



wwPDB EM Validation Summary Report ⓘ

Mar 18, 2026 – 12:07 AM UTC

PDB ID : 9UBR / pdb_00009ubr
EMDB ID : EMD-64015
Title : CryoEM structure of human Galectin-10 with iTrimbody
Authors : Song, J.Y.; Wang, W.
Deposited on : 2025-04-03
Resolution : 2.62 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

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
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

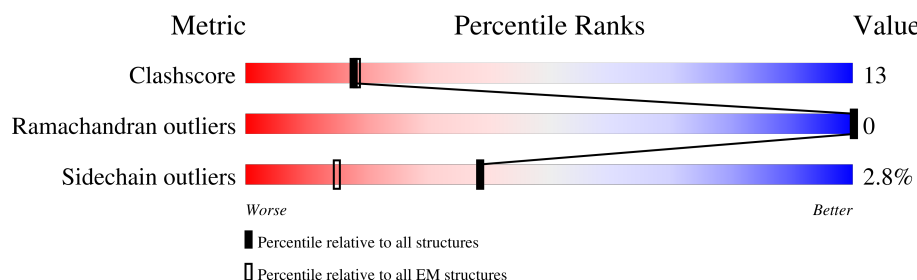
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.62 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)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	260	65% 33% .
1	B	260	67% 33%
1	C	260	70% 28% .
1	D	260	71% 27% .
1	E	260	75% 23% .
1	F	260	68% 31%
2	G	118	75% 25%
2	H	118	81% 19%
2	I	118	77% 23%

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Mol	Chain	Length	Quality of chain
2	J	118	 74% 25% .
2	K	118	 73% 26% .
2	L	118	 76% 23% .
3	M	140	 64% 33% .
3	N	140	 68% 29% ..
3	O	140	 60% 37% .
3	P	140	 76% 24% .
3	Q	140	 69% 30% .
3	R	140	 71% 26% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 23871 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 PrAC-5350A,2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	259	Total 1964	C 1257	N 332	O 365	S 10	0	0
1	B	259	Total 1964	C 1257	N 332	O 365	S 10	0	0
1	C	259	Total 1964	C 1257	N 332	O 365	S 10	0	0
1	D	259	Total 1964	C 1257	N 332	O 365	S 10	0	0
1	E	260	Total 1973	C 1262	N 333	O 368	S 10	0	0
1	F	259	Total 1964	C 1257	N 332	O 365	S 10	0	0

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	87	ILE	LYS	conflict	UNP Q9WXS1
A	91	VAL	LEU	conflict	UNP Q9WXS1
A	95	ALA	GLU	conflict	UNP Q9WXS1
A	116	ALA	GLU	conflict	UNP Q9WXS1
A	119	VAL	PHE	conflict	UNP Q9WXS1
B	87	ILE	LYS	conflict	UNP Q9WXS1
B	91	VAL	LEU	conflict	UNP Q9WXS1
B	95	ALA	GLU	conflict	UNP Q9WXS1
B	116	ALA	GLU	conflict	UNP Q9WXS1
B	119	VAL	PHE	conflict	UNP Q9WXS1
C	87	ILE	LYS	conflict	UNP Q9WXS1
C	91	VAL	LEU	conflict	UNP Q9WXS1
C	95	ALA	GLU	conflict	UNP Q9WXS1
C	116	ALA	GLU	conflict	UNP Q9WXS1
C	119	VAL	PHE	conflict	UNP Q9WXS1
D	87	ILE	LYS	conflict	UNP Q9WXS1
D	91	VAL	LEU	conflict	UNP Q9WXS1

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Chain	Residue	Modelled	Actual	Comment	Reference
D	95	ALA	GLU	conflict	UNP Q9WXS1
D	116	ALA	GLU	conflict	UNP Q9WXS1
D	119	VAL	PHE	conflict	UNP Q9WXS1
E	87	ILE	LYS	conflict	UNP Q9WXS1
E	91	VAL	LEU	conflict	UNP Q9WXS1
E	95	ALA	GLU	conflict	UNP Q9WXS1
E	116	ALA	GLU	conflict	UNP Q9WXS1
E	119	VAL	PHE	conflict	UNP Q9WXS1
F	87	ILE	LYS	conflict	UNP Q9WXS1
F	91	VAL	LEU	conflict	UNP Q9WXS1
F	95	ALA	GLU	conflict	UNP Q9WXS1
F	116	ALA	GLU	conflict	UNP Q9WXS1
F	119	VAL	PHE	conflict	UNP Q9WXS1

