137	ILE	2.4
1	C	86	THR	2.3
1	B	81	ARG	2.2
1	D	70	ILE	2.1
2	c	22	LEU	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.