- Molecule 2 is a protein called hGal10-nanobody.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	118	Total	C	N	O	S	0	0
			876	542	152	178	4		
2	H	118	Total	C	N	O	S	0	0
			876	542	152	178	4		
2	I	118	Total	C	N	O	S	0	0
			876	542	152	178	4		
2	J	118	Total	C	N	O	S	0	0
			876	542	152	178	4		
2	K	118	Total	C	N	O	S	0	0
			876	542	152	178	4		
2	L	118	Total	C	N	O	S	0	0
			876	542	152	178	4		

- Molecule 3 is a protein called Galectin-10.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	M	140	Total	C	N	O	S	0	0
			1137	729	189	212	7		
3	N	140	Total	C	N	O	S	0	0
			1137	729	189	212	7		
3	O	140	Total	C	N	O	S	0	0
			1137	729	189	212	7		
3	P	140	Total	C	N	O	S	0	0
			1137	729	189	212	7		
3	Q	140	Total	C	N	O	S	0	0
			1137	729	189	212	7		

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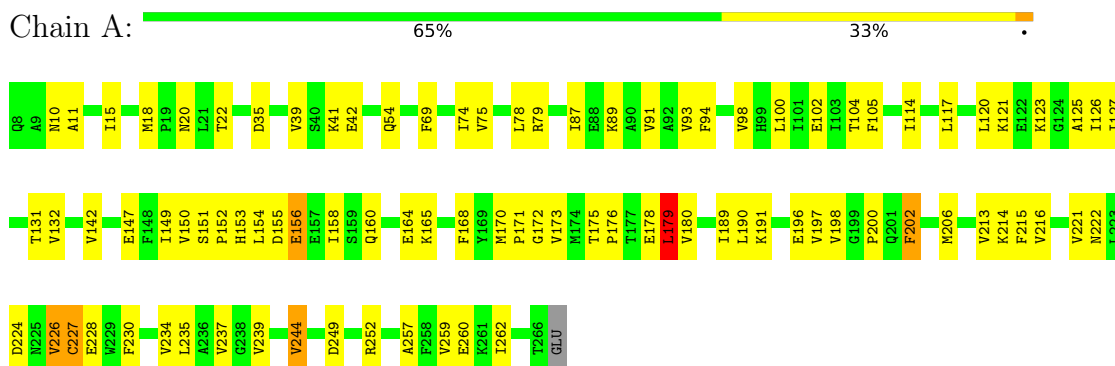
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Mol	Chain	Residues	Atoms					AltConf	Trace
3	R	140	Total	C	N	O	S	0	0
			1137	729	189	212	7		

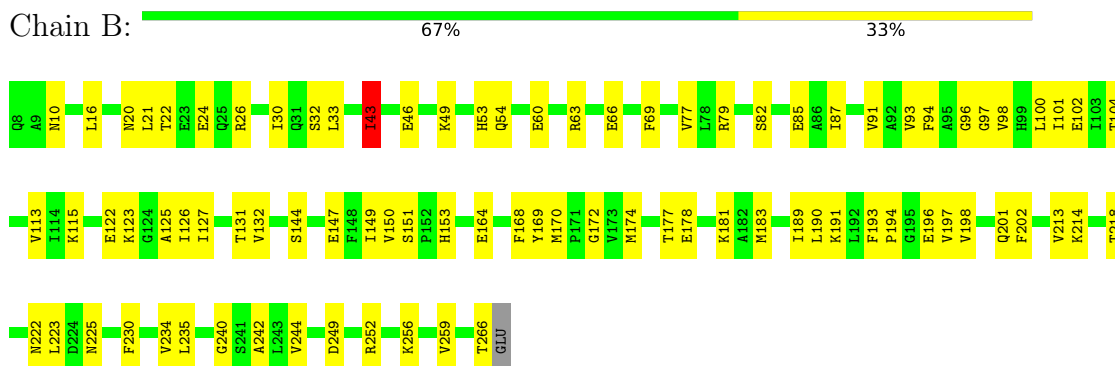
3 Residue-property plots

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. 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. 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.

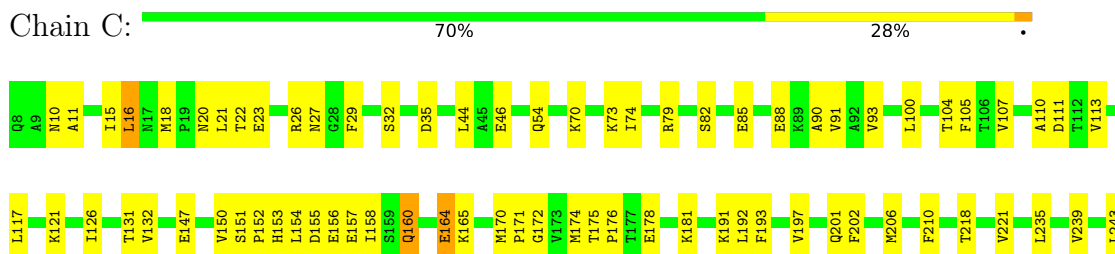
- Molecule 1: PrAC-5350A,2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase



- Molecule 1: PrAC-5350A,2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase



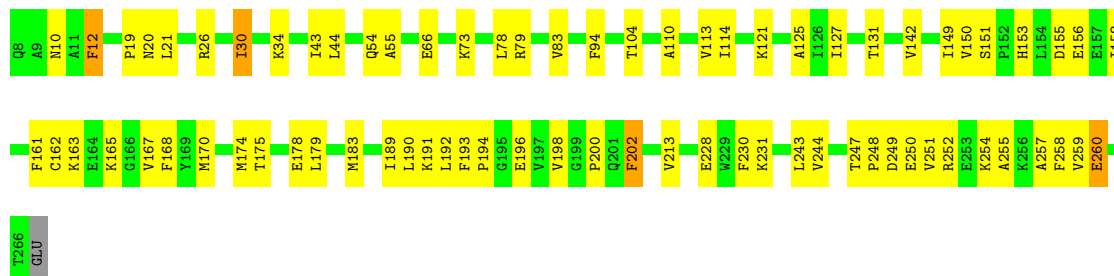
- Molecule 1: PrAC-5350A,2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase





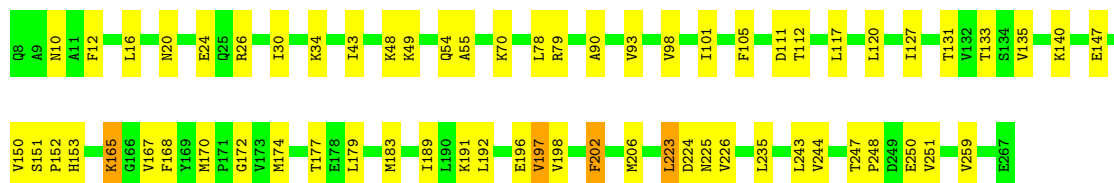
- Molecule 1: PrAC-5350A,2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase

Chain D: 71% 27%



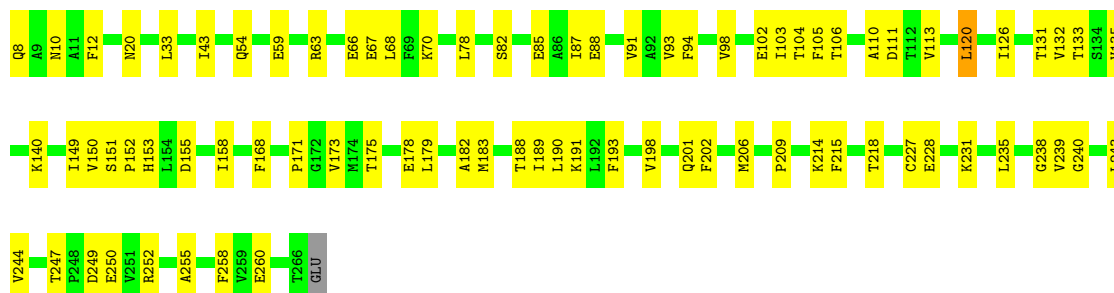
- Molecule 1: PrAC-5350A,2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase

Chain E: 75% 23%



- Molecule 1: PrAC-5350A,2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase

Chain F: 68% 31%



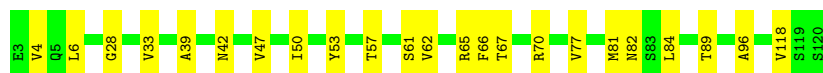
- Molecule 2: hGal10-nanobody

Chain G: 75% 25%



- Molecule 2: hGal10-nanobody

Chain H:  81% 19%



- Molecule 2: hGal10-nanobody

Chain I:  77% 23%



- Molecule 2: hGal10-nanobody

Chain J:  74% 25%



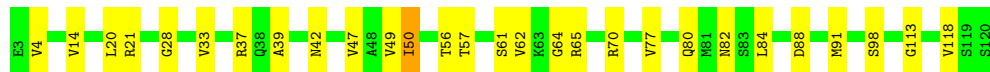
- Molecule 2: hGal10-nanobody

Chain K:  73% 26%



- Molecule 2: hGal10-nanobody

Chain L:  76% 23%



- Molecule 3: Galectin-10

Chain M:  64% 33%



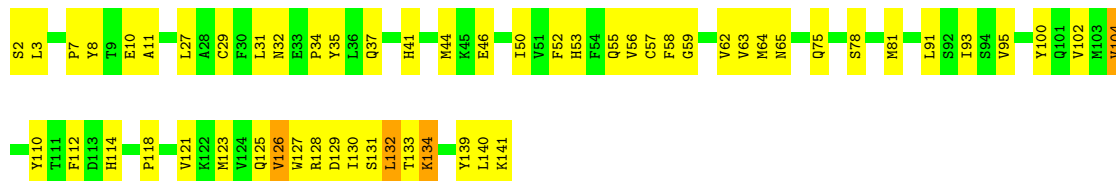
- Molecule 3: Galectin-10

Chain N:  68% 29%

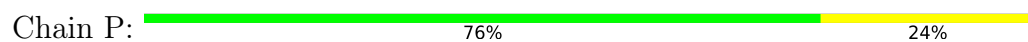




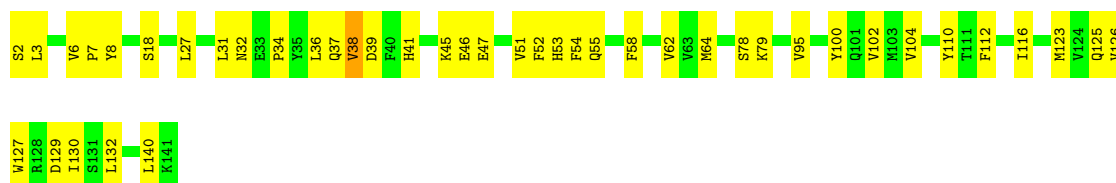
• Molecule 3: Galectin-10



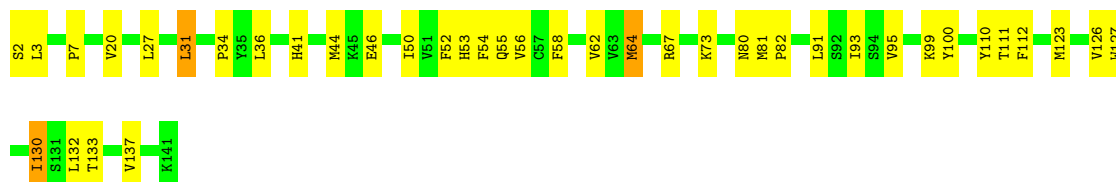
• Molecule 3: Galectin-10



• Molecule 3: Galectin-10



• Molecule 3: Galectin-10



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	700092	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor

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	0.21	0/1997	0.53	5/2693 (0.2%)
1	B	0.21	0/1997	0.57	3/2693 (0.1%)
1	C	0.24	0/1997	0.51	3/2693 (0.1%)
1	D	0.20	0/1997	0.41	2/2693 (0.1%)
1	E	0.23	0/2006	0.54	2/2705 (0.1%)
1	F	0.21	0/1997	0.45	1/2693 (0.0%)
2	G	0.15	0/893	0.41	1/1209 (0.1%)
2	H	0.16	0/893	0.41	0/1209
2	I	0.16	0/893	0.38	0/1209
2	J	0.14	0/893	0.38	0/1209
2	K	0.14	0/893	0.43	1/1209 (0.1%)
2	L	0.22	0/893	0.40	0/1209
3	M	0.23	0/1165	0.66	3/1576 (0.2%)
3	N	0.30	0/1165	0.67	4/1576 (0.3%)
3	O	0.33	0/1165	0.70	0/1576
3	P	0.21	0/1165	0.61	0/1576
3	Q	0.20	0/1165	0.56	1/1576 (0.1%)
3	R	0.21	0/1165	0.49	0/1576
All	All	0.22	0/24339	0.52	26/32880 (0.1%)

There are no bond length outliers.

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	226	VAL	N-CA-C	-11.62	99.60	110.53
1	C	255	ALA	N-CA-C	8.39	121.48	111.33
1	D	260	GLU	N-CA-C	-8.33	102.38	112.54
2	K	47	VAL	N-CA-C	7.58	118.87	111.67
1	B	43	ILE	N-CA-C	-6.83	104.11	110.53

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	1964	0	2027	69	0
1	B	1964	0	2027	65	0
1	C	1964	0	2027	64	0
1	D	1964	0	2027	55	0
1	E	1973	0	2033	45	0
1	F	1964	0	2027	57	0
2	G	876	0	830	23	0
2	H	876	0	830	19	0
2	I	876	0	830	20	0
2	J	876	0	830	23	0
2	K	876	0	830	21	0
2	L	876	0	830	22	0
3	M	1137	0	1117	40	0
3	N	1137	0	1117	32	0
3	O	1137	0	1117	50	0
3	P	1137	0	1117	29	0
3	Q	1137	0	1117	28	0
3	R	1137	0	1117	32	0
All	All	23871	0	23850	638	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 13.

The worst 5 of 638 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)
3:O:11:ALA:HB2	3:O:44:MET:HE1	1.49	0.92
3:P:2:SER:N	3:P:131:SER:HG	1.71	0.89
2:H:33:VAL:HG21	2:H:77:VAL:HG21	1.56	0.88
3:O:57:CYS:O	3:O:81:MET:HE1	1.75	0.85
3:O:127:TRP:O	3:O:127:TRP:CG	2.21	0.84

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 PDB entries followed by that with respect to all EM entries.

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	257/260 (99%)	252 (98%)	5 (2%)	0	100	100
1	B	257/260 (99%)	254 (99%)	3 (1%)	0	100	100
1	C	257/260 (99%)	251 (98%)	6 (2%)	0	100	100
1	D	257/260 (99%)	251 (98%)	6 (2%)	0	100	100
1	E	258/260 (99%)	255 (99%)	3 (1%)	0	100	100
1	F	257/260 (99%)	252 (98%)	5 (2%)	0	100	100
2	G	116/118 (98%)	115 (99%)	1 (1%)	0	100	100
2	H	116/118 (98%)	115 (99%)	1 (1%)	0	100	100
2	I	116/118 (98%)	115 (99%)	1 (1%)	0	100	100
2	J	116/118 (98%)	115 (99%)	1 (1%)	0	100	100
2	K	116/118 (98%)	115 (99%)	1 (1%)	0	100	100
2	L	116/118 (98%)	114 (98%)	2 (2%)	0	100	100
3	M	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
3	N	138/140 (99%)	135 (98%)	3 (2%)	0	100	100
3	O	138/140 (99%)	135 (98%)	3 (2%)	0	100	100
3	P	138/140 (99%)	134 (97%)	4 (3%)	0	100	100
3	Q	138/140 (99%)	131 (95%)	7 (5%)	0	100	100
3	R	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
All	All	3067/3108 (99%)	3011 (98%)	56 (2%)	0	100	100

There are no Ramachandran outliers to report.

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 PDB entries followed by that with respect to all EM entries.

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	210/211 (100%)	205 (98%)	5 (2%)	43	69
1	B	210/211 (100%)	205 (98%)	5 (2%)	43	69
1	C	210/211 (100%)	206 (98%)	4 (2%)	50	74
1	D	210/211 (100%)	206 (98%)	4 (2%)	50	74
1	E	211/211 (100%)	203 (96%)	8 (4%)	29	54
1	F	210/211 (100%)	202 (96%)	8 (4%)	29	54
2	G	92/92 (100%)	91 (99%)	1 (1%)	65	83
2	H	92/92 (100%)	92 (100%)	0	100	100
2	I	92/92 (100%)	91 (99%)	1 (1%)	65	83
2	J	92/92 (100%)	91 (99%)	1 (1%)	65	83
2	K	92/92 (100%)	90 (98%)	2 (2%)	45	70
2	L	92/92 (100%)	91 (99%)	1 (1%)	65	83
3	M	129/129 (100%)	124 (96%)	5 (4%)	28	53
3	N	129/129 (100%)	122 (95%)	7 (5%)	20	40
3	O	129/129 (100%)	122 (95%)	7 (5%)	20	40
3	P	129/129 (100%)	126 (98%)	3 (2%)	44	69
3	Q	129/129 (100%)	124 (96%)	5 (4%)	28	53
3	R	129/129 (100%)	124 (96%)	5 (4%)	28	53
All	All	2587/2592 (100%)	2515 (97%)	72 (3%)	38	64

5 of 72 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	O	133	THR
3	R	133	THR
3	P	51	VAL
3	Q	104	VAL
1	E	225	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	72	HIS

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Mol	Chain	Res	Type
2	H	82	ASN
3	M	53	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 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.